

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 25, 2005, 09:34:25 ; Search time 884.571 Seconds
(without alignments)
1314.676 Million cell updates/sec

Title: US-10-688-489-75
Perfect score: 24
Sequence: 1 tcgcagacggtctctgagggcttac 24

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_scs.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	24	100.0	395	14	AF458358
C 2	24	100.0	451	14	AF458353
C 3	24	100.0	462	14	AF458350
C 4	24	100.0	463	14	AF458344
C 5	24	100.0	463	14	AF458347
C 6	24	100.0	463	14	AF458348
C 7	24	100.0	463	14	AF458355
C 8	24	100.0	463	14	AF458360
C 9	24	100.0	463	14	AF458361
C 10	24	100.0	464	14	AF458361
C 11	24	100.0	464	14	AF458361
C 12	24	100.0	464	14	AF458361
C 13	24	100.0	464	14	AF458361
C 14	24	100.0	464	14	AF458361
C 15	24	100.0	464	14	AF458361
C 16	24	100.0	464	14	AF458361
C 17	24	100.0	464	14	AF458361
C 18	24	100.0	464	14	AF458361
C 19	24	100.0	464	14	AF458361

AY590200	West Nile	14	AY590200	464	14	AY590200	464	14	AY590200	West Nile
AY590201	West Nile	14	AY590201	464	14	AY590201	464	14	AY590201	West Nile
AY590202	West Nile	14	AY590202	464	14	AY590202	464	14	AY590202	West Nile
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AY590204	West Nile	14	AY590204	464	14	AY590204	464	14	AY590204	West Nile
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C 93	24	100.0	11029	14	AF404756	AF404756 West Nile	C 166	22.4	93.3	10977	14	AF069076	AF069076 Japanese
C 94	24	100.0	11029	14	AF404757	AF404757 West Nile	C 167	22.4	93.3	10977	14	AF486638	AF486638 Japanese
C 95	24	100.0	11029	14	AF481864	AF481864 West Nile	C 168	22.4	93.3	10978	14	AY184212	AY184212 Japanese
C 96	24	100.0	11029	14	AF533540	AF533540 West Nile	C 169	22.4	93.3	10989	14	AY268132	AY268132 West Nile
C 97	24	100.0	11029	14	AY289214	AY289214 West Nile	C 170	21.4	89.2	524	14	AF297851	AF297851 Kunjin vi
C 98	24	100.0	11057	14	AY688948	AY688948 West Nile	C 171	20.8	86.7	459	14	AF297851	AF297851 Kunjin vi
C 99	23	95.8	456	14	AF458351	AF458351 Kunjin vi	C 172	20.8	86.7	576	14	AF308515	AF308515 Japanese en
C 100	22.4	93.3	346	14	AF148902	AF148902 Japanese	C 173	20.8	86.7	576	14	AF308515	AF308515 Japanese en
C 101	22.4	93.3	424	14	AF092550	AF092550 Japanese	C 174	20.8	86.7	10963	14	AF308516	AF308516 Japanese
C 102	22.4	93.3	424	14	AF092552	AF092552 Japanese	C 175	20.8	86.7	10976	14	AF316157	AF316157 Japanese
C 103	22.4	93.3	424	14	AF092553	AF092553 Japanese	C 176	20.8	86.7	10977	14	AF315119	AF315119 Japanese
C 104	22.4	93.3	424	14	JEVNSSGAC	JEVNSSGAC Japanese en	C 177	19.4	80.8	129841	2	AF080251	AF080251 Japanese
C 105	22.4	93.3	424	14	JEVNSSGAD	JEVNSSGAD Japanese en	C 178	19.2	80.0	129841	2	AF080251	AF080251 Japanese
C 106	22.4	93.3	424	14	JEVNSSGAE	JEVNSSGAE Japanese en	C 179	19.2	80.0	129841	2	AF080251	AF080251 Japanese
C 107	22.4	93.3	424	14	JEVNSSGAF	JEVNSSGAF Japanese en	C 180	18.8	78.3	165714	8	AF308517	AF308517 Japanese
C 108	22.4	93.3	424	14	JEVNSSGAG	JEVNSSGAG Japanese en	C 181	18.8	78.3	165714	8	AF308517	AF308517 Japanese
C 109	22.4	93.3	424	14	JEVNSSGAH	JEVNSSGAH Japanese en	C 182	18.8	78.3	165714	8	AF308517	AF308517 Japanese
C 110	22.4	93.3	424	14	JEVNSSGAI	JEVNSSGAI Japanese en	C 183	18.8	78.3	165714	8	AF308517	AF308517 Japanese
C 111	22.4	93.3	424	14	JEVNSSGAJ	JEVNSSGAJ Japanese en	C 184	18.8	78.3	165714	8	AF308517	AF308517 Japanese
C 112	22.4	93.3	451	14	AF458352	AF458352 West Nile	C 185	18.2	75.8	103428	9	AC024577	AC024577 Homo sapi
C 113	22.4	93.3	458	14	AF458356	AF458356 Kunjin vi	C 186	18.2	75.8	103428	9	AC024577	AC024577 Homo sapi
C 114	22.4	93.3	463	14	AF458343	AF458343 West Nile	C 187	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 115	22.4	93.3	463	14	AY278556	AY278556 Japanese	C 188	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 116	22.4	93.3	533	14	JEVNSSGAA	JEVNSSGAA Japanese en	C 189	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 117	22.4	93.3	536	14	AF148900	AF148900 Japanese	C 190	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 118	22.4	93.3	545	14	AF297850	AF297850 Kunjin vi	C 191	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 119	22.4	93.3	562	14	FVNSSGAH	FVNSSGAH Kunjin vi	C 192	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 120	22.4	93.3	566	14	VPNG6544P2	VPNG6544P2 Japanese	C 193	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 121	22.4	93.3	572	14	AF306514	AF306514 Japanese	C 194	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 122	22.4	93.3	582	14	AF218068	AF218068 Japanese	C 195	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 123	22.4	93.3	583	14	AF297857	AF297857 Kunjin vi	C 196	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 124	22.4	93.3	583	14	AF297857	AF297857 Kunjin vi	C 197	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 125	22.4	93.3	585	14	AF297840	AF297840 Kunjin vi	C 198	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 126	22.4	93.3	593	14	AF297847	AF297847 Kunjin vi	C 199	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 127	22.4	93.3	593	14	AF297852	AF297852 Kunjin vi	C 200	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 128	22.4	93.3	594	14	AF297853	AF297853 Kunjin vi	C 201	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 129	22.4	93.3	598	14	AF297853	AF297853 Kunjin vi	C 202	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 130	22.4	93.3	600	14	AF297846	AF297846 Kunjin vi	C 203	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 131	22.4	93.3	625	14	AF318291	AF318291 Japanese	C 204	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 132	22.4	93.3	972	14	AF311748	AF311748 Japanese	C 205	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 133	22.4	93.3	10951	14	JEVNLINGCG	JEVNLINGCG Japanese en	C 206	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 134	22.4	93.3	10963	14	AF045551	AF045551 Japanese	C 207	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 135	22.4	93.3	10964	14	AF217620	AF217620 Japanese	C 208	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 136	22.4	93.3	10965	14	AB051292	AB051292 Japanese	C 209	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 137	22.4	93.3	10968	14	AY585242	AY585242 Japanese	C 210	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 138	22.4	93.3	10968	14	AY585242	AY585242 Japanese	C 211	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 139	22.4	93.3	10969	14	AY585243	AY585243 Japanese	C 212	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 140	22.4	93.3	10969	14	JEU15763	JEU15763 Japanese en	C 213	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 141	22.4	93.3	10969	14	JEVCMNAA	JEVCMNAA Japanese en	C 214	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 142	22.4	93.3	10970	14	AF254452	AF254452 Japanese	C 215	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 143	22.4	93.3	10970	14	AF254453	AF254453 Japanese	C 216	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 144	22.4	93.3	10970	14	AY303791	AY303791 Japanese	C 217	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 145	22.4	93.3	10970	14	AY303792	AY303792 Japanese	C 218	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 146	22.4	93.3	10970	14	AY303793	AY303793 Japanese	C 219	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 147	22.4	93.3	10970	14	AY303794	AY303794 Japanese	C 220	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 148	22.4	93.3	10970	14	AY303795	AY303795 Japanese	C 221	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 149	22.4	93.3	10970	14	AY303796	AY303796 Japanese	C 222	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 150	22.4	93.3	10970	14	AY303797	AY303797 Japanese	C 223	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 151	22.4	93.3	10970	14	AY303798	AY303798 Japanese	C 224	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 152	22.4	93.3	10976	14	AF014160	AF014160 Japanese	C 225	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 153	22.4	93.3	10976	14	AF014161	AF014161 Japanese	C 226	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 154	22.4	93.3	10976	14	AF014162	AF014162 Japanese	C 227	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 155	22.4	93.3	10976	14	AF098735	AF098735 Japanese	C 228	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 156	22.4	93.3	10976	14	AF098736	AF098736 Japanese	C 229	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 157	22.4	93.3	10976	14	AF098737	AF098737 Japanese	C 230	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 158	22.4	93.3	10976	14	AF221499	AF221499 Japanese	C 231	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 159	22.4	93.3	10976	14	AF221500	AF221500 Japanese	C 232	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 160	22.4	93.3	10976	14	AF416457	AF416457 Japanese	C 233	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 161	22.4	93.3	10976	14	AF416457	AF416457 Japanese	C 234	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 162	22.4	93.3	10976	14	AF416457	AF416457 Japanese	C 235	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 163	22.4	93.3	10976	14	AF416457	AF416457 Japanese	C 236	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 164	22.4	93.3	10976	14	AF416457	AF416457 Japanese	C 237	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu
C 165	22.4	93.3	10976	14	AF416457	AF416457 Japanese	C 238	17.8	74.2	159100	10	AC107236	AC107236 Mus muscu

C 239	17.2	71.7	302921	2	AC090998	AC090998 Homo sapi	312	16.6	69.2	81020	8	AB026645	AB026645 Arabidops
240	17.2	71.7	347786	1	BX640438	BX640438 Bordetell	C 313	16.6	69.2	83178	2	AC117537	AC117537 Magnaport
241	17.2	71.7	349146	1	BX640438	BX640438 Bordetell	C 314	16.6	69.2	90180	2	AC008176	AC008176 Homo sapi
C 242	16.8	70.0	438	10	MDMH6	X07299 M.musculus	C 315	16.6	69.2	105199	9	AP001576	AP001576 Homo sapi
243	16.8	70.0	2418	3	PELCP8K	L40818 Periplaneta	C 316	16.6	69.2	105999	9	HS73M5	AJ010597 Homo sapi
244	16.8	70.0	2799	6	AR207538	AR207538 Sequence	C 317	16.6	69.2	110000	1	AE000516_23	Continuation (24 o
245	16.8	70.0	2799	6	BD003326	BD003326 Phospholi	C 318	16.6	69.2	110000	1	AE017225_50	Continuation (51 o
246	16.8	70.0	3440	10	BC047268	BC047268 Mus muscu	C 319	16.6	69.2	110000	1	AE017283_12	Continuation (13 o
247	16.8	70.0	3490	6	BD003327	BD003327 Phospholi	C 320	16.6	69.2	110000	1	AE017283_13	Continuation (14 o
248	16.8	70.0	3494	10	MMU87557	U87557 Mus musculu	C 321	16.6	69.2	110000	1	AE017334_50	Continuation (51 o
249	16.8	70.0	3671	10	BC068317	BC068317 Mus muscu	C 322	16.6	69.2	110000	2	AP006490_4	Continuation (5 of
250	16.8	70.0	3832	10	MMFLD2G1	AF052291 Mus muscu	C 323	16.6	69.2	113250	9	AC004900	AC004900 Homo sapi
251	16.8	70.0	13512	1	AE001045	AE001045 Archaeogl	C 324	16.6	69.2	115916	9	AL590618	AL590618 Human DNA
252	16.8	70.0	66886	8	AE016817_14	Continuation (15 o	C 325	16.6	69.2	115916	9	AL590618	AL590618 Human DNA
253	16.8	70.0	98760	70.0	AC133749	AC133749 Homo sapi	C 326	16.6	69.2	115916	9	AL590618	AL590618 Human DNA
C 254	16.8	70.0	110000	8	AE016815_1	Continuation (2 of	C 327	16.6	69.2	132403	2	AC148792	AC148792 Ocolemur
255	16.8	70.0	116932	8	AC074232_1	AC074232 Oryza sat	C 328	16.6	69.2	135855	9	HS135814	AJ010598 Homo sapi
C 256	16.8	70.0	122214	8	AP004033	AP004033 Oryza sat	C 329	16.6	69.2	141529	9	AC011369	AC011369 Homo sapi
C 257	16.8	70.0	123943	10	AL592547	AL592547 Mouse DNA	C 330	16.6	69.2	142233	10	AC125129	AC125129 Mus muscu
258	16.8	70.0	132444	9	AC091878	AC091878 Homo sapi	C 331	16.6	69.2	145729	9	AC117489	AC117489 Homo sapi
C 259	16.8	70.0	141852	8	AP004863	AP004863 Oryza sat	C 332	16.6	69.2	150735	9	AC090687	AC090687 Homo sapi
C 260	16.8	70.0	144339	2	AF290942	AF290942 Homo sapi	C 333	16.6	69.2	151009	2	AC135784	AC135784 Homo sapi
261	16.8	70.0	144393	9	AC102944	AC102944 Homo sapi	C 334	16.6	69.2	152605	2	AC136886	AC136886 Sus scrof
C 262	16.8	70.0	147710	2	AC090070	AC090070 Homo sapi	C 335	16.6	69.2	154195	2	AC142242	AC142242 Acelerix
263	16.8	70.0	155014	2	AC140065	AC140065 Homo sapi	C 336	16.6	69.2	154653	9	AC146050	AC146050 Pan trogl
C 264	16.8	70.0	155161	9	AC083900	AC083900 Homo sapi	C 337	16.6	69.2	159709	9	AC008705	AC008705 Homo sapi
C 265	16.8	70.0	160481	2	AC021784	AC021784 Homo sapi	C 338	16.6	69.2	161589	2	AC136881	AC136881 Sus scrof
C 266	16.8	70.0	162593	2	AC022576	AC022576 Homo sapi	C 339	16.6	69.2	162358	9	AC105748	AC105748 Homo sapi
C 267	16.8	70.0	163965	10	AC132919	AC132919 Mus muscu	C 340	16.6	69.2	164331	2	AC118869	AC118869 Rattus no
C 268	16.8	70.0	165072	2	AC120286	AC120286 Rattus no	C 341	16.6	69.2	166234	9	HS273F12	AL034372 Human DNA
269	16.8	70.0	170591	2	AC022936	AC022936 Homo sapi	C 342	16.6	69.2	166355	9	AP000888	AP000888 Homo sapi
270	16.8	70.0	175202	9	AC022733	AC022733 Homo sapi	C 343	16.6	69.2	166763	2	AC112941	AC112941 Mus muscu
271	16.8	70.0	175491	2	AC129683	AC129683 Rattus no	C 344	16.6	69.2	170465	3	AC091128	AC091128 Drosophil
272	16.8	70.0	175784	9	AP003789	AP003789 Homo sapi	C 345	16.6	69.2	170928	2	AC148803	AC148803 Ocolemur
C 273	16.8	70.0	192938	10	AC125067	AC125067 Mus muscu	C 346	16.6	69.2	177727	2	AC022178	AC022178 Homo sapi
C 274	16.8	70.0	193170	2	AC068652	AC068652 Mus muscu	C 347	16.6	69.2	178804	9	AC113134	AC113134 Homo sapi
275	16.8	70.0	194609	2	AC013775	AC013775 Mus muscu	C 348	16.6	69.2	178965	9	AC098850	AC098850 Homo sapi
276	16.8	70.0	195529	2	AC025714	AC025714 Homo sapi	C 349	16.6	69.2	180783	9	AC128244	AC128244 Rattus no
277	16.8	70.0	201403	9	AC145921	AC145921 Pan trogl	C 350	16.6	69.2	182003	9	AL355987	AL355987 Human DNA
C 278	16.8	70.0	214125	10	AC083948	AC083948 Mus muscu	C 351	16.6	69.2	185902	10	AC122428	AC122428 Mus muscu
C 279	16.8	70.0	241775	2	AC131140	AC131140 Rattus no	C 352	16.6	69.2	187438	3	AC010711	AC010711 Drosophil
C 280	16.8	70.0	246006	2	AC102141	AC102141 Mus muscu	C 353	16.6	69.2	191174	10	AC116586	AC116586 Mus muscu
C 281	16.8	70.0	251571	2	AC114093	AC114093 Rattus no	C 354	16.6	69.2	191727	10	AC150744	AC150744 Mus muscu
C 282	16.8	70.0	259978	2	AC073819	AC073819 Mus muscu	C 355	16.6	69.2	195007	9	CNS06C81	AL391749 Human chr
C 283	16.8	70.0	270738	2	AC095854	AC095854 Rattus no	C 356	16.6	69.2	195202	2	AC132669	AC132669 Rattus no
C 284	16.8	70.0	274766	2	AC135283	AC135283 Rattus no	C 357	16.6	69.2	196086	10	AC104889	AC104889 Mus muscu
C 285	16.8	70.0	286178	2	AC091290	AC091290 Mus muscu	C 358	16.6	69.2	198552	2	AC025638	AC025638 Homo sapi
C 286	16.8	70.0	300029	8	AE017114	AE017114 Oryza sat	C 359	16.6	69.2	198965	2	AC148961	AC148961 Callithri
287	16.6	69.2	183	11	BV171141	BV171141 sqmm40750	C 360	16.6	69.2	200151	2	AC151872	AC151872 Lemur cat
C 288	16.6	69.2	345	14	AY089756	AY089756 Hepatitis	C 361	16.6	69.2	201512	9	AL391833	AL391833 Mus muscu
C 289	16.6	69.2	345	14	AY089758	AY089758 Hepatitis	C 362	16.6	69.2	202083	2	AC023833	AC023833 Mus muscu
C 290	16.6	69.2	597	6	CQ524047	CQ524047 Sequence	C 363	16.6	69.2	202383	2	AC139291	AC139291 Mus muscu
291	16.6	69.2	723	6	AX381068	AX381068 Sequence	C 364	16.6	69.2	203226	2	AC105479	AC105479 Rattus no
292	16.6	69.2	1021	3	TVCP1	X77218 T.vaginalis	C 365	16.6	69.2	207086	10	AL596117	AL596117 Mouse DNA
C 293	16.6	69.2	1261	5	GDH0X42	X74323 G.gallus nr	C 366	16.6	69.2	209111	9	CNS00YVG	AC096821 Human chr
294	16.6	69.2	1283	9	AK098639	AK098639 Homo sapi	C 367	16.6	69.2	212111	2	AC094482	AC094482 Rattus no
C 295	16.6	69.2	1381	8	AY096674	AY096674 Arabidops	C 368	16.6	69.2	213244	10	AC113016	AC113016 Mus muscu
C 296	16.6	69.2	1758	8	AY050889	AY050889 Arabidops	C 369	16.6	69.2	227877	2	AC109725	AC109725 Rattus no
C 297	16.6	69.2	1832	8	AY084738	AY084738 Arabidops	C 370	16.6	69.2	228232	2	AC090293	AC090293 Mus muscu
C 298	16.6	69.2	1837	1	STWMPRYNA	M37055 Streptomyce	C 371	16.6	69.2	228742	2	AC134190	AC134190 Rattus no
299	16.6	69.2	2238	3	AB006454	AB006454 Patinopoc	C 372	16.6	69.2	228940	2	AC126890	AC126890 Rattus no
C 300	16.6	69.2	2922	3	TTT276471	TTT276471 Tetrahyme	C 373	16.6	69.2	229710	2	AC130229	AC130229 Rattus no
C 301	16.6	69.2	3000	9	AK095805	AK095805 Homo sapi	C 374	16.6	69.2	231736	2	AC117323	AC117323 Rattus no
C 302	16.6	69.2	5870	6	CQ363854	CQ363854 Sequence	C 375	16.6	69.2	231750	2	AC095594	AC095594 Rattus no
C 303	16.6	69.2	11199	1	AE001061	AE001061 Archaeogl	C 376	16.6	69.2	232649	2	AC108267	AC108267 Rattus no
C 304	16.6	69.2	12439	1	AE009153	AE009153 Agrobacte	C 377	16.6	69.2	233784	2	AC130877	AC130877 Rattus no
C 305	16.6	69.2	12606	1	AE008118	AE008118 Agrobacte	C 378	16.6	69.2	238653	2	AC099453	AC099453 Rattus no
C 306	16.6	69.2	37586	6	AX191745	AX191745 Sequence	C 379	16.6	69.2	239875	2	AC126827	AC126827 Rattus no
C 307	16.6	69.2	37959	9	BX537333	BX537333 Human DNA	C 380	16.6	69.2	240091	2	AC137350	AC137350 Rattus no
C 308	16.6	69.2	43489	2	AC019833	AC019833 Drosophil	C 381	16.6	69.2	241859	2	AC136406	AC136406 Rattus no
309	16.6	69.2	61880	2	AC021135	AC021135 Homo sapi	C 382	16.6	69.2	243329	5	AC145979	AC145979 Gallus ga
C 310	16.6	69.2	61880	2	AC021135	AC021135 Homo sapi	C 383	16.6	69.2	244978	9	AF241726	AF241726 Homo sapi
311	16.6	69.2	69776	9	AL953870	AL953870 Human DNA	C 384	16.6	69.2	250023	2	AC111499	AC111499 Rattus no

385	16.6	69.2	253176	2	AC094477	AC094477 Rattus no	C 458	16.2	67.5	2459	6	CQ842165	CQ842165 Sequence
386	16.6	69.2	254778	2	AC126532	AC126532 Rattus no	C 459	16.2	67.5	2459	9	AKI25202	AKI25202 Homo sapi
387	16.6	69.2	258207	2	AC115279	AC115279 Rattus no		16.2	67.5	2666	10	MUSEPO	L77979 Mus musculus
388	16.6	69.2	260860	2	AC125982	AC125982 Rattus no	460	16.2	67.5	2666	10	BC052881	BC052881 Mus muscu
389	16.6	69.2	263088	2	AC130872	AC130872 Rattus no	462	16.2	67.5	2694	10	MUSEPP	D78153 Mus musculus
390	16.6	69.2	264504	1	AE017041	AE017041 Bacillus	463	16.2	67.5	3831	6	CO581577	CO581577 Sequence
391	16.6	69.2	268718	2	AC106377	AC106377 Rattus no	464	16.2	67.5	4004	3	AY119106	AY119106 Drosophila
392	16.6	69.2	279912	2	AC126572	AC126572 Rattus no	465	16.2	67.5	4369	1	AF057021	AF057021 Salmonella
393	16.6	69.2	286205	2	CR759869	CR759869 Danio rer	C 466	16.2	67.5	5561	9	HUMIL28	AF057021 Salmonella
394	16.6	69.2	296500	1	SC0939128	SC0939128 Streptomy	C 467	16.2	67.5	5737	6	A37269	A37269 Sequence 9
395	16.6	69.2	304282	1	AE016910	AE016910 Chromobac	C 468	16.2	67.5	5737	6	HUMIL2	J00264 Homo sapien
396	16.6	69.2	306050	1	EX248341	EX248341 Mycobacte	469	16.2	67.5	6566	6	CO581576	CO581576 Sequence
397	16.6	69.2	318699	3	AE003470	AE003470 Drosophila	C 470	16.2	67.5	6566	6	CO581576	CO581576 Sequence
398	16.6	69.2	340000	9	HS21C010	HS21C010 Homo sapi	C 471	16.2	67.5	6884	9	HSIL05	X06935 Human inter
399	16.6	69.2	346186	1	EX842578	EX842578 Mycobacte	C 472	16.2	67.5	6884	9	HSIL05	X06935 Human inter
400	16.4	68.3	1839	6	CQ804202	CQ804202 Sequence	C 473	16.2	67.5	9798	14	AE093615	AF359939 Homo sapi
401	16.4	68.3	1870	8	BT001966	BT001966 Arabidops	C 474	16.2	67.5	9798	14	AE093615	AF359939 Homo sapi
402	16.4	68.3	1929	6	AX412678	AX412678 Arabidops	C 475	16.2	67.5	12232	1	AE013121	AE013121 Thermoana
403	16.4	68.3	1929	6	AX506546	AX506546 Sequence	C 476	16.2	67.5	14659	1	HTH243655	AJ743655 Methanoba
404	16.4	68.3	1929	6	AX652042	AX652042 Sequence	C 477	16.2	67.5	18573	9	HSOXD3	AJ743655 Methanoba
405	16.4	68.3	2039	8	AF350282	AF350282 Arabidops	C 478	16.2	67.5	21721	6	AR410075	Y09980 H.sapiens H
406	16.4	68.3	2161	8	AY062544	AY062544 Arabidops	C 479	16.2	67.5	21721	6	AR410075	Y09980 H.sapiens H
407	16.4	68.3	2193	8	BT000695	BT000695 Arabidops	C 480	16.2	67.5	21721	6	AR410075	Y09980 H.sapiens H
408	16.4	68.3	2872	8	AK118741	AK118741 Arabidops	C 481	16.2	67.5	22976	6	AR410057	BD062437 LSR recep
409	16.4	68.3	11039	1	AE005828	AE005828 Caulobact	C 482	16.2	67.5	22976	6	AR410057	BD062437 LSR recep
410	16.4	68.3	12347	1	AE005387	AE005387 Escherich	C 483	16.2	67.5	22976	6	AR410057	BD062437 LSR recep
411	16.4	68.3	17829	9	AP001438	AP001438 Homo sapi	C 484	16.2	67.5	22976	6	AR410057	BD062437 LSR recep
412	16.4	68.3	35236	3	U61944	U61944 Caenorhabdi	C 485	16.2	67.5	23187	6	AR253031	AX100598 Sequence
413	16.4	68.3	48091	2	AC1100171	AC1100171 Mus muscu	C 486	16.2	67.5	23187	6	AR253031	AX100598 Sequence
414	16.4	68.3	64470	2	AC100171	AC100171 Mus muscu	C 487	16.2	67.5	24057	1	AE008725	AE008725 Salmonell
415	16.4	68.3	79569	9	AC092449	AC092449 Homo sapi	C 488	16.2	67.5	41936	6	AX335752	AX335752 Sequence
416	16.4	68.3	88452	2	AC138690	AC138690 Homo sapi	C 489	16.2	67.5	41936	6	AX335752	AX335752 Sequence
417	16.4	68.3	91938	8	ATFE20M13	ATFE20M13 Arabidops	C 490	16.2	67.5	4328	9	CH19R30879	AD000684 Homo sapi
418	16.4	68.3	100000	9	AP000020	AP000020 Homo sapi	C 491	16.2	67.5	4328	9	CH19R30879	AD000684 Homo sapi
419	16.4	68.3	107740	8	AP000162	AP000162 Homo sapi	C 492	16.2	67.5	51463	2	AC095742	AC095742 Sequence
420	16.4	68.3	126083	9	AC069558	AC069558 Genomic S	C 493	16.2	67.5	51463	2	AC095742	AC095742 Sequence
421	16.4	68.3	130058	8	AC105337	AC105337 Homo sapi	C 494	16.2	67.5	71894	2	AC027754	AC027754 Homo sapi
422	16.4	68.3	138841	9	AC078840	AC078840 Oryza sat	C 495	16.2	67.5	71894	2	AC027754	AC027754 Homo sapi
423	16.4	68.3	148841	9	AC110794	AC110794 Homo sapi	C 496	16.2	67.5	71894	2	AC027754	AC027754 Homo sapi
424	16.4	68.3	156795	2	AC023537	AC023537 Homo sapi	C 497	16.2	67.5	71894	2	AC027754	AC027754 Homo sapi
425	16.4	68.3	158896	2	AC144354	AC144354 Homo sapi	C 498	16.2	67.5	71894	2	AC027754	AC027754 Homo sapi
426	16.4	68.3	159598	9	AP004386	AP004386 Homo sapi	C 499	16.2	67.5	86026	8	AC144727	AC144727 Medicago
427	16.4	68.3	176952	8	AC084023	AC084023 Oryza sat	C 499	16.2	67.5	86026	8	AC144727	AC144727 Medicago
428	16.4	68.3	177341	2	AC079764	AC079764 Homo sapi	C 500	16.2	67.5	95720	2	AC149154	AC149154 Xenopus t
429	16.4	68.3	177737	2	AC146859	AC146859 Homo sapi		16.2	67.5	95720	2	AC149154	AC149154 Xenopus t
430	16.4	68.3	179071	2	AC146655	AC146655 Homo sapi		16.2	67.5	95720	2	AC149154	AC149154 Xenopus t
431	16.4	68.3	191424	9	BS000127	BS000127 Pan trogl		16.2	67.5	95720	2	AC149154	AC149154 Xenopus t
432	16.4	68.3	198177	9	AC069127	AC069127 Homo sapi		16.2	67.5	95720	2	AC149154	AC149154 Xenopus t
433	16.4	68.3	198176	2	AC069127	AC069127 Homo sapi		16.2	67.5	95720	2	AC149154	AC149154 Xenopus t
434	16.4	68.3	199476	2	AC143053	AC143053 Macaca mu		16.2	67.5	95720	2	AC149154	AC149154 Xenopus t
435	16.4	68.3	199789	8	ATCHR1V89	ATCHR1V89 Arabidops		16.2	67.5	95720	2	AC149154	AC149154 Xenopus t
436	16.4	68.3	200946	2	AC148421	AC148421 Meleagris		16.2	67.5	95720	2	AC149154	AC149154 Xenopus t
437	16.4	68.3	213584	2	AC135700	AC135700 Rattus no		16.2	67.5	95720	2	AC149154	AC149154 Xenopus t
438	16.4	68.3	229583	10	AL844566	AL844566 Mouse DNA		16.2	67.5	95720	2	AC149154	AC149154 Xenopus t
439	16.4	68.3	257071	1	AP002558	AP002558 Escherich		16.2	67.5	95720	2	AC149154	AC149154 Xenopus t
440	16.4	68.3	257918	2	AC130780	AC130780 Rattus no		16.2	67.5	95720	2	AC149154	AC149154 Xenopus t
441	16.4	68.3	261278	2	AC107586	AC107586 Rattus no		16.2	67.5	95720	2	AC149154	AC149154 Xenopus t
442	16.4	68.3	262632	2	AC119780	AC119780 Rattus no		16.2	67.5	95720	2	AC149154	AC149154 Xenopus t
443	16.4	68.3	301934	8	AE017110	AE017110 Oryza sat		16.2	67.5	95720	2	AC149154	AC149154 Xenopus t
444	16.4	68.3	340000	9	AP001731	AP001731 Homo sapi		16.2	67.5	95720	2	AC149154	AC149154 Xenopus t
445	16.2	67.5	571	10	CLUPS	CLUPS C.longicaud		16.2	67.5	95720	2	AC149154	AC149154 Xenopus t
446	16.2	67.5	636	6	CNS01A6C	CNS01A6C Botrytis		16.2	67.5	95720	2	AC149154	AC149154 Xenopus t
447	16.2	67.5	921	6	AR347653	AR347653 Sequence		16.2	67.5	95720	2	AC149154	AC149154 Xenopus t
448	16.2	67.5	1350	8	BT002231	BT002231 Arabidops		16.2	67.5	95720	2	AC149154	AC149154 Xenopus t
449	16.2	67.5	1591	8	AF372951	AF372951 Arabidops		16.2	67.5	95720	2	AC149154	AC149154 Xenopus t
450	16.2	67.5	1815	6	AR271274	AR271274 Sequence		16.2	67.5	95720	2	AC149154	AC149154 Xenopus t
451	16.2	67.5	1815	6	AR274520	AR274520 Sequence		16.2	67.5	95720	2	AC149154	AC149154 Xenopus t
452	16.2	67.5	1815	6	AR274520	AR274520 Sequence		16.2	67.5	95720	2	AC149154	AC149154 Xenopus t
453	16.2	67.5	1815	6	AX283089	AX283089 Sequence		16.2	67.5	95720	2	AC149154	AC149154 Xenopus t
454	16.2	67.5	1836	10	RNO245648	RNO245648 Rattus no		16.2	67.5	95720	2	AC149154	AC149154 Xenopus t
455	16.2	67.5	1966	8	AY645664	AY645664 Fusarium		16.2	67.5	95720	2	AC149154	AC149154 Xenopus t
456	16.2	67.5	2180	8	AY645666	AY645666 Fusarium		16.2	67.5	95720	2	AC149154	AC149154 Xenopus t
457	16.2	67.5	2345	10	MMU087620	MMU087620 Mus musculus		16.2	67.5	95720	2	AC149154	AC149154 Xenopus t

ALIGNMENTS

LOCUS	AP458358	395 bp	RNA	linear	VRL 18-JUN-2003
DEFINITION	West Nile virus strain AnMg798 nonstructural protein 5 gene, partial cds.				
ACCESSION	AF458358				
VERSION	AF458358.1				
KEYWORDS	GI:21636495				
SOURCE	West Nile virus (WNV)				
ORGANISM	West Nile virus				
REFERENCE	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group.				
AUTHORS	1 (bases 1 to 395)				
TITLE	Beasley, D.W., Li, L., Suderman, M.T. and Barrett, A.D.				
JOURNAL	Mouse neuroinvasive phenotype of West Nile virus strains varies depending upon virus genotype				
MEDLINE	Virology 296 (1), 17-23 (2002)				
PUBMED	12036314				
REFERENCE	2 (bases 1 to 395)				
AUTHORS	Beasley, D.W.C., Li, L., Suderman, M.T. and Barrett, A.D.				
TITLE	Direct Submission				
JOURNAL	Submitted (14-DEC-2001) Department of Pathology and WHO Collaborating Center for Tropical Diseases, The University of Texas Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA				

FEATURES	source	Location/Qualifiers
QY	1	TCGAGACGGTCTTGAGGGCTTAC 24
Db	393	TCGAGACGGTCTTGAGGGCTTAC 370
RESULT 3		
AF458350/c		
LOCUS		
DEFINITION		West Nile virus strain And-27875 nonstructural protein 5 gene, partial cds.
ACCESSION		AF458350
VERSION		AF458350.1
KEYWORDS		GI:21636479
SOURCE		West Nile virus (WNV)
ORGANISM		West Nile virus
REFERENCE		Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group.
AUTHORS		1 (bases 1 to 462)
TITLE		Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
JOURNAL		Mouse neuroinvasive phenotype of West Nile virus strains varies depending upon virus genotype
MEDLINE		Virology 296 (1), 17-23 (2002)
PUBMED		22033887
REFERENCE		2 (bases 1 to 462)
AUTHORS		Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE		Direct Submission
JOURNAL		Submitted (14-DEC-2001) Department of Pathology and WHO Collaborating Center for Tropical Diseases, The University of Texas Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
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Db	337	TCGAGACGGTCTTGAGGGCTTAC 314
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AF458353/c		
LOCUS		
DEFINITION		West Nile virus strain G-15578 nonstructural protein 5 gene, partial cds.
ACCESSION		AF458353
VERSION		AF458353.1
KEYWORDS		GI:21636485
SOURCE		West Nile virus (WNV)
ORGANISM		West Nile virus
REFERENCE		Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group.
AUTHORS		1 (bases 1 to 451)
TITLE		Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
JOURNAL		Mouse neuroinvasive phenotype of West Nile virus strains varies depending upon virus genotype
MEDLINE		Virology 296 (1), 17-23 (2002)
PUBMED		22033887
REFERENCE		2 (bases 1 to 451)
AUTHORS		Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE		Direct Submission
JOURNAL		Submitted (14-DEC-2001) Department of Pathology and WHO Collaborating Center for Tropical Diseases, The University of Texas Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
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QY	1	TCGAGACGGTCTTGAGGGCTTAC 24
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AF458344/c		
LOCUS		
DEFINITION		West Nile virus strain 68856 nonstructural protein 5 gene, partial cds.
ACCESSION		AF458344
VERSION		AF458344.1
KEYWORDS		GI:21636467
SOURCE		West Nile virus (WNV)
ORGANISM		West Nile virus
REFERENCE		Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group.
AUTHORS		1 (bases 1 to 463)
TITLE		Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
JOURNAL		Mouse neuroinvasive phenotype of West Nile virus strains varies depending upon virus genotype
MEDLINE		Virology 296 (1), 17-23 (2002)
PUBMED		22033887
REFERENCE		2 (bases 1 to 451)
AUTHORS		Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE		Direct Submission
JOURNAL		Submitted (14-DEC-2001) Department of Pathology and WHO Collaborating Center for Tropical Diseases, The University of Texas Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
FEATURES		Location/Qualifiers
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QY	1	TCGAGACGGTCTTGAGGGCTTAC 24
Db		

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depending upon virus genotype
Virology 296 (1), 17-23 (2002)
MEDLINE 22033887
PUBMED 12036314
REFERENCE 2 (bases 1 to 463)
AUTHORS Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-2001) Department of Pathology and WHO
Collaborating Center for Tropical Diseases, The University of Texas
Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
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QY 1 TCCGAGACGGTTCGAGGCGCTTAC 24
Db 405 TCCGAGACGGTTCGAGGCGCTTAC 382

RESULT 5
AF458347/c
LOCUS West Nile virus strain EthAn4766 nonstructural protein 5 gene,
DEFINITION partial cds.
ACCESSION AF458347
VERSION GI:21636473
KEYWORDS
SOURCE West Nile virus (WNV)
ORGANISM
    Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
    Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 463)
AUTHORS Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
TITLE Mouse neuroinvasive phenotype of West Nile virus strains varies
    depending upon virus genotype
JOURNAL Virology 296 (1), 17-23 (2002)
MEDLINE 22033887
PUBMED 12036314
REFERENCE 2 (bases 1 to 463)
AUTHORS Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
TITLE Mouse neuroinvasive phenotype of West Nile virus strains varies
    depending upon virus genotype
JOURNAL Virology 296 (1), 17-23 (2002)
MEDLINE 22033887
PUBMED 12036314
REFERENCE 2 (bases 1 to 463)
AUTHORS Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-2001) Department of Pathology and WHO
Collaborating Center for Tropical Diseases, The University of Texas
Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
FEATURES
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QY 1 TCCGAGACGGTTCGAGGCGCTTAC 24
Db 405 TCCGAGACGGTTCGAGGCGCTTAC 382

RESULT 5
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LOCUS West Nile virus strain EthAn4766 nonstructural protein 5 gene,
DEFINITION partial cds.
ACCESSION AF458347
VERSION GI:21636473
KEYWORDS
SOURCE West Nile virus (WNV)
ORGANISM
    Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
    Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 463)
AUTHORS Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
TITLE Mouse neuroinvasive phenotype of West Nile virus strains varies
    depending upon virus genotype
JOURNAL Virology 296 (1), 17-23 (2002)
MEDLINE 22033887
PUBMED 12036314
REFERENCE 2 (bases 1 to 463)
AUTHORS Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-2001) Department of Pathology and WHO
Collaborating Center for Tropical Diseases, The University of Texas
Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
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Db 405 TCCGAGACGGTTCGAGGCGCTTAC 382

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QY 1 TCCGAGACGGTTCGAGGCGCTTAC 24
Db 405 TCCGAGACGGTTCGAGGCGCTTAC 382

RESULT 6
AF458348/c
LOCUS West Nile virus strain IBAn7019 nonstructural protein 5 gene,
DEFINITION partial cds.
ACCESSION AF458348
VERSION GI:21636475
KEYWORDS
SOURCE West Nile virus (WNV)
ORGANISM
    Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
    Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 463)
AUTHORS Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
TITLE Mouse neuroinvasive phenotype of West Nile virus strains varies
    depending upon virus genotype
JOURNAL Virology 296 (1), 17-23 (2002)
MEDLINE 22033887
PUBMED 12036314
REFERENCE 2 (bases 1 to 463)
AUTHORS Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-2001) Department of Pathology and WHO
Collaborating Center for Tropical Diseases, The University of Texas
Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
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        Best Local Similarity 100.0%; Pred. No. 0.43;
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QY 1 TCCGAGACGGTTCGAGGCGCTTAC 24
Db 405 TCCGAGACGGTTCGAGGCGCTTAC 382

RESULT 7
AF458355/c
LOCUS West Nile virus strain Egypt101 nonstructural protein 5 gene,
DEFINITION partial cds.

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Db 106 TCCGAGACGGTTCCTGAGGGCTTAC 83

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DEFINITION West Nile virus strain 03001087 3' UTR, partial sequence.
ACCESSION AY590192
VERSION AY590192.1 GI:47121679
KEYWORDS
SOURCE West Nile virus (WNV)
ORGANISM West Nile virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 464)
AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
TITLE Genetic and phenotypic variation of West Nile virus in New York,
2000-2003
JOURNAL Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE 2 (bases 1 to 464)
AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
TITLE Direct Submission
JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
FEATURES
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Db 106 TCCGAGACGGTTCCTGAGGGCTTAC 83

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LOCUS AY590193 464 bp RNA linear VRL 30-MAY-2004
DEFINITION West Nile virus strain 03001426 3' UTR, partial sequence.
ACCESSION AY590193
VERSION AY590193.1 GI:47121680
KEYWORDS
SOURCE West Nile virus (WNV)
ORGANISM West Nile virus

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Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group.

REFERENCE 1 (bases 1 to 464)
AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and Kramer,L.D.

TITLE Genetic and phenotypic variation of West Nile virus in New York, 2000-2003

JOURNAL Am. J. Trop. Med. Hyg. (2004) In press

REFERENCE 2 (bases 1 to 464)
AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and Kramer,L.D.

TITLE Direct Submission

JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA

FEATURES
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Db 106 TCCGAGACGGTTCTGAGGGCTTAC 83

RESULT 14
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LOCUS West Nile virus strain 03001516 3' UTR, partial sequence.

REFERENCE 1 (bases 1 to 464)
AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and Kramer,L.D.

TITLE Genetic and phenotypic variation of West Nile virus in New York, 2000-2003

JOURNAL Am. J. Trop. Med. Hyg. (2004) In press

REFERENCE 2 (bases 1 to 464)
AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and Kramer,L.D.

TITLE Direct Submission

JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA

FEATURES
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Db 106 TCCGAGACGGTTCTGAGGGCTTAC 83

RESULT 15
AY590195/c

LOCUS West Nile virus strain 03001543 3' UTR, partial sequence.

REFERENCE 1 (bases 1 to 464)
AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and Kramer,L.D.

TITLE Genetic and phenotypic variation of West Nile virus in New York, 2000-2003

JOURNAL Am. J. Trop. Med. Hyg. (2004) In press

REFERENCE 2 (bases 1 to 464)
AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and Kramer,L.D.

TITLE Direct Submission

JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA

FEATURES
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Db 106 TCCGAGACGGTTCTGAGGGCTTAC 83

RESULT 16
AY590196/c

LOCUS West Nile virus strain 03001619 3' UTR, partial sequence.

REFERENCE 1 (bases 1 to 464)
AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and Kramer,L.D.

TITLE Genetic and phenotypic variation of West Nile virus in New York, 2000-2003

JOURNAL Am. J. Trop. Med. Hyg. (2004) In press

REFERENCE 2 (bases 1 to 464)
AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and Kramer,L.D.

TITLE Direct Submission

JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA

FEATURES
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/organism="West Nile virus"
/viroion

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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 106 TCCGAGACGGTCTGAGGGCTTAC 83

RESULT 20
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 KEYWORDS
 SOURCE
 ORGANISM
 West Nile virus (WNV)
 West Nile virus
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 Flavivirus; Japanese encephalitis virus group.
 1 (bases 1 to 464)
 Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
 Kramer,L.D.
 TITLE Genetic and phenotypic variation of West Nile virus in New York,
 2000-2003
 JOURNAL Am. J. Trop. Med. Hyg. (2004) In press
 REFERENCE 2 (bases 1 to 464)
 Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
 Kramer,L.D.
 TITLE Direct Submission
 JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
 Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA

FEATURES
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 /strain="03001816"
 /specific_host="American crow"
 /db_xref="taxon:11082"
 /country="USA"
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 Best Local Similarity 100.0%; Pred. No. 0.43;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 106 TCCGAGACGGTCTGAGGGCTTAC 83

RESULT 21
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 LOCUS
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 ACCESSION AY590201
 VERSION AY590201.1 GI:47121688
 KEYWORDS
 SOURCE
 ORGANISM
 West Nile virus (WNV)
 West Nile virus
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 Flavivirus; Japanese encephalitis virus group.
 1 (bases 1 to 464)
 Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
 Kramer,L.D.
 TITLE Genetic and phenotypic variation of West Nile virus in New York,
 2000-2003
 JOURNAL Am. J. Trop. Med. Hyg. (2004) In press
 REFERENCE 2 (bases 1 to 464)
 Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
 Kramer,L.D.
 TITLE Direct Submission
 JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
 Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA

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 /virion
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QY 1 TCCGAGACGGTCTGAGGGCTTAC 24
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 Db 106 TCCGAGACGGTCTGAGGGCTTAC 83

RESULT 22
 AY590202/c
 LOCUS
 DEFINITION West Nile virus strain 03001895 3' UTR, partial sequence.
 ACCESSION AY590202
 VERSION AY590202.1 GI:47121689
 KEYWORDS
 SOURCE
 ORGANISM
 West Nile virus (WNV)
 West Nile virus
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 Flavivirus; Japanese encephalitis virus group.
 1 (bases 1 to 464)
 Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
 Kramer,L.D.
 TITLE Genetic and phenotypic variation of West Nile virus in New York,
 2000-2003
 JOURNAL Am. J. Trop. Med. Hyg. (2004) In press
 REFERENCE 2 (bases 1 to 464)
 Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
 Kramer,L.D.
 TITLE Direct Submission
 JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
 Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA

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 Best Local Similarity 100.0%; Pred. No. 0.43;
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QY 1 TCCGAGACGGTCTGAGGGCTTAC 24
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RESULT 23
 AY590203/c
 LOCUS
 DEFINITION West Nile virus strain 03001956 3' UTR, partial sequence.
 ACCESSION AY590203
 VERSION AY590203.1 GI:47121690
 KEYWORDS

Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA

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RESULT 22
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 LOCUS
 DEFINITION West Nile virus strain 03001895 3' UTR, partial sequence.
 ACCESSION AY590202
 VERSION AY590202.1 GI:47121689
 KEYWORDS
 SOURCE
 ORGANISM
 West Nile virus (WNV)
 West Nile virus
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 Flavivirus; Japanese encephalitis virus group.
 1 (bases 1 to 464)
 Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
 Kramer,L.D.
 TITLE Genetic and phenotypic variation of West Nile virus in New York,
 2000-2003
 JOURNAL Am. J. Trop. Med. Hyg. (2004) In press
 REFERENCE 2 (bases 1 to 464)
 Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
 Kramer,L.D.
 TITLE Direct Submission
 JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
 Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA

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 /virion
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 Best Local Similarity 100.0%; Pred. No. 0.43;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 106 TCCGAGACGGTCTGAGGGCTTAC 83

RESULT 23
 AY590203/c
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 DEFINITION West Nile virus strain 03001956 3' UTR, partial sequence.
 ACCESSION AY590203
 VERSION AY590203.1 GI:47121690
 KEYWORDS

SOURCE West Nile virus (WNV)
 ORGANISM West Nile virus
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 Flavivirus; Japanese encephalitis virus group.
 REFERENCE 1 (bases 1 to 464)
 AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
 Kramer,L.D.
 TITLE Genetic and phenotypic variation of West Nile virus in New York,
 2000-2003
 JOURNAL Am. J. Trop. Med. Hyg. (2004) In press
 REFERENCE 2 (bases 1 to 464)
 AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
 Kramer,L.D.
 TITLE Direct Submission
 JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
 Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
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 Db 106 TCCGAGACGGTTCGAGGGCTTAC 83
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 AY590204/c
 LOCUS West Nile virus strain 03001986 3' UTR, partial sequence.
 DEFINITION
 ACCESSION AY590204
 VERSION AY590204.1 GI:47121691
 KEYWORDS
 ORGANISM West Nile virus (WNV)
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 Flavivirus; Japanese encephalitis virus group.
 REFERENCE 1 (bases 1 to 464)
 AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
 Kramer,L.D.
 TITLE Genetic and phenotypic variation of West Nile virus in New York,
 2000-2003
 JOURNAL Am. J. Trop. Med. Hyg. (2004) In press
 REFERENCE 2 (bases 1 to 464)
 AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
 Kramer,L.D.
 TITLE Direct Submission
 JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
 Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
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 Db 106 TCCGAGACGGTTCGAGGGCTTAC 83
 RESULT 26
 AY590206/c
 LOCUS West Nile virus strain 03002031 3' UTR, partial sequence.
 DEFINITION
 ACCESSION AY590206
 VERSION AY590206.1 GI:47121693
 KEYWORDS
 ORGANISM West Nile virus (WNV)
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 Flavivirus; Japanese encephalitis virus group.
 REFERENCE 1 (bases 1 to 464)
 AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
 Kramer,L.D.
 TITLE Genetic and phenotypic variation of West Nile virus in New York,
 2000-2003
 JOURNAL Am. J. Trop. Med. Hyg. (2004) In press
 REFERENCE 2 (bases 1 to 464)
 AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
 Kramer,L.D.
 TITLE Direct Submission

Best Local Similarity 100.0%; Pred. No. 0.43;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 106 TCCGAGACGGTTCGAGGGCTTAC 83
 RESULT 25
 AY590205/c
 LOCUS West Nile virus strain 03002018 3' UTR, partial sequence.
 DEFINITION
 ACCESSION AY590205
 VERSION AY590205.1 GI:47121692
 KEYWORDS
 ORGANISM West Nile virus (WNV)
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 Flavivirus; Japanese encephalitis virus group.
 REFERENCE 1 (bases 1 to 464)
 AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
 Kramer,L.D.
 TITLE Genetic and phenotypic variation of West Nile virus in New York,
 2000-2003
 JOURNAL Am. J. Trop. Med. Hyg. (2004) In press
 REFERENCE 2 (bases 1 to 464)
 AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
 Kramer,L.D.
 TITLE Direct Submission
 JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
 Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
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 Db 106 TCCGAGACGGTTCGAGGGCTTAC 83
 RESULT 26
 AY590206/c
 LOCUS West Nile virus strain 03002031 3' UTR, partial sequence.
 DEFINITION
 ACCESSION AY590206
 VERSION AY590206.1 GI:47121693
 KEYWORDS
 ORGANISM West Nile virus (WNV)
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 Flavivirus; Japanese encephalitis virus group.
 REFERENCE 1 (bases 1 to 464)
 AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
 Kramer,L.D.
 TITLE Genetic and phenotypic variation of West Nile virus in New York,
 2000-2003
 JOURNAL Am. J. Trop. Med. Hyg. (2004) In press
 REFERENCE 2 (bases 1 to 464)
 AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
 Kramer,L.D.
 TITLE Direct Submission

JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
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 |||||
 Db 106 TCCGAGACGGTTCTGAGGGCTTAC 83
RESULT 27
AY590207/c
LOCUS AY590207 464 bp RNA linear VRL 30-MAY-2004
DEFINITION West Nile virus strain 03002035 3' UTR, partial sequence.
ACCESSION AY590207
VERSION AY590207.1 GI:47121694
KEYWORDS
SOURCE
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 West Nile virus
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
REFERENCE
 1 (bases 1 to 464)
 Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
 Kramer,L.D.
TITLE
 Genetic and phenotypic variation of West Nile virus in New York,
 2000-2003
JOURNAL Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE 2 (bases 1 to 464)
 Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
 Kramer,L.D.
TITLE Direct Submission
JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
 Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
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 |||||
 Db 106 TCCGAGACGGTTCTGAGGGCTTAC 83
RESULT 28
AY590208/c
LOCUS AY590208 464 bp RNA linear VRL 30-MAY-2004
DEFINITION West Nile virus strain 03002066 3' UTR, partial sequence.
ACCESSION AY590208
VERSION AY590208.1 GI:47121695

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Query Match          100.0%; Score 24; DB 14; Length 464;
Best Local Similarity 100.0%; Pred. No. 0.43; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0;

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Db 106 TCCGAGACGGTTCAGGGCTTAC 83

RESULT 30
AF458349/c
LOCUS
DEFINITION
West Nile virus strain ArB3575/82 nonstructural protein 5 gene,
partial cds.
ACCESSION
AF458349
VERSION
AF458349.1 GI:21636477
SOURCE
West Nile virus (WNV)
ORGANISM
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
1 (bases 1 to 481)
AUTHORS
Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
TITLE
Mouse neuroinvasive phenotype of West Nile virus strains varies
depending upon virus genotype
JOURNAL
Virology 296 (1), 17-23 (2002)
MEDLINE
22033887
PUBMED
12036314
REFERENCE
2 (bases 1 to 481)
AUTHORS
Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE
Direct Submission
JOURNAL
Submitted (14-DEC-2001) Department of Pathology and WHO
Collaborating Center for Tropical Diseases, The University of Texas
Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
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Best Local Similarity 100.0%; Pred. No. 0.43; Indels 0; Gaps 0;
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RESULT 32
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DEFINITION
West Nile virus strain ArD-76104 nonstructural protein 5 gene,
partial cds.
ACCESSION
AF458345
VERSION
AF458345.1 GI:21636469
KEYWORDS
SOURCE
West Nile virus (WNV)
ORGANISM
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
1 (bases 1 to 483)
AUTHORS
Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
TITLE
Mouse neuroinvasive phenotype of West Nile virus strains varies
depending upon virus genotype
JOURNAL
Virology 296 (1), 17-23 (2002)
MEDLINE
22033887
PUBMED
12036314
REFERENCE
2 (bases 1 to 483)
AUTHORS
Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE
Direct Submission
JOURNAL
Submitted (14-DEC-2001) Department of Pathology and WHO
Collaborating Center for Tropical Diseases, The University of Texas
Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
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Matches 24; Conservative 0; Mismatches 0;

QY 1 TCCGAGACGGTTCAGGGCTTAC 24
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Db 106 TCCGAGACGGTTCAGGGCTTAC 83

RESULT 30
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LOCUS
DEFINITION
West Nile virus strain ArB3575/82 nonstructural protein 5 gene,
partial cds.
ACCESSION
AF458349
VERSION
AF458349.1 GI:21636477
SOURCE
West Nile virus (WNV)
ORGANISM
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
1 (bases 1 to 481)
AUTHORS
Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
TITLE
Mouse neuroinvasive phenotype of West Nile virus strains varies
depending upon virus genotype
JOURNAL
Virology 296 (1), 17-23 (2002)
MEDLINE
22033887
PUBMED
12036314
REFERENCE
2 (bases 1 to 481)
AUTHORS
Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE
Direct Submission
JOURNAL
Submitted (14-DEC-2001) Department of Pathology and WHO
Collaborating Center for Tropical Diseases, The University of Texas
Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
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Matches 24; Conservative 0; Mismatches 0;

QY 1 TCCGAGACGGTTCAGGGCTTAC 24
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Db 423 TCCGAGACGGTTCAGGGCTTAC 400

RESULT 31
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DEFINITION
West Nile virus strain H-442 nonstructural protein 5 gene, partial
cds.
ACCESSION
AF458359
VERSION
AF458359.1 GI:21636497
KEYWORDS
SOURCE
West Nile virus (WNV)
ORGANISM
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
1 (bases 1 to 481)
AUTHORS
Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
TITLE
Mouse neuroinvasive phenotype of West Nile virus strains varies
depending upon virus genotype
JOURNAL
Virology 296 (1), 17-23 (2002)
MEDLINE
22033887
PUBMED
12036314
REFERENCE
2 (bases 1 to 481)
AUTHORS
Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE
Direct Submission
JOURNAL
Submitted (14-DEC-2001) Department of Pathology and WHO
Collaborating Center for Tropical Diseases, The University of Texas
Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
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ORIGIN
Query Match          100.0%; Score 24; DB 14; Length 481;
Best Local Similarity 100.0%; Pred. No. 0.43; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0;

QY 1 TCCGAGACGGTTCAGGGCTTAC 24
    |||||
Db 423 TCCGAGACGGTTCAGGGCTTAC 400

RESULT 32
AF458345/c
LOCUS
DEFINITION
West Nile virus strain ArD-76104 nonstructural protein 5 gene,
partial cds.
ACCESSION
AF458345
VERSION
AF458345.1 GI:21636469
KEYWORDS
SOURCE
West Nile virus (WNV)
ORGANISM
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
1 (bases 1 to 483)
AUTHORS
Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
TITLE
Mouse neuroinvasive phenotype of West Nile virus strains varies
depending upon virus genotype
JOURNAL
Virology 296 (1), 17-23 (2002)
MEDLINE
22033887
PUBMED
12036314
REFERENCE
2 (bases 1 to 483)
AUTHORS
Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE
Direct Submission
JOURNAL
Submitted (14-DEC-2001) Department of Pathology and WHO
Collaborating Center for Tropical Diseases, The University of Texas
Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
FEATURES
source
1..483
/organism="West Nile virus"
/virion
/mol_type="genomic RNA"
/strain="ArD-76104"
/db_xref="taxon:11082"
<1..174
CDS

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/note="NS5"
/codon_start=1
/product="nonstructural protein 5"
/protein_id="AA070011.1"
/db_xref="GI:21636470"
/translation="DIWCGSLIGTRTRATWAENIHVAINQVRSVIGEEKYVDYMSSLR
RYEDTIVVEDTVL"
175. .>483

3' UTR
ORIGIN
Query Match 100.0%; Score 24; DB 14; Length 483;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTGAGGGCTTAC 24
|||||
Db 425 TCCGAGACGGTTCTGAGGGCTTAC 402

RESULT 33
AF458357/c
LOCUS
DEFINITION
West Nile virus strain SPU-116/89 nonstructural protein 5 gene,
partial cds.
ACCESSION
AF458357
VERSION
AF458357.1 GI:21636493
KEYWORDS
SOURCE
ORGANISM
West Nile virus (WNV)
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
1 (bases 1 to 483)
Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
Mouse neuroinvasive phenotype of West Nile virus strains varies
depending upon virus genotype
Virology 296 (1), 17-23 (2002)
MEDLINE
22033887
PUBMED
12036314
REFERENCE
2 (bases 1 to 483)
Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
Direct Submission
Submitted (14-DEC-2001) Department of Pathology and WHO
Collaborating Center for Tropical Diseases, The University of Texas
Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
Location/Qualifiers
1. .483
/organism="West Nile virus"
/virion
/mol_type="genomic RNA"
/strain="SPU-116/89"
/db_xref="taxon:11082"
<1. .174
/note="NS5"
/codon_start=1
/product="nonstructural protein 5"
/protein_id="AA070023.1"
/db_xref="GI:21636494"
/translation="DIWCGSLIGTRTRATWAENIHVAINQVRSVIGEEKYVDYMSSLR
RYEDTIVVEDTVL"
175. .>483

CDS
Query Match 100.0%; Score 24; DB 14; Length 483;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTGAGGGCTTAC 24
|||||
Db 426 TCCGAGACGGTTCTGAGGGCTTAC 403

RESULT 35
AF297854/c
LOCUS
DEFINITION
Kunjin virus isolate WK436 nonstructural protein 5 gene, partial
cgs.
ACCESSION
AF297854
VERSION
AF297854.1 GI:11991998
KEYWORDS
SOURCE
ORGANISM
Kunjin virus
Kunjin virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
1 (bases 1 to 542)
Scherrret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
The relationships between West Nile and Kunjin viruses
Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE
21469816
PUBMED
11585335
REFERENCE
2 (bases 1 to 542)
Scherrret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
Definitive studies of the relationships between West Nile and

```

Kunjin viruses
Unpublished
3 (bases 1 to 542)
REFERENCE
AUTHORS Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE Direct Submission
JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University
of Queensland, St Lucia, QLD 4072, Australia
FEATURES
source Location/Qualifiers
1..542
/organism="Kunjin virus"
/mol_type="genomic RNA"
/isolate="WK436"
/db_xref="taxon:11077"
<1..243
/note="NS5"
/codon_start=1
/product="nonstructural protein 5"
/protein_id="AAG42392.1"
/db_xref="GI:11991999"
/translation="NEWEDKTPVEKWSDPVYSGKREDIWGSLIGTRARATWAENIQ
VAINQVRSIIIGDEKYVDYMSWKRYEDTTLVEDTVL"

ORIGIN
Query Match 100.0%; Score 24; DB 14; Length 542;
Best Local Similarity 100.0%; Pred. No. 0.42; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCGAGGCGTTAC 24
|||||
Db 469 TCCGAGACGGTTCGAGGCGTTAC 446

RESULT 36
KUNNS5GAA/c
LOCUS Kunjin virus nonstructural protein (NS5) gene, 3' end of cds. VRL 07-JUN-1996
DEFINITION Kunjin virus nonstructural protein (NS5) gene, 3' end of cds.
ACCESSION L48978
VERSION L48978.1 GI:1066802
KEYWORDS NS5 gene; nonstructural protein.
SOURCE Kunjin virus
ORGANISM Kunjin virus
Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 587)
AUTHORS Poldinger,M., Hall,R.A. and Mackenzie,J.S.
TITLE Molecular characterization of the Japanese encephalitis serocomplex
of the flavivirus genus
JOURNAL Virology 218 (2), 417-421 (1996)
MEDLINE 96193756
PUBMED 8610471
COMMENT Original source text: Kunjin virus (strain MRM61C) cDNA to genomic
RNA.
FEATURES
source Location/Qualifiers
1..587
/organism="Kunjin virus"
/mol_type="genomic RNA"
/strain="MRM61C"
/db_xref="taxon:11077"
1..237
/gene="NS5"
<1..237
/gene="NS5"
/codon_start=1
/product="nonstructural protein"
/protein_id="AAB02077.1"
/db_xref="GI:1066802"
/translation="NEWEDKTPVEKWSDPVYSGKREDIWGSLIGTRARATWAENIQVA
INQVRSIIIGDEKYVDYMSWKRYEDTTLVEDTVL"

ORIGIN
Query Match 100.0%; Score 24; DB 14; Length 587;
Best Local Similarity 100.0%; Pred. No. 0.42; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCGAGGCGTTAC 24
|||||
Db 461 TCCGAGACGGTTCGAGGCGTTAC 438

RESULT 37
KUNNS5GAB/c
LOCUS Kunjin virus nonstructural protein (NS5) gene, 3' end of cds. VRL 07-JUN-1996
DEFINITION Kunjin virus nonstructural protein (NS5) gene, 3' end of cds.
ACCESSION L48979
VERSION L48979.1 GI:1066804
KEYWORDS NS5 gene; nonstructural protein.
SOURCE Kunjin virus
ORGANISM Kunjin virus
Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 587)
AUTHORS Poldinger,M., Hall,R.A. and Mackenzie,J.S.
TITLE Molecular characterization of the Japanese encephalitis serocomplex
of the flavivirus genus
JOURNAL Virology 218 (2), 417-421 (1996)
MEDLINE 96193756
PUBMED 8610471
COMMENT Original source text: Kunjin virus (strain MRM16) cDNA to genomic
RNA.
FEATURES
source Location/Qualifiers
1..587
/organism="Kunjin virus"
/mol_type="genomic RNA"
/strain="MRM16"
/db_xref="taxon:11077"
1..237
/gene="NS5"
<1..237
/gene="NS5"
/codon_start=1
/product="nonstructural protein"
/protein_id="AAB02078.1"
/db_xref="GI:1066805"
/translation="WMEDKTPVEKWSDPVYSGKREDIWGSLIGTRARATWAENIQVA
INQVRSIIIGDEKYVDYMSWKRYEDTTLVEDTVL"

ORIGIN
Query Match 100.0%; Score 24; DB 14; Length 587;
Best Local Similarity 100.0%; Pred. No. 0.42; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCGAGGCGTTAC 24
|||||
Db 461 TCCGAGACGGTTCGAGGCGTTAC 438

RESULT 38
AF196543/c
LOCUS West Nile virus isolate Mgan798 polyprotein gene, partial cds.
DEFINITION West Nile virus isolate Mgan798 polyprotein gene, partial cds.
ACCESSION AF196543
VERSION AF196543.1 GI:15865595
KEYWORDS
SOURCE West Nile virus
ORGANISM West Nile virus
Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 591)
AUTHORS Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE The relationships between West Nile and Kunjin viruses
JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE 21469816
PUBMED 11585535
REFERENCE 2 (bases 1 to 591)

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCGAGGCGTTAC 24
|||||
Db 461 TCCGAGACGGTTCGAGGCGTTAC 438

RESULT 37
KUNNS5GAB/c
LOCUS Kunjin virus nonstructural protein (NS5) gene, 3' end of cds. VRL 07-JUN-1996
DEFINITION Kunjin virus nonstructural protein (NS5) gene, 3' end of cds.
ACCESSION L48979
VERSION L48979.1 GI:1066804
KEYWORDS NS5 gene; nonstructural protein.
SOURCE Kunjin virus
ORGANISM Kunjin virus
Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 587)
AUTHORS Poldinger,M., Hall,R.A. and Mackenzie,J.S.
TITLE Molecular characterization of the Japanese encephalitis serocomplex
of the flavivirus genus
JOURNAL Virology 218 (2), 417-421 (1996)
MEDLINE 96193756
PUBMED 8610471
COMMENT Original source text: Kunjin virus (strain MRM16) cDNA to genomic
RNA.
FEATURES
source Location/Qualifiers
1..587
/organism="Kunjin virus"
/mol_type="genomic RNA"
/strain="MRM16"
/db_xref="taxon:11077"
1..237
/gene="NS5"
<1..237
/gene="NS5"
/codon_start=1
/product="nonstructural protein"
/protein_id="AAB02078.1"
/db_xref="GI:1066805"
/translation="WMEDKTPVEKWSDPVYSGKREDIWGSLIGTRARATWAENIQVA
INQVRSIIIGDEKYVDYMSWKRYEDTTLVEDTVL"

ORIGIN
Query Match 100.0%; Score 24; DB 14; Length 587;
Best Local Similarity 100.0%; Pred. No. 0.42; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCGAGGCGTTAC 24
|||||
Db 461 TCCGAGACGGTTCGAGGCGTTAC 438

RESULT 38
AF196543/c
LOCUS West Nile virus isolate Mgan798 polyprotein gene, partial cds.
DEFINITION West Nile virus isolate Mgan798 polyprotein gene, partial cds.
ACCESSION AF196543
VERSION AF196543.1 GI:15865595
KEYWORDS
SOURCE West Nile virus
ORGANISM West Nile virus
Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 591)
AUTHORS Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE The relationships between West Nile and Kunjin viruses
JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE 21469816
PUBMED 11585535
REFERENCE 2 (bases 1 to 591)

AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
TITLE Definitive studies of the relationships between West Nile and Kunjin viruses
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 591)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
TITLE Direct Submission
JOURNAL Submitted (20-OCT-1999) Department of Microbiology and Parasitology, University of Queensland, St. Lucia, Brisbane, QLD 4072, Australia

FEATURES
 source Location/Qualifiers
 1..591
 /organism="West Nile virus"
 /mol_type="genomic RNA"
 /isolate="Mgan798"
 /db_xref="taxon:11082"
 <1..255
 /codon_start=1
 /product="polyprotein"
 /protein_id="AAU09961.1"
 /db_xref="GI:15865596"
 /translation="WIEENWENKTPVERWSDIPYSGKREDIWCGSLIGTRTRATWA ENHVAINQVRSVIGEEKYVDYMSLRREYDITVVEDTVL"
 mat_peptide <1..252
 3'UTR 256..>591
 ORIGIN
 Query Match 100.0%; Score 24; DB 14; Length 591;
 Best Local Similarity 100.0%; Pred. No. 0.42;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 TCCGAGACGGTCTCGAGGCTTAC 24
 419 TCCGAGACGGTCTCGAGGCTTAC 396

RESULT 39
WNFNS5GAA/c
LOCUS West Nile virus nonstructural protein (NS5) gene, 3' end of cds.
DEFINITION L48977
ACCESSION L48977.1 GI:1066867
VERSION NS5 gene; nonstructural protein.
KEYWORDS West Nile virus
SOURCE West Nile virus
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 593)
AUTHORS Poidinger,M., Hall,R.A. and Mackenzie,J.S.
TITLE Molecular characterization of the Japanese encephalitis serocomplex of the flavivirus genus
JOURNAL Virology 218 (2), 417-421 (1996)
MEDLINE 96193756
PUBMED 8610471
COMMENT Original source text: West Nile virus (strain Sarafend) cDNA to genomic RNA.

FEATURES
 source Location/Qualifiers
 1..593
 /organism="West Nile virus"
 /mol_type="genomic RNA"
 /strain="Sarafend"
 /db_xref="taxon:11082"
 1..250
 /gene="NS5"
 <1..250
 /gene="NS5"
 /codon_start=2
 /product="nonstructural protein"
 /protein_id="AA02101.1"
 /db_xref="GI:1066868"

gene
CDS

ORIGIN
 Query Match 100.0%; Score 24; DB 14; Length 593;
 Best Local Similarity 100.0%; Pred. No. 0.42;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCCGAGACGGTCTCGAGGCTTAC 24
 426 TCCGAGACGGTCTCGAGGCTTAC 403

RESULT 40
AF297844/c
LOCUS Kunjin virus isolate CH16549E nonstructural protein 5 gene, partial cds.
DEFINITION AF297844
ACCESSION AF297844.1 GI:11991978
VERSION Kunjin virus
KEYWORDS Kunjin virus
SOURCE Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group.
ORGANISM 1 (bases 1 to 601)
REFERENCE Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V., Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
AUTHORS The relationships between West Nile and Kunjin viruses
TITLE Emerging Infect. Dis. 7 (4), 697-705 (2001)
JOURNAL 21469816
MEDLINE 11585535
PUBMED 11585535
REFERENCE 2 (bases 1 to 601)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.
TITLE Definitive studies of the relationships between West Nile and Kunjin viruses
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 601)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.
TITLE Direct Submission
JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University of Queensland, St Lucia, QLD 4072, Australia

FEATURES
 source Location/Qualifiers
 1..601
 /organism="Kunjin virus"
 /mol_type="genomic RNA"
 /isolate="CH16549E"
 /db_xref="taxon:11077"
 <1..242
 /note="NS5"
 /codon_start=3
 /product="nonstructural protein 5"
 /protein_id="AAG42382.1"
 /db_xref="GI:11991979"
 /translation="EWMDTTPVEKWSVPYSGKREDIWCGSLIGTRARATWAEDIQV AINQVRSIIGDEKYVDYMSLRRIEYITLVEDTVL"

CDS

ORIGIN
 Query Match 100.0%; Score 24; DB 14; Length 601;
 Best Local Similarity 100.0%; Pred. No. 0.42;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCCGAGACGGTCTCGAGGCTTAC 24
 468 TCCGAGACGGTCTCGAGGCTTAC 445

RESULT 41
KUNNS5/c
LOCUS Kunjin virus (strain Sarawak) nonstructural protein (NS5) gene, 3'
DEFINITION

/product="nonstructural protein 5"
/protein_id="AAG42394.1"
/db_xref="GI:11992003"
/translations="WIDENEMEDKTPVEKMSDVPYSGKREDIWCGSLIGTRARATWA
ENIQVAINQVRSIIIGDEKYVDYMSLSKRYEDTILVEDTVL"

ORIGIN

Query Match 100.0%; Score 24; DB 14; Length 609;
Best Local Similarity 100.0%; Pred. No. 0.42; Mismatches 0; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCGAGACGGTTCTGAGGGCTTAC 24
|||||
Db 490 TCCGAGACGGTTCTGAGGGCTTAC 467

RESULT 44

AF297845/c
LOCUS
Kunjin virus isolate CX255 nonstructural protein 5 gene, partial
cds.

ACCESSION AF297845
VERSION AF297845.1 GI:11991980

KEYWORDS
SOURCE
ORGANISM
Kunjin virus

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 616)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.

TITLE The relationships between West Nile and Kunjin viruses
JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE 21469816
PUBMED 11585535

REFERENCE 2 (bases 1 to 616)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.

TITLE Definitive studies of the relationships between West Nile and
Kunjin viruses

JOURNAL Unpublished
REFERENCE 3 (bases 1 to 616)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.

TITLE Direct Submission
JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University
of Queensland, St Lucia, QLD 4072, Australia

FEATURES

source
1..616
Location/Qualifiers
/organism="Kunjin virus"
/mol_type="genomic RNA"
/isolate="CX255"
/db_xref="taxon:11077"
<1..226

CDS

/notes="NS5"
/codon_start=2
/product="nonstructural protein 5"
/protein_id="AAG42393.1"
/db_xref="GI:11991981"
/translations="TTPVEKMSDVPYSGKPEDIWCGSLIGTRARATWAENIQVATQV
RSIIIGDEKYVDYMTLSKRYEDTILVEDTVL"

ORIGIN

Query Match 100.0%; Score 24; DB 14; Length 616;
Best Local Similarity 100.0%; Pred. No. 0.42; Mismatches 0; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTGAGGGCTTAC 24
|||||

Db 452 TCCGAGACGGTTCTGAGGGCTTAC 429
|||||

RESULT 45

AF297859/c

LOCUS
Kunjin virus isolate MRM5373 nonstructural protein 5 gene, partial
cds.

ACCESSION AF297859
VERSION AF297859.1 GI:11992008

KEYWORDS
SOURCE
ORGANISM
Kunjin virus

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 620)

AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.

TITLE The relationships between West Nile and Kunjin viruses
JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE 21469816
PUBMED 11585535

REFERENCE 2 (bases 1 to 620)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.

TITLE Definitive studies of the relationships between West Nile and
Kunjin viruses

JOURNAL Unpublished
REFERENCE 3 (bases 1 to 620)

AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.

TITLE Direct Submission
JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University
of Queensland, St Lucia, QLD 4072, Australia

FEATURES

source
1..620
Location/Qualifiers
/organism="Kunjin virus"
/mol_type="genomic RNA"
/isolate="MRM5373"
/db_xref="taxon:11077"
<1..251

CDS

/note="NS5"
/codon_start=3
/product="nonstructural protein 5"
/protein_id="AAG42397.1"
/db_xref="GI:11992009"
/translations="EENEMWEDKTPVEKMSDVPYSGKREDIWCGSLIGTRARATWAEN
IQVAINQVRSIIIGDEKYVDYMSLSKRYEDTILVEDTVL"

ORIGIN

Query Match 100.0%; Score 24; DB 14; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.42; Mismatches 0; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTGAGGGCTTAC 24
|||||

Db 477 TCCGAGACGGTTCTGAGGGCTTAC 454
|||||

RESULT 46

AF297842/c
LOCUS
Kunjin virus isolate CHI6514C nonstructural protein 5 gene, partial
cds.

ACCESSION AF297842
VERSION AF297842.1 GI:11991974

KEYWORDS
SOURCE
ORGANISM
Kunjin virus

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 622)

AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.

TITLE The relationships between West Nile and Kunjin viruses
JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE 21469816

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PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
11585535
2 (bases 1 to 622)
Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
Definitive studies of the relationships between West Nile and
Kunjin viruses
Unpublished
3 (bases 1 to 622)
Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
Direct Submission
Submitted (22-AUG-2000) Microbiology and Parasitology, University
of Queensland, St Lucia, QLD 4072, Australia
Location/Qualifiers
1. .622
/organism="Kunjin virus"
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DEFINITION
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
FEATURES
source
AF297843
Kunjin virus isolate CH16532C nonstructural protein 5 gene, partial
cds.
AF297843.1 GI:11991976
Kunjin virus
Kunjin virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
1 (bases 1 to 623)
Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
The relationships between West Nile and Kunjin viruses
Emerging Infect. Dis. 7 (4), 697-705 (2001)
21469816
MEDLINE
PUBMED
11585535
2 (bases 1 to 623)
Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
Definitive studies of the relationships between West Nile and
Kunjin viruses
Unpublished
3 (bases 1 to 623)
Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
Direct Submission
Submitted (22-AUG-2000) Microbiology and Parasitology, University
of Queensland, St Lucia, QLD 4072, Australia
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LOCUS
DEFINITION
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
FEATURES
source
KUNNONCODB
Kunjin virus 3' UTR.
L24512
VERSION
L24512.1 GI:403464
KEYWORDS
SOURCE
Kunjin virus
Kunjin virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
1 (bases 1 to 627)
Coia,G., Parker,M.D., Speight,G., Byrne,M.E. and Westaway,E.G.
Nucleotide and complete amino acid sequences of Kunjin virus:
definitive gene order and characteristics of the virus-specified
proteins
J. Gen. Virol. 69 (Pt 1), 1-21 (1988)
88089524
MEDLINE
PUBMED
2826659
2 (bases 1 to 627)
Khromykh,A.A. and Westaway,E.G.
Completion of Kunjin virus RNA sequence and recovery of an
infectious RNA transcribed from stably cloned full-length cDNA
J. Virol. 68 (7), 4580-4588 (1994)
94267921
MEDLINE
PUBMED
8207832
COMMENT
Original source text: Kunjin virus (strain MRM 61C) mature RNA.
Location/Qualifiers
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DEFINITION
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VERSION					
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ORGANISM	Kunjin virus				
REFERENCE	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;				
AUTHORS	Flavivirus; Japanese encephalitis virus group.				
TITLE	Schretter,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,				
JOURNAL	Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.				
MEDLINE	The relationships between West Nile and Kunjin viruses				
PUBMED	Emerging Infect. Dis. 7 (4), 697-705 (2001)				
REFERENCE	2 (bases 1 to 633)				
AUTHORS	Schretter,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.				
TITLE	and Hall,R.A.				
JOURNAL	Definitive studies of the relationships between West Nile and				
REFERENCE	Kunjin viruses				
AUTHORS	Unpublished				
TITLE	3 (bases 1 to 633)				
JOURNAL	Schretter,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.				
REFERENCE	and Hall,R.A.				
TITLE	Direct Submission				
JOURNAL	Submitted (22-AUG-2000) Microbiology and Parasitology, University				
FEATURES	of Queensland, St Lucia, QLD 4072, Australia				
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SOURCE	West Nile virus				
ORGANISM	West Nile virus				
REFERENCE	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;				
AUTHORS	Flavivirus; Japanese encephalitis virus group.				
TITLE	Jia,X.Y., Briese,T., Jordan,I., Rambaut,A., Chi,H.C.,				
JOURNAL	Mackenzie,J.S., Hall,R.A., Scherret,J. and Lipkin,W.I.				
MEDLINE	Genetic analysis of West Nile New York 1999 encephalitis virus				
PUBMED	Lancet 354 (9194), 1971-1972 (1999)				
REFERENCE	20086017				
AUTHORS	10622305				
	2 (bases 1 to 644)				
	Schretter,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,				
	Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.				

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 25, 2005, 09:32:36 ; Search time 229.143 Seconds
(without alignments)
620.023 Million cell updates/sec

Title: US-10-688-489-75

Perfect score: 24

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 500 summaries

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- 3: Geneseqn2000s:*
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- 8: Geneseqn2003s:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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9	24	100.0	10975	12	ADN98022 West Nile
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11	24	100.0	11029	10	ABV74821 West Nile
12	24	100.0	11029	12	ADN98023 West Nile
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14	23	95.8	50	12	ADN36763 West Nile
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16	22.4	93.3	10968	12	ADN07437 Japanese
17	22.4	93.3	18563	12	ADN07466 Japanese
18	22.4	93.3	18563	12	ADN07465 Japanese
19	22.4	93.3	18565	12	ADN07467 Japanese
20	22.4	93.3	19038	12	ADN07468 Japanese

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C 23	22	91.7	22	12	ADN36755	Adn36755 West Nile
C 24	22	91.7	49	12	ADN36764	Adn36764 West Nile
C 25	21	87.5	23	12	ADN36827	Adn36827 West Nile
C 26	20.8	86.7	10976	3	ABE50890	AbE50890 Japanese
C 27	19	79.2	19	12	ADN36794	Adn36794 West Nile
C 28	17	79.2	87	12	ADN36779	Adn36779 West Nile
C 29	17.6	73.3	1661	10	ADD31012	Add31012 Plant yie
C 30	17.6	73.3	1661	12	ADI43924	Adi43924 Plant tra
C 31	17.6	73.3	1661	12	ADI61330	Adi61330 CDNA enco
C 32	17.6	73.3	1661	12	ADO01998	Ado01998 Thalecres
C 33	17.6	73.3	1823	3	AAC36549	Aac36549 Arabidops
C 34	17.6	73.3	1823	3	AAC35016	Aac35016 Arabidops
C 35	17	70.8	17	6	ACN03369	Acn03369 WNV Inozy
C 36	17	70.8	17	6	ACN05431	Acn05431 WNV DNAYz
C 37	17	70.8	17	6	ACN07305	Acn07305 WNV Amber
C 38	17	70.8	17	6	ACN14217	Acn14217 WNV minus
C 39	17	70.8	17	6	ACN14216	Acn14216 WNV minus
C 40	17	70.8	17	6	ACN03368	Acn03368 WNV Inozy
C 41	17	70.8	17	6	ACN12333	Acn12333 WNV minus
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C 44	17	70.8	17	6	ACN07446	Acn07446 WNV minus
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C 145	16.2	67.5	22421	11	ABD20510	Human pul	C 218	15.8	65.8	96593	10	AD84205	
C 146	16.2	67.5	22421	11	ABD20510	Human pul	C 219	15.8	65.8	96593	10	AD84205	
C 147	16.2	67.5	22421	11	ABD20510	Human pul	C 220	15.8	65.8	96593	10	AD84205	
C 148	16.2	67.5	22421	11	ABD20510	Human pul	C 221	15.8	65.8	96593	10	AD84205	
C 149	16.2	67.5	22421	11	ABD20510	Human pul	C 222	15.8	65.8	96593	10	AD84205	
C 150	16.2	67.5	22421	11	ABD20510	Human pul	C 223	15.8	65.8	96593	10	AD84205	
C 151	16.2	67.5	22421	11	ABD20510	Human pul	C 224	15.8	65.8	96593	10	AD84205	
C 152	16.2	67.5	22421	11	ABD20510	Human pul	C 225	15.8	65.8	96593	10	AD84205	
C 153	16.2	67.5	22421	11	ABD20510	Human pul	C 226	15.8	65.8	96593	10	AD84205	
C 154	16.2	67.5	22421	11	ABD20510	Human pul	C 227	15.8	65.8	96593	10	AD84205	
C 155	16.2	67.5	22421	11	ABD20510	Human pul	C 228	15.8	65.8	96593	10	AD84205	
C 156	16.2	67.5	22421	11	ABD20510	Human pul	C 229	15.8	65.8	96593	10	AD84205	
C 157	16.2	67.5	22421	11	ABD20510	Human pul	C 230	15.8	65.8	96593	10	AD84205	
C 158	16.2	67.5	22421	11	ABD20510	Human pul	C 231	15.8	65.8	96593	10	AD84205	
C 159	16.2	67.5	22421	11	ABD20510	Human pul	C 232	15.8	65.8	96593	10	AD84205	
C 160	16.2	67.5	22421	11	ABD20510	Human pul	C 233	15.8	65.8	96593	10	AD84205	
C 161	16.2	67.5	22421	11	ABD20510	Human pul	C 234	15.8	65.8	96593	10	AD84205	
C 162	16.2	67.5	22421	11	ABD20510	Human pul	C 235	15.8	65.8	96593	10	AD84205	
C 163	16.2	67.5	22421	11	ABD20510	Human pul	C 236	15.8	65.8	96593	10	AD84205	
C 164	16.2	67.5	22421	11	ABD20510	Human pul	C 237	15.8	65.8	96593	10	AD84205	
C 165	16.2	67.5	22421	11	ABD20510	Human pul	C 238	15.8	65.8	96593	10	AD84205	
C 166	16.2	67.5	22421	11	ABD20510	Human pul	C 239	15.8	65.8	96593	10	AD84205	

C 240	15.6	65.0	3112	13	ADS48608	Adsa48608 Bacterial	3113	15.6	65.0	5243	10	ADE98306	Cancer-li	
C 241	15.6	65.0	3147	12	ADO42366	Ado42366 Human NOV	314	15.6	65.0	5264	10	ADE98382	Cancer-li	
C 242	15.6	65.0	3147	12	ADO42688	Ado42688 Human NOV	315	15.6	65.0	5271	10	ADE98329	Cancer-li	
C 243	15.6	65.0	3327	8	ACA46115	Acc46115 Human dit	316	15.6	65.0	5280	10	ADE98384	Cancer-li	
C 244	15.6	65.0	3389	4	AHH14332	Aah14352 Human CDN	317	15.6	65.0	5285	10	ADE98379	Cancer-li	
C 245	15.6	65.0	3398	11	ACN89794	Acn89794 Breast ca	318	15.6	65.0	5287	10	ADE98334	Cancer-li	
C 246	15.6	65.0	3607	3	ACA87845	Aac87845 B. thurin	319	15.6	65.0	5319	6	ABL68493	Cancer-ca	
C 247	15.6	65.0	3642	8	ACC46098	Acc46098 Human dit	320	15.6	65.0	5339	6	ADE98332	Cancer-li	
C 248	15.6	65.0	3642	8	ACC46098	Acc46098 Human dit	321	15.6	65.0	5359	8	ACC42351	Human MAP	
C 249	15.6	65.0	3741	12	ADI16315	Adi16315 Human nuc	322	15.6	65.0	5361	10	ADE98381	Cancer-li	
C 250	15.6	65.0	3877	4	ABK42634	Abk42634 Genomic s	323	15.6	65.0	5366	10	ADE98351	Cancer-li	
C 251	15.6	65.0	3877	5	ABA20095	Abao20095 Human ner	324	15.6	65.0	5368	10	ADE98328	Cancer-li	
C 252	15.6	65.0	3877	9	ABD60790	Abd60790 Connectiv	325	15.6	65.0	5382	10	ADE98378	Cancer-li	
C 253	15.6	65.0	3879	4	ABK42632	Abk42632 Genomic s	326	15.6	65.0	5390	10	ADFO9690	Human mod	
C 254	15.6	65.0	3879	9	ADB60788	Abd60788 Connectiv	327	15.6	65.0	5390	12	ADI24469	Human mod	
C 255	15.6	65.0	3943	6	AAS16294	Aas16294 cDNA enco	328	15.6	65.0	5390	13	ADS88604	Human hou	
C 256	15.6	65.0	3961	12	ADI16314	Adi16314 Human nuc	329	15.6	65.0	5407	10	ADP81470	Human hou	
C 257	15.6	65.0	4017	6	ABN96532	Abn96532 Gene #303	330	15.6	65.0	5434	10	ADE98336	Cancer-li	
C 258	15.6	65.0	4031	8	ACC42350	Acc42350 Human MAP	331	15.6	65.0	5436	10	ADE98331	Cancer-li	
C 259	15.6	65.0	4078	10	ACA56554	Aca56554 Human eig	332	15.6	65.0	5463	10	ADE98353	Cancer-li	
C 260	15.6	65.0	4078	10	ADI56350	Adi56350 Human pol	333	15.6	65.0	5531	10	ADE98325	Cancer-li	
C 261	15.6	65.0	4285	5	AAS76622	Aas76622 DNA enco	334	15.6	65.0	5584	10	ADE98350	Cancer-li	
C 262	15.6	65.0	4526	10	ADP98368	Adp98368 Cancer-li	C 335	15.6	65.0	6138	6	ABV73472	Human cyt	
C 263	15.6	65.0	4535	11	ACN45003	Acn45003 Human mkn	C 336	15.6	65.0	6141	6	ABV73471	Human cyt	
C 264	15.6	65.0	4550	13	ACN42872	Acn42872 Human dia	C 337	15.6	65.0	7032	4	ABK42542	Genomic s	
C 265	15.6	65.0	4553	6	ABL61993	Abi61993 Colon ade	C 338	15.6	65.0	7032	9	ADB60698	Connectiv	
C 266	15.6	65.0	4553	6	ABL62500	Abi62500 Colon ade	C 339	15.6	65.0	7646	6	ABV73469	Human cyt	
C 267	15.6	65.0	4553	6	ABK64849	Abk64849 Human ben	C 340	15.6	65.0	8622	3	AAA95912	Human KLK	
C 268	15.6	65.0	4553	11	ADJ131649	Adj131649 Human CDN	341	15.6	65.0	8622	8	ACC70054	Nucleotid	
C 269	15.6	65.0	4607	10	ADP98371	Adp98371 Cancer-li	342	15.6	65.0	8622	12	ADN05515	Antipsori	
C 270	15.6	65.0	4628	10	ADP98365	Adp98365 Cancer-li	C 343	15.6	65.0	11990	6	ABL61824	Colon ade	
C 271	15.6	65.0	4693	10	ADP98314	Adp98314 Cancer-li	C 344	15.6	65.0	11990	6	ABL69703	Prostate	
C 272	15.6	65.0	4709	10	ADP98340	Adp98340 Cancer-li	C 345	15.6	65.0	11990	8	ACA64920	Human des	
C 273	15.6	65.0	4728	10	ADP98367	Adp98367 Cancer-li	C 346	15.6	65.0	16570	6	ABV73470	Human cyt	
C 274	15.6	65.0	4774	10	ADP98327	Adp98327 Cancer-li	C 347	15.6	65.0	16878	3	AAA81515	N mening	
C 275	15.6	65.0	4777	10	ADP98343	Adp98343 Cancer-li	C 348	15.6	65.0	18318	2	AAI41418	HCW Tole	
C 276	15.6	65.0	4795	10	ADP98311	Adp98311 Cancer-li	349	15.6	65.0	18876	10	ADI23928	Streptomy	
C 277	15.6	65.0	4809	10	ADP98370	Adp98370 Cancer-li	C 350	15.6	65.0	19407	4	AAK81438	Human imm	
C 278	15.6	65.0	4825	10	ADP98366	Adp98366 Cancer-li	C 351	15.6	65.0	19407	5	ABA15879	Human ner	
C 279	15.6	65.0	4830	10	ADP98345	Adp98345 Cancer-li	C 352	15.6	65.0	23815	4	AAK85169	Human imm	
C 280	15.6	65.0	4876	10	ADP98376	Adp98376 Cancer-li	C 353	15.6	65.0	23815	4	AAK68678	Human imm	
C 281	15.6	65.0	4886	10	ADP98349	Adp98349 Cancer-li	C 354	15.6	65.0	24167	5	ABA16132	Human ner	
C 282	15.6	65.0	4888	12	ADO42372	Ado42372 Human NOV	C 355	15.6	65.0	28564	10	ADE54773	Human gen	
C 283	15.6	65.0	4895	10	ADP98313	Adp98313 Cancer-li	356	15.6	65.0	32502	4	AAS59542	Propionib	
C 284	15.6	65.0	4906	10	ADP98369	Adp98369 Cancer-li	C 357	15.6	65.0	32502	8	ACF64471	Propionib	
C 285	15.6	65.0	4911	10	ADP98339	Adp98339 Cancer-li	C 358	15.6	65.0	34269	4	AAK68677	Human imm	
C 286	15.6	65.0	4927	10	ADP98344	Adp98344 Cancer-li	C 359	15.6	65.0	34269	4	AAK85168	Human imm	
C 287	15.6	65.0	4944	10	ADP98308	Adp98308 Cancer-li	C 360	15.6	65.0	37590	4	AAS12439	DNA enco	
C 288	15.6	65.0	4967	10	ADP98354	Adp98354 Cancer-li	C 361	15.6	65.0	52787	12	ADQ97354	Mouse can	
C 289	15.6	65.0	4976	10	ADP98326	Adp98326 Cancer-li	C 362	15.6	65.0	59999	13	ADR28249	Human low	
C 290	15.6	65.0	4979	10	ADP98342	Adp98342 Cancer-li	C 363	15.6	65.0	61944	10	ADI23920	Streptomy	
C 291	15.6	65.0	4981	10	ADP98386	Adp98386 Cancer-li	C 364	15.6	65.0	110000	3	AAA81490	Continuation (10 o	
C 292	15.6	65.0	4988	10	ADP98346	Adp98346 Cancer-li	C 365	15.6	65.0	110000	12	ADN45845	Continuation (9 of	
C 293	15.6	65.0	4992	10	ADP98312	Adp98312 Cancer-li	C 366	15.6	65.0	110000	12	ADN47591	Continuation (12 o	
C 294	15.6	65.0	4997	10	ADP98310	Adp98310 Cancer-li	C 367	15.6	65.0	110000	12	ADN46123	Continuation (9 of	
C 295	15.6	65.0	5008	10	ADP98338	Adp98338 Cancer-li	C 368	15.6	65.0	110000	12	ADN47209	Continuation (12 o	
C 296	15.6	65.0	5062	10	ADP98383	Adp98383 Cancer-li	C 369	15.6	65.0	110000	12	ADN46464	Continuation (9 of	
C 297	15.6	65.0	5069	10	ADP98330	Adp98330 Cancer-li	C 370	15.6	65.0	110000	12	ADN47960	Continuation (12 o	
C 298	15.6	65.0	5072	10	ADP98315	Adp98315 Cancer-li	C 371	15.6	65.0	110000	13	ABD32721	Human can	
C 299	15.6	65.0	5076	10	ADP98341	Adp98341 Cancer-li	372	15.6	65.0	146733	12	ADQ97410	Mouse can	
C 300	15.6	65.0	5078	10	ADP98374	Adp98374 Cancer-li	373	15.6	65.0	185695	8	ABQ77405	Human THB	
C 301	15.6	65.0	5083	10	ADP98380	Adp98380 Cancer-li	C 374	15.6	65.0	219352	13	ABD33098	Murine ca	
C 302	15.6	65.0	5088	10	ADP98348	Adp98348 Cancer-li	C 375	15.6	65.0	229354	6	ABQ74179	Human cyt	
C 303	15.6	65.0	5094	10	ADP98309	Adp98309 Cancer-li	C 376	15.6	65.0	349880	3	AAF21609	Neisseria	
C 304	15.6	65.0	5137	10	ADP98333	Adp98333 Cancer-li	C 377	15.6	65.0	349880	3	AAF21608	Neisseria	
C 305	15.6	65.0	5146	10	ADP98307	Adp98307 Cancer-li	C 378	15.6	65.0	64.2	694	10	ABQ81849	Bifidobac
C 306	15.6	65.0	5164	10	ADP98377	Adp98377 Cancer-li	C 379	15.6	65.0	1937	5	ABV24796	Human end	
C 307	15.6	65.0	5169	10	ADP98352	Adp98352 Cancer-li	C 380	15.4	64.2	1968	9	ADB09644	Allolococ	
C 308	15.6	65.0	5175	10	ADP98373	Adp98373 Cancer-li	C 381	15.4	64.2	1968	9	ADB09642	Allolococ	
C 309	15.6	65.0	5183	10	ADP98385	Adp98385 Cancer-li	382	15.4	64.2	1968	12	ADJ27112	Allolococ	
C 310	15.6	65.0	5185	10	ADP98347	Adp98347 Cancer-li	383	15.4	64.2	5017	4	AAH18661	Human CDN	
C 311	15.6	65.0	5190	10	ADP98335	Adp98335 Cancer-li	384	15.4	64.2					
C 312	15.6	65.0	5232	10	ADP98337	Adp98337 Cancer-li	385	15.4	64.2					

C 386	15.4	64.2	92076	13	ABD33368	Abd33368 Murine ca	C 459	15.2	63.3	1619	6	ABL61992	AbL61992 Colon ade
387	15.4	64.2	110000	9	ADBI2064_10	Continuation (11 o	C 460	15.2	63.3	1633	13	ADS49320	AdS49320 Bacterial
388	15.2	63.3	160	6	AAAC42743	Abn42743 Human spl	C 461	15.2	63.3	1665	3	AAAF37070	Aaaf37070 Human PRO
389	15.2	63.3	147	3	AAAC18009	Aac18009 Human sec	C 462	15.2	63.3	1665	4	AAAF54312	Aaf54312 DNA encod
390	15.2	63.3	221	3	AAAC16163	Aac16163 Human sec	C 463	15.2	63.3	1665	4	AAAF54312	Aaf54312 DNA encod
391	15.2	63.3	251	12	ACH85841	Ach85841 Human gen	C 464	15.2	63.3	1665	4	AAAF6067	Aaaf6067 Human DNA
392	15.2	63.3	344	6	ABK29694	Abk29694 Colon ade	C 465	15.2	63.3	1665	4	AAAF92100	Aaf92100 Human PRO
393	15.2	63.3	348	5	ABAI13864	Abai13864 Human ner	C 466	15.2	63.3	1665	6	ABS74420	AbS74420 Human cDN
394	15.2	63.3	375	2	AAV88984	Aav88984 Human ner	C 467	15.2	63.3	1665	8	ACA89517	AcA89517 cDNA enco
C 395	15.2	63.3	421	4	AAAO7054	Aao7054 Human pan	C 468	15.2	63.3	1665	8	ACA73527	AcA73527 Human sec
C 396	15.2	63.3	421	4	AAK88795	Aak88795 Human dig	C 469	15.2	63.3	1665	8	ACA05842	AcA05842 Human sec
C 397	15.2	63.3	429	10	ABX37842	Abx37842 N. gonorr	C 470	15.2	63.3	1665	8	ACA66676	AcA66676 cDNA enco
C 398	15.2	63.3	429	10	ABX39565	Abx39565 N. gonorr	C 471	15.2	63.3	1665	8	ACA91206	AcA91206 Novel hum
C 399	15.2	63.3	437	6	AAV89768	Aav89768 EST clone	C 472	15.2	63.3	1665	8	ACD81583	AcD81583 Human cDN
C 400	15.2	63.3	441	6	ABN77830	Abn77830 Human ORF	C 473	15.2	63.3	1665	8	ACF20251	AcF20251 Human sec
C 401	15.2	63.3	442	9	ACH50617	Ach50617 Human mam	C 474	15.2	63.3	1665	8	ACF19637	AcF19637 Human sec
C 402	15.2	63.3	457	8	ACA23582	AcA23582 Prokaryot	C 475	15.2	63.3	1665	8	ACD21925	AcD21925 Human sec
C 403	15.2	63.3	459	9	ACH29596	Ach29596 Human adu	C 476	15.2	63.3	1665	8	ACF13090	AcF13090 Human sec
C 404	15.2	63.3	468	9	ACH38754	Ach38754 Human adu	C 477	15.2	63.3	1665	8	ACD25193	AcD25193 Human sec
C 405	15.2	63.3	489	9	ACH16066	Ach16066 Human foe	C 478	15.2	63.3	1665	8	ACF00242	AcF00242 Human sec
C 406	15.2	63.3	513	4	ABA60756	AbA60756 Human adu	C 479	15.2	63.3	1665	8	ACA60405	AcA60405 Novel hum
C 407	15.2	63.3	513	4	AAI40648	Aai40648 Probe #93	C 480	15.2	63.3	1665	8	ACA72299	AcA72299 Novel hum
C 408	15.2	63.3	513	4	AAK34932	Aak34932 Human bon	C 481	15.2	63.3	1665	8	ACD04823	AcD04823 Novel hum
C 409	15.2	63.3	513	4	AAK09041	Aak09041 Human bra	C 482	15.2	63.3	1665	8	ACD18284	AcD18284 Human sec
C 410	15.2	63.3	547	4	AAI61295	Aai61295 Human pol	C 483	15.2	63.3	1665	8	ACD08291	AcD08291 Human sec
C 411	15.2	63.3	555	12	ACH72085	Ach72085 Human gen	C 484	15.2	63.3	1665	8	ACA88725	AcA88725 Novel hum
C 412	15.2	63.3	557	12	ACH76980	Ach76980 Human gen	C 485	15.2	63.3	1665	8	ACA70167	AcA70167 Human sec
C 413	15.2	63.3	576	8	ABS55823	AbS55823 Human Ank	C 486	15.2	63.3	1665	8	ACD12389	AcD12389 Novel hum
C 414	15.2	63.3	576	12	ADE91297	AdE91297 cDNA clon	C 487	15.2	63.3	1665	8	ACC74304	AcC74304 Human sec
C 415	15.2	63.3	583	2	AAAX21005	Aax21005 Polynucle	C 488	15.2	63.3	1665	8	ACD15932	AcD15932 Human sec
C 416	15.2	63.3	672	4	AAAX21005	Aax21005 Human cDN	C 489	15.2	63.3	1665	8	ACD25500	AcD25500 Novel hum
C 417	15.2	63.3	672	8	ABX73272	Abx73272 Human nov	C 490	15.2	63.3	1665	8	ACD17977	AcD17977 Human sec
C 418	15.2	63.3	818	8	ABX05210	Abx05210 Human nov	C 491	15.2	63.3	1665	8	ACC88264	AcC88264 Human sec
C 419	15.2	63.3	942	3	AAAC34540	Aac34540 Arabidops	C 492	15.2	63.3	1665	8	ACD21618	AcD21618 Human sec
C 420	15.2	63.3	956	4	AAAS33313	Aas33313 DNA encod	C 493	15.2	63.3	1665	8	ACA18685	AcA18685 Human sec
C 421	15.2	63.3	962	6	AAAI4641	Aai4641 Arabidops	C 494	15.2	63.3	1665	8	ACA58852	AcA58852 cDNA enco
C 422	15.2	63.3	1002	4	AAAI2452	Aai2452 DNA encod	C 495	15.2	63.3	1665	8	ABX98295	Abx98295 Human cDN
C 423	15.2	63.3	1035	12	ADL03456	Adl03456 DNA encod	C 496	15.2	63.3	1665	8	ACD14046	AcD14046 Human PRO
C 424	15.2	63.3	1078	4	AAK51908	Aak51908 Human pol	C 497	15.2	63.3	1665	8	ACD09826	AcD09826 Human sec
C 425	15.2	63.3	1158	6	AAAD2889	Aad2889 Human DNA	C 498	15.2	63.3	1665	8	ACC88571	AcC88571 Human sec
C 426	15.2	63.3	1158	6	ABS55822	AbS55822 Human cDN	C 499	15.2	63.3	1665	8	ACD21311	AcD21311 Human sec
C 427	15.2	63.3	1158	10	ADH62620	Adh62620 Human tel	C 500	15.2	63.3	1665	8	ABX75683	Abx75683 Human cDN
C 428	15.2	63.3	1158	12	ADB91296	AdB91296 cDNA enco						ACA64028	cDNA enco
C 429	15.2	63.3	1202	4	AAAS33131	Aas33131 DNA encod							
C 430	15.2	63.3	1208	4	AAI59509	Aai59509 Human pol							
C 431	15.2	63.3	1244	3	AAAC40734	Aac40734 Arabidops							
C 432	15.2	63.3	1286	4	AAH99099	Aah99099 Human EST							
C 433	15.2	63.3	1368	11	ACH99857	Ach99857 Klebsiell							
C 434	15.2	63.3	1392	6	AAH48351	Aah48351 Human FOA							
C 435	15.2	63.3	1392	6	ABA96942	AbA96942 Human den							
C 436	15.2	63.3	1392	13	ADSS9699	AdS9699 Bacterial							
C 437	15.2	63.3	1400	4	AAH21249	Aah21249 Human KCN							
C 438	15.2	63.3	1416	8	ACA32300	AcA32300 Prokaryot							
C 439	15.2	63.3	1419	5	AAAS65954	Aas65954 DNA encod							
C 440	15.2	63.3	1452	10	AAAS3677	AdA3677 Human cod							
C 441	15.2	63.3	1466	4	AAH32618	Aah32618 Human sec							
C 442	15.2	63.3	1475	12	ADQ22740	AdQ22740 Human sof							
C 443	15.2	63.3	1475	12	ADQ23254	AdQ23254 Human sof							
C 444	15.2	63.3	1492	2	AAZ00814	Aaz00814 Human sec							
C 445	15.2	63.3	1492	8	ADA39903	Ada39903 Human sec							
C 446	15.2	63.3	1492	8	ACC50492	Acc50492 Human sec							
C 447	15.2	63.3	1492	8	ABZ71274	Abz71274 Human sec							
C 448	15.2	63.3	1492	9	ADB91180	AdB91180 Human sec							
C 449	15.2	63.3	1492	10	ADC73557	AdC73557 Human sec							
C 450	15.2	63.3	1492	10	ADD37614	Add37614 Human sec							
C 451	15.2	63.3	1492	10	ADA56093	Ada56093 Gene enco							
C 452	15.2	63.3	1504	10	ADD46911	Add46911 Rat gene							
C 453	15.2	63.3	1504	10	ADE56589	AdE56589 Rat gene							
C 454	15.2	63.3	1504	10	ADD46915	Add46915 Rat gene							
C 455	15.2	63.3	1504	10	ADE56593	AdE56593 Rat gene							
C 456	15.2	63.3	1508	11	ADM02282	Adm02282 Human cDN							
C 457	15.2	63.3	1588	10	ADC30473	AdC30473 Human nov							
C 458	15.2	63.3	1616	5	AAAS73650	Aas73650 DNA encod							

ALIGNMENTS

RESULT 1
ADN36752
ID ADN36752 standard; DNA; 24 BP.
XX
AC ADN36752;
XX
15-JUL-2004 (first entry)
DE West Nile virus detection-related oligonucleotide probe SeqID74.
XX
DE hybridisation assay probe; nucleic acid detection;
KW target-complementary sequence; flavivirus; West Nile virus; WNV;
KW RNA virus; infection; meningitis; encephalitis;
XX high throughput screening; probe; ss.
OS West Nile virus.
XX
FN WO2004036190-A2.
XX
PD 29-APR-2004.
XX
PF 10-OCT-2003; 2003WO-US033639.
XX
PR 16-OCT-2002; 2002US-0418891P.
PR 25-NOV-2002; 2002US-0429006P.
PR 24-FEB-2003; 2003US-0449810P.

XX PA (GENP-) GEN-PROBE INC.
 XX PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
 XX DR WPI; 2004-389590/36.
 XX PT New hybridization assay probe comprising target-complementary sequence of
 PT bases, useful in detecting flavivirus, e.g. West Nile virus.
 XX PS Claim 27; SEQ ID NO 74; 135pp; English.
 XX CC This invention relates to a novel hybridisation assay probe, for
 CC detecting a nucleic acid, which is a probe sequence that comprises a
 CC target-complementary sequence of bases, and optionally one or more base
 CC sequences that are not complementary to the nucleic acid that is to be
 CC detected. The hybridisation assay probes and the kits are useful in
 CC detecting and amplifying a target nucleic acid sequence, for example
 CC flavivirus like West Nile virus, that may be present in a biological
 CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
 CC birds and culex mosquitoes, with humans and horses serving as incidental
 CC hosts. Infection of humans can lead to meningitis or encephalitis. The
 CC invention may allow for accurate and efficient high throughput screening.
 CC The present sequence is that of an oligonucleotide probe which is related
 CC to the invention.
 XX SQ Sequence 24 BP; 4 A; 6 C; 8 G; 6 T; 0 U; 0 Other;
 Query Match 100.0%; Score 24; DB 12; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.08; Indels 0; Gaps 0;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCCGAGACGGTTCGAGGGCTTAC 24
 Db 1 TCCGAGACGGTTCGAGGGCTTAC 24
 RESULT 2
 ADN36753
 ID ADN36753 standard; DNA; 24 BP.
 AC ADN36753;
 XX 15-JUL-2004 (first entry)
 DE West Nile virus detection-related oligonucleotide probe SeqID75.
 KW hybridisation assay probe; nucleic acid detection;
 KW target-complementary sequence; flavivirus; West Nile virus; WNV;
 KW RNA virus; infection; meningitis; encephalitis;
 KW high throughput screening; probe; ss.
 XX West Nile virus.
 OS WO2004036190-A2.
 XX 29-APR-2004.
 PF 10-OCT-2003; 2003WO-US033639.
 XX 16-OCT-2002; 2002US-0418891P.
 PR 25-NOV-2002; 2002US-0429006P.
 PR 24-FEB-2003; 2003US-0449810P.
 XX (GENP-) GEN-PROBE INC.
 XX Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
 XX WPI; 2004-389590/36.
 XX PT New hybridization assay probe comprising target-complementary sequence of
 PT bases, useful in detecting flavivirus, e.g. West Nile virus.
 XX PS Claim 27; SEQ ID NO 74; 135pp; English.
 XX CC This invention relates to a novel hybridisation assay probe, for
 CC detecting a nucleic acid, which is a probe sequence that comprises a
 CC target-complementary sequence of bases, and optionally one or more base
 CC sequences that are not complementary to the nucleic acid that is to be
 CC detected. The hybridisation assay probes and the kits are useful in
 CC detecting and amplifying a target nucleic acid sequence, for example
 CC flavivirus like West Nile virus, that may be present in a biological
 CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
 CC birds and culex mosquitoes, with humans and horses serving as incidental
 CC hosts. Infection of humans can lead to meningitis or encephalitis. The
 CC invention may allow for accurate and efficient high throughput screening.
 CC The present sequence is that of an oligonucleotide probe which is related
 CC to the invention.
 XX SQ Sequence 24 BP; 4 A; 6 C; 8 G; 6 T; 0 U; 0 Other;
 Query Match 100.0%; Score 24; DB 12; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.08; Indels 0; Gaps 0;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCCGAGACGGTTCGAGGGCTTAC 24
 Db 1 TCCGAGACGGTTCGAGGGCTTAC 24
 RESULT 3
 ADN36751
 ID ADN36751 standard; DNA; 48 BP.
 AC ADN36751;
 XX 15-JUL-2004 (first entry)
 DE West Nile virus detection-related oligonucleotide probe SeqID73.
 KW hybridisation assay probe; nucleic acid detection;
 KW target-complementary sequence; flavivirus; West Nile virus; WNV;
 KW RNA virus; infection; meningitis; encephalitis;
 KW high throughput screening; probe; ss.
 XX West Nile virus.
 OS WO2004036190-A2.
 XX 29-APR-2004.
 PF 10-OCT-2003; 2003WO-US033639.
 XX 16-OCT-2002; 2002US-0418891P.
 PR 25-NOV-2002; 2002US-0429006P.
 PR 24-FEB-2003; 2003US-0449810P.
 XX (GENP-) GEN-PROBE INC.
 XX Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
 XX WPI; 2004-389590/36.
 XX PT New hybridization assay probe comprising target-complementary sequence of
 PT bases, useful in detecting flavivirus, e.g. West Nile virus.
 XX PS Claim 18; SEQ ID NO 73; 135pp; English.
 XX CC This invention relates to a novel hybridisation assay probe, for
 CC detecting a nucleic acid, which is a probe sequence that comprises a
 CC target-complementary sequence of bases, and optionally one or more base
 CC sequences that are not complementary to the nucleic acid that is to be
 CC detected. The hybridisation assay probes and the kits are useful in
 CC detecting and amplifying a target nucleic acid sequence, for example
 CC flavivirus like West Nile virus, that may be present in a biological
 CC sample. West Nile virus (WNV) is an RNA virus that primarily infects

PS Claim 26; SEQ ID NO 75; 135pp; English.
 XX CC This invention relates to a novel hybridisation assay probe, for
 CC detecting a nucleic acid, which is a probe sequence that comprises a
 CC target-complementary sequence of bases, and optionally one or more base
 CC sequences that are not complementary to the nucleic acid that is to be
 CC detected. The hybridisation assay probes and the kits are useful in
 CC detecting and amplifying a target nucleic acid sequence, for example
 CC flavivirus like West Nile virus, that may be present in a biological
 CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
 CC birds and culex mosquitoes, with humans and horses serving as incidental
 CC hosts. Infection of humans can lead to meningitis or encephalitis. The
 CC invention may allow for accurate and efficient high throughput screening.
 CC The present sequence is that of an oligonucleotide probe which is related
 CC to the invention.
 XX SQ Sequence 24 BP; 4 A; 6 C; 8 G; 6 T; 0 U; 0 Other;
 Query Match 100.0%; Score 24; DB 12; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.08; Indels 0; Gaps 0;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCCGAGACGGTTCGAGGGCTTAC 24
 Db 1 TCCGAGACGGTTCGAGGGCTTAC 24
 RESULT 3
 ADN36751
 ID ADN36751 standard; DNA; 48 BP.
 AC ADN36751;
 XX 15-JUL-2004 (first entry)
 DE West Nile virus detection-related oligonucleotide probe SeqID73.
 KW hybridisation assay probe; nucleic acid detection;
 KW target-complementary sequence; flavivirus; West Nile virus; WNV;
 KW RNA virus; infection; meningitis; encephalitis;
 KW high throughput screening; probe; ss.
 XX West Nile virus.
 OS WO2004036190-A2.
 XX 29-APR-2004.
 PF 10-OCT-2003; 2003WO-US033639.
 XX 16-OCT-2002; 2002US-0418891P.
 PR 25-NOV-2002; 2002US-0429006P.
 PR 24-FEB-2003; 2003US-0449810P.
 XX (GENP-) GEN-PROBE INC.
 XX Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
 XX WPI; 2004-389590/36.
 XX PT New hybridization assay probe comprising target-complementary sequence of
 PT bases, useful in detecting flavivirus, e.g. West Nile virus.
 XX PS Claim 18; SEQ ID NO 73; 135pp; English.
 XX CC This invention relates to a novel hybridisation assay probe, for
 CC detecting a nucleic acid, which is a probe sequence that comprises a
 CC target-complementary sequence of bases, and optionally one or more base
 CC sequences that are not complementary to the nucleic acid that is to be
 CC detected. The hybridisation assay probes and the kits are useful in
 CC detecting and amplifying a target nucleic acid sequence, for example
 CC flavivirus like West Nile virus, that may be present in a biological
 CC sample. West Nile virus (WNV) is an RNA virus that primarily infects

CC birds and culex mosquitoes, with humans and horses serving as incidental
 CC hosts. Infection of humans can lead to meningitis or encephalitis. The
 CC invention may allow for accurate and efficient high throughput screening.
 CC The present sequence is that of an oligonucleotide probe which is related
 CC to the invention.

XX
 SQ Sequence 48 BP; 8 A; 12 C; 13 G; 15 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 12; Length 48;
 Best Local Similarity 100.0%; Pred. No. 0.096;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTGAGGGCTTAC 24
 |||||
 Db 1 TCCGAGACGGTTCTGAGGGCTTAC 24

RESULT 4
 ADN36762
 ID ADN36762 standard; DNA; 51 BP.

XX AC ADN36762;

XX DT 15-JUL-2004 (first entry)

XX DE West Nile virus detection-related oligonucleotide probe SeqID84.

XX KW hybridisation assay probe; nucleic acid detection;

XX KW target-complementary sequence; flavivirus; West Nile virus; WNV;

XX KW RNA virus; infection; meningitis; encephalitis;

XX KW high throughput screening; probe; ss.

XX OS West Nile virus.

XX OS Enterobacteria phage T7.

XX FH Key Location/Qualifiers

FT misc_feature 1..27

FT /*tag= a

FT /*note= "T7 promoter sequence"

FT misc_feature 28..51

FT /*tag= b

FT /*note= "WNV-complimentary sequence"

XX WO2004036190-A2.

XX PD 29-APR-2004.

XX PF 10-OCT-2003; 2003WO-US033639.

XX PR 16-OCT-2002; 2002US-0418891P.

XX PR 25-NOV-2002; 2002US-0429006P.

XX PR 24-FEB-2003; 2003US-0449810P.

XX PA (GENP-) GEN-PROBE INC.

XX PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;

XX WPI; 2004-389590/36.

XX PT New hybridization assay probe comprising target-complementary sequence of
 bases, useful in detecting flavivirus, e.g. West Nile virus.

XX PS Disclosure; SEQ ID NO 84; 135pp; English.

XX CC This invention relates to a novel hybridisation assay probe, for
 CC detecting a nucleic acid, which is a probe sequence that comprises a
 CC target-complementary sequence of bases, and optionally one or more base
 CC sequences that are not complementary to the nucleic acid that is to be
 CC detected. The hybridisation assay probes and the kits are useful in
 CC detecting and amplifying a target nucleic acid sequence, for example
 CC flavivirus like West Nile virus, that may be present in a biological
 CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
 CC birds and culex mosquitoes, with humans and horses serving as incidental

CC hosts. Infection of humans can lead to meningitis or encephalitis. The
 CC invention may allow for accurate and efficient high throughput screening.
 CC The present sequence is that of an oligonucleotide probe which is related
 CC to the invention.

XX SQ Sequence 51 BP; 15 A; 10 C; 13 G; 13 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 12; Length 51;
 Best Local Similarity 100.0%; Pred. No. 0.088;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTGAGGGCTTAC 24
 |||||
 Db 28 TCCGAGACGGTTCTGAGGGCTTAC 51

RESULT 5

ADN36750

ID ADN36750 standard; DNA; 70 BP.

XX AC ADN36750;

XX DT 15-JUL-2004 (first entry)

XX DE West Nile virus detection-related oligonucleotide probe SeqID72.

XX KW hybridisation assay probe; nucleic acid detection;

XX KW target-complementary sequence; flavivirus; West Nile virus; WNV;

XX KW RNA virus; infection; meningitis; encephalitis;

XX KW high throughput screening; probe; ss.

XX OS West Nile virus.

XX OS WO2004036190-A2.

XX PD 29-APR-2004.

XX PF 10-OCT-2003; 2003WO-US033639.

XX PR 16-OCT-2002; 2002US-0418891P.

XX PR 25-NOV-2002; 2002US-0429006P.

XX PR 24-FEB-2003; 2003US-0449810P.

XX PA (GENP-) GEN-PROBE INC.

XX PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;

XX WPI; 2004-389590/36.

XX PT New hybridization assay probe comprising target-complementary sequence of
 bases, useful in detecting flavivirus, e.g. West Nile virus.

XX PS Disclosure; SEQ ID NO 72; 135pp; English.

XX CC This invention relates to a novel hybridisation assay probe, for
 CC detecting a nucleic acid, which is a probe sequence that comprises a
 CC target-complementary sequence of bases, and optionally one or more base
 CC sequences that are not complementary to the nucleic acid that is to be
 CC detected. The hybridisation assay probes and the kits are useful in
 CC detecting and amplifying a target nucleic acid sequence, for example
 CC flavivirus like West Nile virus, that may be present in a biological
 CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
 CC birds and culex mosquitoes, with humans and horses serving as incidental
 CC hosts. Infection of humans can lead to meningitis or encephalitis. The
 CC invention may allow for accurate and efficient high throughput screening.
 CC The present sequence is that of an oligonucleotide probe which is related
 CC to the invention.

XX SQ Sequence 70 BP; 11 A; 19 C; 20 G; 20 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 12; Length 70;

Best Local Similarity 100.0%; Pred. No. 0.092;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTGAGGGCTTAC 24
 Db 1 TCCGAGACGGTCTGAGGGCTTAC 24

RESULT 6
 ADR32078/c
 ID ADR32078 standard; DNA; 10945 BP.
 XX
 AC ADR32078;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Genomic DNA of a West Nile virus.
 XX
 KW analysis; target; real time PCR; ds; genomic.
 XX
 OS West Nile virus.
 XX
 PN WO2004072230-A2.
 XX
 PD 26-AUG-2004.
 XX
 PF 10-FEB-2004; 2004WO-US0002012.
 XX
 PR 10-FEB-2003; 2003US-00361004.
 XX
 PA (CLEA-) CLEARANT INC.
 XX
 PI Mckenney K, Gillmeister L, Marlowe K, Armistead D;
 XX
 DR WPI; 2004-625843/60.
 XX
 PT Analyzing a target nucleic acid sequence in a biological material by real
 PT time PCR using nucleic acid primers that are separated by at least 750
 PT nucleic acid residues in the target sequence.
 XX
 PS Disclosure; SEQ ID NO 5; 96pp; English.
 XX
 CC The invention relates to a novel method for analysing a target nucleic
 CC acid sequence in a biological material. The method comprises adding at
 CC least two nucleic acid primers that hybridise under stringent conditions
 CC to predetermined nucleic acid sequences of the target nucleic acid
 CC sequence that are separated by at least 750 nucleic acid residues,
 CC amplifying the target nucleic acid sequence by PCR, and detecting and
 CC quantifying the target nucleic acid sequence. The methods and
 CC compositions of the present invention are useful for analysing a target
 CC nucleic acid sequence in a biological material by real time PCR using
 CC nucleic acid primers that are separated by at least 750 nucleic acid
 CC residues in the target sequence. This polynucleotide sequence represents
 CC the genomic DNA of a West Nile virus used in the target analysis method
 CC of the invention.
 XX
 SQ Sequence 10945 BP; 2999 A; 2457 C; 3143 G; 2346 T; 0 U; 0 Other;
 Query Match 100.0%; Score 24; DB 13; Length 10945;
 Best Local Similarity 100.0%; Pred. No. 0.18; Indels 0; Gaps 0;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTGAGGGCTTAC 24
 Db 10587 TCCGAGACGGTCTGAGGGCTTAC 10564

RESULT 7
 ADR67768/c
 ID ADR67768 standard; DNA; 10945 BP.
 XX
 AC ADR67768;
 XX
 DT 18-NOV-2004 (first entry)
 XX

DE West Nile virus DNA detected by novel detection method.
 XX ds; detection; pathogen.
 XX
 OS West Nile virus.
 XX
 PN WO2004072231-A2.
 XX
 PD 26-AUG-2004.
 XX
 PF 10-FEB-2004; 2004WO-US0002013.
 XX
 PR 10-FEB-2003; 2003US-00361002.
 XX
 PA (CLEA-) CLEARANT INC.
 XX
 PI Mckenney K, Gillmeister L, Marlowe K, Armistead D;
 XX
 DR WPI; 2004-625844/60.
 XX
 CC Determining level of potentially active biological pathogens in
 CC biological material, by adding nucleic acid primer pairs to biological
 CC material, amplifying target nucleic acid by PCR, detecting and
 CC quantifying target nucleic acid.
 XX
 PS Disclosure; SEQ ID NO 5; 111pp; English.
 XX
 CC The invention relates to a method of determining (MI) level of
 CC potentially active biological pathogens in biological material, involves
 CC adding at least two nucleic acid primer pairs to biological material,
 CC amplifying target nucleic acid sequences by PCR, and detecting and
 CC quantifying target nucleic acid sequences, where quantity of the nucleic
 CC acid sequences is proportional to number of biological pathogens in
 CC biological material. (MI) is useful for determining level of potentially
 CC active biological pathogens in a biological material such as cells,
 CC tissues, blood or blood components, proteins, enzymes, immunoglobulins,
 CC botanicals, food, ligaments, tendons, nerves, bone, teeth, skin grafts,
 CC bone marrow, heart valves, cartilage, corneas, arteries, veins, organs,
 CC lipids, carbohydrates, collagen, chitin and its derivatives, forensic
 CC samples, mummified material, human or animal remains, stem cells, islet
 CC of Langerhans cells, cells for transplantation, red blood cells, white
 CC blood cells or platelets. The biological pathogen is chosen from
 CC bacteria, viruses, fungi and single cell parasites. The biological
 CC pathogen is chosen from Aspergillus, Candida, Histoplasma,
 CC Saccharomyces, Coccidioides, Cryptococcus, Escherichia, Bacillus,
 CC Campylobacter, Helicobacter, Listeria, Clostridium, Streptococcus,
 CC Enterococcus, Staphylococcus, Brucella, Haemophilus, Salmonella,
 CC Yersinia, Pseudomonas, Serratia, Enterobacter, Klebsiella, Proteus,
 CC Citrobacter, Corynebacterium, Propionibacterium and Coxiella. The
 CC biological pathogen is chosen from Adeno-associated virus (AAV),
 CC California encephalitis virus, Coronavirus, Coxsackievirus-A,
 CC Coxsackievirus-B, Eastern equine encephalitis virus (EEEV), Echovirus,
 CC Hantavirus, Hepatitis A virus (HAV), Hepatitis C virus (HCV), Hepatitis
 CC delta virus (HDV), Hepatitis E virus (HEV), Hepatitis G virus (HGV), HIV,
 CC Human T-lymphotrophic virus (HTLV), Influenza virus (Flu virus), Measles
 CC virus (Rubella), Mumps virus, Norwalk virus, Parainfluenza virus, Polio
 CC virus, Rabies virus, Respiratory Syncytial virus, Rhinovirus, Rubella
 CC virus, Saint Louis encephalitis virus, Western equine encephalitis virus
 CC (WEEV), yellow fever virus, Adenovirus, Cytomegalovirus (CMV), Epstein-
 CC Barr virus (EBV), Hepatitis B virus (HBV), Herpes simplex virus 1, Herpes
 CC simplex virus 2, Molluscum contagiosum, Papilloma virus (HPV), Smallpox
 CC virus (Variola), Vaccinia virus, Venezuelan equine encephalitis virus
 CC (VEEV), Ebola virus, West Nile virus, Human parvovirus B19 and Rotavirus.
 CC (MI) is useful for determining the effectiveness of a sterilization
 CC process applied to a biological material. (MI) is useful in determining
 CC whether the biological pathogen is inactive or active. (MI) enables
 CC determination of whether the particular biological pathogen is present in
 CC a biological material as shown by amplification of first target sequence
 CC and whether the biological pathogen is inactive or active. (MI) enables
 CC evaluation of the effectiveness of sterilization processes, and
 CC determination of both the original level and the residual level of
 CC potentially active biological pathogens. This sequence corresponds to a
 CC West Nile virus DNA detected by the method of the invention.

XX SQ Sequence 10945 BP; 2959 A; 2457 C; 3143 G; 2346 T; 0 U; 0 Other;
 Query Match 100.0%; Score 24; DB 13; Length 10945;
 Best Local Similarity 100.0%; Pred. No. 0.18;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCAGGGCTTAC 24
 |||||
 Db 10587 TCCGAGACGGTTCAGGGCTTAC 10564

RESULT 8
 ADK13681/c
 ID ADK13681 standard; DNA; 10962 BP.
 XX AC ADK13681;
 XX AC
 XX AC
 DT 20-MAY-2004 (first entry)
 XX DE West Nile Virus DNA sequence, SEQ ID 1.
 XX DE
 KW Virucide; Immunosuppressant; flavivirus;
 KW envelope protein domain III polypeptide; envelope protein; gene; ss.
 XX OS West Nile virus.
 XX OS
 FH Key Location/Qualifiers
 CDS 97..10389
 FT /*tag= a
 FT /*product= "West Nile Virus protein"
 XX PN WO2004016586-A2.
 XX PD
 PD 26-FEB-2004.
 XX PF
 PF 18-AUG-2003; 2003WO-US025681.
 XX PR
 PR 16-AUG-2002; 2002US-0403893P.
 PR 06-FEB-2003; 2003US-0445581P.
 XX PS
 PS (TEXA) UNIV TEXAS SYSTEM.
 XX PI Barrett A, Beasley D, Holbrook M;
 XX PI
 XX WPI; 2004-203756/19.
 DR P-PSDB; ADK13682.
 XX DR
 PT Diagnosing flavivirus infection by contacting a sample from a human or
 PT animal with a flavivirus envelope protein domain III polypeptide, and
 PT detecting formation of an immunocomplex between the envelope protein and
 PT antibodies in the sample.
 XX PS
 PS Disclosure; SEQ ID NO 1; 110pp; English.
 XX PS
 CC The present invention relates to a method for screening for a flavivirus
 CC in a subject or animal host. The method comprises: contacting a sample
 CC from the subject with a composition comprising a flavivirus envelope
 CC protein domain III polypeptide (ADK13683-ADK13701) under conditions that
 CC permit formation of specific immunocomplex between an antibody in the
 CC sample and the envelope protein domain III polypeptide; and detecting
 CC whether a specific immunocomplex is formed. The present sequence is the
 CC coding sequence for West Nile Virus protein, from which E protein
 CC envelope protein domain III polypeptide (ADK13683) is derived.
 XX CC
 XX SQ Sequence 10962 BP; 2997 A; 2497 C; 3100 G; 2368 T; 0 U; 0 Other;
 Query Match 100.0%; Score 24; DB 12; Length 10962;
 Best Local Similarity 100.0%; Pred. No. 0.18;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCAGGGCTTAC 24
 |||||
 Db 10587 TCCGAGACGGTTCAGGGCTTAC 10564

RESULT 10
 ABZ68481/c
 ID ABZ68481 standard; DNA; 11029 BP.
 XX AC ABZ68481;
 XX AC
 XX DT 22-APR-2003 (first entry)
 XX DE Nucleotide sequence of the genome of West Nile virus IS-98-ST1.
 XX DE
 XX WNV; IS-98-ST1; Flavivirus; infection; encephalitis; gene; ss.
 XX XX

Db 10564 TCCGAGACGGTTCAGGGCTTAC 10541

RESULT 9
 ADN98022/c
 ID ADN98022 standard; DNA; 10975 BP.
 XX AC ADN98022;
 XX AC
 XX DT 29-JUL-2004 (first entry)
 XX DE West Nile Virus isolate 2741 complete genome sequence.
 XX DE
 KW ds; West Nile Virus; envelope protein; glycoprotein E; flavivirus;
 KW Japanese encephalitis virus; Dengue virus; St Louis encephalitis virus.
 XX OS West Nile virus.
 XX OS
 PN WO2004040263-A2.
 XX PD 13-MAY-2004.
 XX PD
 XX 31-OCT-2003; 2003WO-US034823.
 XX PF
 PF 31-OCT-2002; 2002US-0422755P.
 XX PR
 PR 06-JUN-2003; 2003US-0476513P.
 XX PR
 XX (HEAL-) HEALTH RES INC.
 XX PA
 XX PI Wong SJ, Pei-Yong S;
 XX PI
 XX WPI; 2004-400223/37.
 DR GENBANK; AF206518.
 XX DR
 PT New diagnostic kit comprising West Nile Virus (WNV) envelope protein
 PT reactive with antibody against WNV and cross-reactive with antibody
 PT against a flavivirus, useful in diagnosing flavivirus infection caused by
 PT DENV, WNV, JEV or SLEV.
 XX PS
 PS Disclosure; Fig 37; 212pp; English.
 XX PS
 CC The invention relates to a diagnostic kit comprising at least one
 CC isolated and purified polypeptide comprising a West Nile Virus (WNV)
 CC envelope (E) protein or its immunogenic fragment having a native
 CC conformation or non-denatured structure and that is reactive with
 CC antibodies against WNV and cross-reactive with antibodies against a
 CC flavivirus. The diagnostic kit is useful in diagnosing flavivirus
 CC infection caused by DENV, WNV, JEV or SLEV. This sequence corresponds to
 CC the complete nucleotide sequence of the WNV isolate 2741.
 XX CC
 XX SQ Sequence 10975 BP; 3007 A; 2460 C; 3149 G; 2359 T; 0 U; 0 Other;
 Query Match 100.0%; Score 24; DB 12; Length 10975;
 Best Local Similarity 100.0%; Pred. No. 0.18;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCAGGGCTTAC 24
 |||||
 Db 10611 TCCGAGACGGTTCAGGGCTTAC 10588

RESULT 10
 ABZ68481/c
 ID ABZ68481 standard; DNA; 11029 BP.
 XX AC ABZ68481;
 XX AC
 XX DT 22-APR-2003 (first entry)
 XX DE Nucleotide sequence of the genome of West Nile virus IS-98-ST1.
 XX DE
 XX WNV; IS-98-ST1; Flavivirus; infection; encephalitis; gene; ss.
 XX XX

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OS West Nile virus.
XX Key Location/Qualifiers
XX CDS 97..10397
XX FT /*tag= a
XX FT /product= "polyprotein"
XX
XX WO200281511-A1.
XX
XX 17-OCT-2002.
XX
XX 04-APR-2002; 2002WO-FR001168.
XX
XX 04-APR-2001; 2001FR-00004599.
XX
XX 06-SEP-2001; 2001FR-00011525.
XX
XX (INSP ) INST PASTEUR.
XX (KIMR-) KIMRON VETERINARY INST.
XX
XX Despres P, Deubel V, Guenet J, Drouet M, Malkinson M, Banet C;
XX Frenkiel M, Courageot M, Coulibaly F, Catteau A, Flamand M, Weber P;
XX Ceccaldi P;
XX
XX WPI; 2003-058498/05.
XX P-PSDB; ABP70647.
XX
XX New neurovirulent strain of West Nile virus, useful in diagnosis and
XX screening for antiviral agents, also related nucleic acids, proteins and
XX antibodies.
XX
XX Claim 1; Page 34-49; 68pp; French.
XX
XX The present sequence represents the genome of a strain of West Nile virus
XX (WNV), designated IS-98-ST1. This strain is a neuroinvasive and
XX neurovirulent strain of WNV. Polynucleotides and polypeptides derived
XX from the IS-98-ST1 genome are useful for diagnosis and prognosis of
XX Flavivirus infection, specifically WNV-mediated encephalitis. They are
XX also useful to raise specific antibodies, for recombinant expression of
XX WNV proteins or peptides (for diagnosis, production of antibodies and
XX identification of specific binding partners in cells), for identifying
XX cellular genes implicated in resistance to viral infection, and for
XX screening for anti-Flavivirus agents
XX
XX Sequence 11029 BP; 3019 A; 2471 C; 3167 G; 2372 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 24; DB 8; Length 11029;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTGAGGGCTTAC 24
|||
Db 10629 TCCGAGACGGTTCTGAGGGCTTAC 10606

RESULT 11
ABV74821/c
ID ABV74821 standard; DNA; 11029 BP.
XX
XX ABV74821;
XX
XX 28-MAR-2003 (first entry)
XX
XX West Nile virus strain NY99-flamingo 382-99 complete genome.
XX
XX Virucide; hepatotropic; antinflammatory; antiviral; OAS;
XX 2'-5'-oligoadenylate synthase; Flavivirus infection; gene; ss.
XX
XX West Nile Virus.
XX
XX Key Location/Qualifiers
XX CDS 97..10398
XX FT /*tag= a
XX FT /product= "West Nile Virus protein"

```

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XX WO200281741-A2.
XX
XX 17-OCT-2002.
XX
XX 04-APR-2002; 2002WO-FR001169.
XX
XX 04-APR-2001; 2001FR-00004598.
XX
XX (INSP ) INST PASTEUR.
XX (CNRS ) CNRS CENT NAT RECH SCI.
XX
XX Guenet J, Mashimo T, Simon-Chazottes D, Montagutelli X;
XX Frenkiel M, Despres P, Deubel V, Bonhomme F, Lucas M;
XX WPI; 2003-058566/05.
XX P-PSDB; ABB98821.
XX
XX Identifying stimulators of oligoadenylate synthase family genes, useful
XX as antiviral agents against Flavivirus, also mutated genes responsible
XX for sensitivity to virus.
XX
XX Example 1; Page 52-67; 93pp; French.
XX
XX The present invention relates to a method for identifying compounds (I)
XX that can stimulate a gene of the OAS (2'-5'-oligoadenylate synthase)
XX family. The method comprises: (a) inducing expression of the OAS gene in
XX a culture of cells from a non-human mammal (Flvr/Flvr or Flvr/Flva;
XX indicating resistance or sensitivity to Flavivirus infection); (b)
XX treating cells with test compound; and (c) measuring activity of OAS gene
XX relative to a control. (I) are potentially useful as antiviral agents for
XX treating infections by Flaviviruses (e.g. hepatitis C; dengue; yellow
XX fever and various forms of encephalitis). Genomic OAS DNA and derived
XX cDNA, also the encoded proteins, are useful: (a) for treating Flavivirus
XX infection; (b) in screening for anti-Flavivirus agents; and (c) for
XX evaluating sensitivity of subjects to Flavivirus infection and their
XX likely response to interferon treatment, e.g. to identify patients at
XX risk of developing severe forms of such infections. The present sequence
XX is West Nile Virus strain NY99-flamingo 382-99 (IS-98-ST1) complete
XX genome, which was used in an example from the invention. West Nile Virus
XX is one such Flavivirus
XX
XX Sequence 11029 BP; 3019 A; 2471 C; 3167 G; 2372 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 24; DB 10; Length 11029;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTGAGGGCTTAC 24
|||
Db 10629 TCCGAGACGGTTCTGAGGGCTTAC 10606

RESULT 12
ADN98023/c
ID ADN98023 standard; DNA; 11029 BP.
XX
XX ADN98023;
XX
XX 29-JUL-2004 (first entry)
XX
XX West Nile Virus isolate 3356 complete genome sequence.
XX
XX ds; West Nile Virus; envelope protein; glycoprotein E; flavivirus;
XX Japanese encephalitis virus; Dengue virus; St Louis encephalitis virus.
XX
XX West Nile virus.
XX
XX WO2004040263-A2.
XX
XX 13-MAY-2004.
XX
XX 31-OCT-2003; 2003WO-US034823.

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XX PR 31-OCT-2002; 2002US-0422755P.
XX PR 06-JUN-2003; 2003US-0476513P.
XX PA (HEAL-) HEALTH RES INC.
XX PI Wong SJ, Pei-Yong S;
XX PI WPI; 2004-400223/37.
XX DR GENBANK; AF404756.
XX PT New diagnostic kit comprising West Nile Virus (WNV) envelope protein
XX PT reactive with antibody against WNV and cross-reactive with antibody
XX PT against a flavivirus; useful in diagnosing flavivirus infection caused by
XX PT DENV, WNV, JEV or SLEV.
XX PS Disclosure; Fig 38; 212pp; English.
XX SQ Sequence 11029 BP; 3017 A; 2466 C; 3172 G; 2374 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 12; Length 11029;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTGAGGGCTTAC 24
DB 10629 TCCGAGACGGTTCTGAGGGCTTAC 10606

RESULT 13
ADN36754
ID ADN36754 standard; DNA; 23 BP.
XX AC ADN36754;
XX DT 15-JUL-2004 (first entry)
XX DE West Nile virus detection-related oligonucleotide probe SeqID76.
XX KW hybridisation assay probe; nucleic acid detection;
XX KW target-complementary sequence; flavivirus; West Nile virus; WNV;
XX KW RNA virus; infection; meningitis; encephalitis;
XX KW high throughput screening; probe; ss.
XX OS West Nile virus.
XX PN WO2004036190-A2.
XX PD 29-APR-2004.
XX PF 10-OCT-2003; 2003WO-US033639.
XX PR 16-OCT-2002; 2002US-0418891P.
XX PR 25-NOV-2002; 2002US-0429006P.
XX PR 24-FEB-2003; 2003US-0449810P.
XX PA (GENP-) GEN-PROBE INC.
XX PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX PI WPI; 2004-389590/36.
XX DR WPI; 2004-389590/36.
XX PT New hybridization assay probe comprising target-complementary sequence of
XX PT bases, useful in detecting flavivirus, e.g. West Nile virus.

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XX PS Claim 26; SEQ ID NO 76; 135pp; English.
XX CC This invention relates to a novel hybridisation assay probe, for
XX CC detecting a nucleic acid, which is a probe sequence that comprises a
XX CC target-complementary sequence of bases, and optionally one or more base
XX CC sequences that are not complementary to the nucleic acid that is to be
XX CC detected. The hybridisation assay probes and the kits are useful in
XX CC detecting and amplifying a target nucleic acid sequence, for example
XX CC flavivirus like West Nile virus, that may be present in a biological
XX CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
XX CC birds and culex mosquitoes, with humans and horses serving as incidental
XX CC hosts. Infection of humans can lead to meningitis or encephalitis. The
XX CC invention may allow for accurate and efficient high throughput screening.
XX CC The present sequence is that of an oligonucleotide probe which is related
XX CC to the invention.
XX SQ Sequence 23 BP; 4 A; 5 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 95.8%; Score 23; DB 12; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTGAGGGCTTAC 23
DB 1 TCCGAGACGGTTCTGAGGGCTTAC 23

RESULT 14
ADN36763
ID ADN36763 standard; DNA; 50 BP.
XX AC ADN36763;
XX DT 15-JUL-2004 (first entry)
XX DE West Nile virus detection-related PCR primer SeqID85.
XX KW hybridisation assay probe; nucleic acid detection;
XX KW target-complementary sequence; flavivirus; West Nile virus; WNV;
XX KW RNA virus; infection; meningitis; encephalitis;
XX KW high throughput screening; PCR; primer; ss.
XX OS West Nile virus.
XX PN Enterobacteria phage T7.
XX FH Key Location/Qualifiers
FT misc_feature 1..27
FT /tag= a
FT /note= "T7 promoter sequence"
FT misc_feature 28..50
FT /tag= b
FT /note= "WNV-complimentary sequence"
XX PN WO2004036190-A2.
XX PD 29-APR-2004.
XX PF 10-OCT-2003; 2003WO-US033639.
XX PR 16-OCT-2002; 2002US-0418891P.
XX PR 25-NOV-2002; 2002US-0429006P.
XX PR 24-FEB-2003; 2003US-0449810P.
XX PA (GENP-) GEN-PROBE INC.
XX PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX PI WPI; 2004-389590/36.
XX DR WPI; 2004-389590/36.
XX PT New hybridization assay probe comprising target-complementary sequence of
XX PT bases, useful in detecting flavivirus, e.g. West Nile virus.

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PS Example 4; SEQ ID NO 85; 135pp; English.

XX This invention relates to a novel hybridisation assay probe, for
CC detecting a nucleic acid, which is a probe sequence that comprises a
CC target-complementary sequence of bases, and optionally one or more base
CC sequences that are not complementary to the nucleic acid that is to be
CC detected. The hybridisation assay probes and the kits are useful in
CC detecting and amplifying a target nucleic acid sequence, for example
CC flavivirus like West Nile virus, that may be present in a biological
CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC birds and culex mosquitoes, with humans and horses serving as incidental
CC hosts. Infection of humans can lead to meningitis or encephalitis. The
CC invention may allow for accurate and efficient high throughput screening.
CC The present sequence is that of a PCR primer which is related to the
CC invention.

SQ Sequence 50 BP; 15 A; 9 C; 13 G; 13 T; 0 U; 0 Other;

Query Match 95.8%; Score 23; DB 12; Length 50;

Best Local Similarity 100.0%; Pred. No. 0.27; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTGAGGGCTTA 23

DB 28 TCCGAGACGGTCTGAGGGCTTA 50

RESULT 15

ADO07431/C

ID ADO07431 standard; DNA; 10818 BP.

XX AC ADO07431;

XX 15-JUL-2004 (first entry)

XX Japanese Encephalitis virus JEV coding sequence SEQ ID NO: 9.
DE antiinflammatory; neuroprotective; gene therapy;
XX Japanese Encephalitis virus; JEV; ds; gene; vaccine;
KW Japanese encephalitis.

XX Japanese encephalitis virus.

XX WO2004033690-A1.

XX 22-APR-2004.

XX 09-OCT-2003; 2003WO-KR002081.

XX 09-OCT-2002; 2002KR-00061589.

XX (CICD-) CID CO LTD.

XX (LEES/) LEE S H.

XX Lee SH, Lee Y, Yun S;

XX WPI; 2004-340933/31.

XX New Japanese encephalitis virus genomic RNA, useful in developing
PT vaccines for and in diagnosing and treating Japanese encephalitis.
PT
XX
PS Example 2; Page 145-152; 265pp; English.
XX The present invention relates to a genomic RNA of the Korean Japanese
CC Encephalitis Virus (JEV) isolate, composed of a 5' and 3' nontranslated
CC region (NTR) and a single polypeptide coding region. The JEV genomic RNA,
CC JEV cDNA and reagents are useful in developing vaccines for and in
CC diagnosing and treating Japanese encephalitis. The present sequence is a
CC sequence of the invention.

XX Sequence 10818 BP; 2991 A; 2491 C; 3075 G; 2261 T; 0 U; 0 Other;

XX Query Match 93.3%; Score 22.4; DB 12; Length 10818;

Best Local Similarity 95.8%; Pred. No. 1.1; Mismatches 23; Conservative 0; Indels 1; Gaps 0;

QY 1 TCCGAGACGGTCTGAGGGCTTAC 24

DB 10523 TCCGAGACGGTCTGAGGGCTTTC 10500

RESULT 16

ADO07437/C

ID ADO07437 standard; DNA; 10968 BP.

XX AC ADO07437;

XX 15-JUL-2004 (first entry)

XX Japanese Encephalitis virus JEV coding sequence SEQ ID NO: 15.

XX antiinflammatory; neuroprotective; gene therapy;

XX Japanese Encephalitis virus; JEV; ds; gene; vaccine;

XX Japanese encephalitis.

XX Japanese encephalitis virus.

XX WO2004033690-A1.

XX 22-APR-2004.

XX 09-OCT-2003; 2003WO-KR002081.

XX 09-OCT-2002; 2002KR-00061589.

XX (CICD-) CID CO LTD.

XX (LEES/) LEE S H.

XX Lee SH, Lee Y, Yun S;

XX WPI; 2004-340933/31.

XX New Japanese encephalitis virus genomic RNA, useful in developing
PT vaccines for and in diagnosing and treating Japanese encephalitis.
PT
XX
PS Claim 3; Page 154-161; 265pp; English.
XX The present invention relates to a genomic RNA of the Korean Japanese
CC Encephalitis Virus (JEV) isolate, composed of a 5' and 3' nontranslated
CC region (NTR) and a single polypeptide coding region. The JEV genomic RNA,
CC JEV cDNA and reagents are useful in developing vaccines for and in
CC diagnosing and treating Japanese encephalitis. The present sequence is a
CC sequence of the invention.

XX Sequence 10968 BP; 3032 A; 2518 C; 3117 G; 2301 T; 0 U; 0 Other;

XX Query Match 93.3%; Score 22.4; DB 12; Length 10968;

XX Best Local Similarity 95.8%; Pred. No. 1.1; Mismatches 23; Conservative 0; Indels 1; Gaps 0;

QY 1 TCCGAGACGGTCTGAGGGCTTAC 24

DB 10573 TCCGAGACGGTCTGAGGGCTTTC 10550

RESULT 17

ADO07466/C

ID ADO07466 standard; DNA; 18563 BP.

XX AC ADO07466;

XX 15-JUL-2004 (first entry)

XX Japanese Encephalitis virus JEV coding sequence SEQ ID NO: 44.

XX antiinflammatory; neuroprotective; gene therapy;

KW Japanese Encephalitis virus; JEV; ds; gene; vaccine;
KW Japanese encephalitis.
XX
OS Japanese encephalitis virus.
XX WO2004033690-A1.
XX
XX
XX PD 22-APR-2004.
XX
XX PF 09-OCT-2003; 2003WO-KR002081.
XX
XX PR 09-OCT-2002; 2002KR-00061589.
XX
XX PA (CIDC-) CID CO LTD.
XX PA (LEES/) LEE S H.
XX
XX PI Lee SH, Lee Y, Yun S;
XX WPI; 2004-340933/31.
XX
XX PT New Japanese encephalitis virus genomic RNA, useful in developing
XX PT vaccines for and in diagnosing and treating Japanese encephalitis.
XX
XX Claim 12; Page 193-206; 265pp; English.
XX
XX CC The present invention relates to a genomic RNA of the Korean Japanese
XX CC Encephalitis Virus (JEV) isolate, composed of a 5' and 3' nontranslated
XX CC region (NTR) and a single polypeptide coding region. The JEV genomic RNA,
XX CC JEV cDNA and reagents are useful in developing vaccines for and in
XX CC diagnosing and treating Japanese encephalitis. The present sequence is a
XX CC sequence of the invention.
XX
XX SQ Sequence 18563 BP; 4943 A; 4211 C; 4929 G; 4480 T; 0 U; 0 Other;
XX
XX Query Match 93.3%; Score 22.4; DB 12; Length 18563;
XX Best Local Similarity 95.8%; Pred. No. 1.2;
XX Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 TCCGAGACGGTTCGAGGGCTTAC 24
XX DB 10573 TCCGAGACGGTTCGAGGGCTTTC 10550
XX
XX RESULT 18
XX ADO07465/C
XX ID ADO07465 standard; DNA; 18563 BP.
XX
XX AC ADO07465;
XX
XX DT 15-JUL-2004 (first entry)
XX
XX DE Japanese Encephalitis virus JEV coding sequence SEQ ID NO: 43.
XX
XX KW antiinflammatory; neuroprotective; gene therapy;
XX KW Japanese Encephalitis virus; JEV; ds; gene; vaccine;
XX KW Japanese encephalitis.
XX
XX OS Japanese encephalitis virus.
XX
XX PN WO2004033690-A1.
XX
XX PD 22-APR-2004.
XX
XX PF 09-OCT-2003; 2003WO-KR002081.
XX
XX PR 09-OCT-2002; 2002KR-00061589.
XX
XX PA (CIDC-) CID CO LTD.
XX PA (LEES/) LEE S H.
XX
XX PI Lee SH, Lee Y, Yun S;
XX WPI; 2004-340933/31.
XX
XX DR

XX New Japanese encephalitis virus genomic RNA, useful in developing
XX PT vaccines for and in diagnosing and treating Japanese encephalitis.
XX
XX PS Claim 12; Page 180-193; 265pp; English.
XX
XX CC The present invention relates to a genomic RNA of the Korean Japanese
XX CC Encephalitis Virus (JEV) isolate, composed of a 5' and 3' nontranslated
XX CC region (NTR) and a single polypeptide coding region. The JEV genomic RNA,
XX CC JEV cDNA and reagents are useful in developing vaccines for and in
XX CC diagnosing and treating Japanese encephalitis. The present sequence is a
XX CC sequence of the invention.
XX
XX SQ Sequence 18563 BP; 4944 A; 4211 C; 4929 G; 4479 T; 0 U; 0 Other;
XX
XX Query Match 93.3%; Score 22.4; DB 12; Length 18563;
XX Best Local Similarity 95.8%; Pred. No. 1.2;
XX Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 TCCGAGACGGTTCGAGGGCTTAC 24
XX DB 10573 TCCGAGACGGTTCGAGGGCTTTC 10550
XX
XX RESULT 19
XX ADO07467/C
XX ID ADO07467 standard; DNA; 18565 BP.
XX
XX AC ADO07467;
XX
XX DT 15-JUL-2004 (first entry)
XX
XX DE Japanese Encephalitis virus JEV coding sequence SEQ ID NO: 45.
XX
XX KW antiinflammatory; neuroprotective; gene therapy;
XX KW Japanese Encephalitis virus; JEV; ds; gene; vaccine;
XX KW Japanese encephalitis.
XX
XX OS Japanese encephalitis virus.
XX
XX PN WO2004033690-A1.
XX
XX PD 22-APR-2004.
XX
XX PF 09-OCT-2003; 2003WO-KR002081.
XX
XX PR 09-OCT-2002; 2002KR-00061589.
XX
XX PA (CIDC-) CID CO LTD.
XX PA (LEES/) LEE S H.
XX
XX PI Lee SH, Lee Y, Yun S;
XX WPI; 2004-340933/31.
XX
XX PT New Japanese encephalitis virus genomic RNA, useful in developing
XX PT vaccines for and in diagnosing and treating Japanese encephalitis.
XX
XX PS Claim 12; Page 206-219; 265pp; English.
XX
XX CC The present invention relates to a genomic RNA of the Korean Japanese
XX CC Encephalitis Virus (JEV) isolate, composed of a 5' and 3' nontranslated
XX CC region (NTR) and a single polypeptide coding region. The JEV genomic RNA,
XX CC JEV cDNA and reagents are useful in developing vaccines for and in
XX CC diagnosing and treating Japanese encephalitis. The present sequence is a
XX CC sequence of the invention.
XX
XX SQ Sequence 18565 BP; 4944 A; 4211 C; 4929 G; 4481 T; 0 U; 0 Other;
XX
XX Query Match 93.3%; Score 22.4; DB 12; Length 18565;
XX Best Local Similarity 95.8%; Pred. No. 1.2;
XX Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;


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Qy 1 TCCGAGACGGTCTCTGAGGGCTTAC 24
Db 10573 TCCGAGACGGTCTCTGAGGGCTTTC 10550

RESULT 20
ADO07468/c
ID ADO07468 standard; DNA; 19038 BP.
XX AC ADO07468;
XX 15-JUL-2004 (first entry)
XX Japanese Encephalitis virus JEV coding sequence SEQ ID NO: 46.
XX antiinflammatory; neuroprotective; gene therapy;
KW Japanese Encephalitis virus; JEV; ds; gene; vaccine;
KW Japanese encephalitis.
XX OS Japanese encephalitis virus.
XX WO2004033690-A1.
XX 22-APR-2004.
XX 09-OCT-2003; 2003WO-KR002081.
XX 09-OCT-2002; 2002KR-00061589.
XX (CIBC-) CID CO LTD.
XX (LEES/) LEE S H.
XX Lee SH, Lee Y, Yun S;
XX WPI; 2004-340933/31.
XX New Japanese encephalitis virus genomic RNA, useful in developing
PT vaccines for and in diagnosing and treating Japanese encephalitis.
XX Claim 12; Page 232-245; 265pp; English.
XX The present invention relates to a genomic RNA of the Korean Japanese
CC Encephalitis Virus (JEV) isolate, composed of a 5' and 3' nontranslated
CC region (NTR) and a single polypeptide coding region. The JEV genomic RNA,
CC JEV cDNA and reagents are useful in developing vaccines for and in
CC diagnosing and treating Japanese encephalitis. The present sequence is a
CC sequence of the invention.
XX SQ Sequence 19038 BP; 5059 A; 4310 C; 5055 G; 4614 T; 0 U; 0 Other;

Query Match 93.3%; Score 22.4; DB 12; Length 19038;
Best Local Similarity 95.8%; Pred. No. 1.2;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTCTCTGAGGGCTTAC 24
Db 10573 TCCGAGACGGTCTCTGAGGGCTTTC 10550

RESULT 22
ADO07470/c
ID ADO07470 standard; DNA; 19040 BP.
XX AC ADO07470;
XX 15-JUL-2004 (first entry)
XX Japanese Encephalitis virus JEV coding sequence SEQ ID NO: 48.
XX antiinflammatory; neuroprotective; gene therapy;
KW Japanese Encephalitis virus; JEV; ds; gene; vaccine;
KW Japanese encephalitis.
XX OS Japanese encephalitis virus.
XX WO2004033690-A1.
XX 22-APR-2004.
XX 09-OCT-2003; 2003WO-KR002081.
XX 09-OCT-2002; 2002KR-00061589.
XX (CIBC-) CID CO LTD.
XX (LEES/) LEE S H.
XX Lee SH, Lee Y, Yun S;
XX WPI; 2004-340933/31.
XX New Japanese encephalitis virus genomic RNA, useful in developing
PT vaccines for and in diagnosing and treating Japanese encephalitis.

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XX

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Query Match          91.7%; Score 22; DB 12; Length 49;
Best Local Similarity 100.0%; Pred. No. 0.82;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCCGAGACGGTCTGAGGGCTT 22
DB      28 TCCGAGACGGTCTGAGGGCTT 49

RESULT 25
ADN36827
ID      ADN36827 standard; RNA; 23 BP.
XX
AC
XX
XX
DT      15-JUL-2004 (first entry)
XX
XX      West Nile virus detection-related oligonucleotide probe SeqID149.
XX
XX      hybridisation assay probe; nucleic acid detection;
KW      target-complementary sequence; flavivirus; West Nile virus; WNV;
KW      RNA virus; infection; meningitis; encephalitis;
KW      high throughput screening; probe; ss.
XX
OS      West Nile virus.
XX
PH      Key          Location/Qualifiers
FT      modified_base 1..23      /*tag= a
FT      /mod_base= OTHER
FT      /note= "OTHER= 2'-methoxyethoxy (2'-MOE) nucleotides"
XX
PN      W02004036190-A2.
XX
PD      29-APR-2004.
XX
XX      10-OCT-2003; 2003WO-US033639.
XX
XX      16-OCT-2002; 2002US-0418991P.
PR
XX      25-NOV-2002; 2002US-0429006P.
PR
XX      24-FEB-2003; 2003US-0449810P.
XX
XX      (GENP-) GEN-PROBE INC.
XX
XX      Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
PI
XX
XX      WPI; 2004-389590/36.
DR
XX
XX      New hybridization assay probe comprising target-complementary sequence of
PT      bases, useful in detecting flavivirus, e.g. West Nile virus.
PT
XX
XX      Example 1; SEQ ID NO 149; 135pp; English.
PS
XX
XX      This invention relates to a novel hybridisation assay probe, for
CC      detecting a nucleic acid, which is a probe sequence that comprises a
CC      target-complementary sequence of bases, and optionally one or more base
CC      sequences that are not complementary to the nucleic acid that is to be
CC      detected. The hybridisation assay probes and the kits are useful in
CC      detecting and amplifying a target nucleic acid sequence, for example
CC      flavivirus like West Nile virus, that may be present in a biological
CC      sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC      birds and culex mosquitoes, with humans and horses serving as incidental
CC      hosts. Infection of humans can lead to meningitis or encephalitis. The
CC      invention may allow for accurate and efficient high throughput screening.
CC      The present sequence is that of an oligonucleotide probe which is related
CC      to the invention.
XX
SQ      Sequence 23 BP; 5 A; 4 C; 8 G; 0 T; 6 U; 0 Other;

Query Match          87.5%; Score 21; DB 12; Length 23;
Best Local Similarity 76.2%; Pred. No. 2.3;
Matches 16; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      4 GAGACGGTCTGAGGGCTTAC 24
DB      1 GAGACGGUUCUGAGGGCUUAC 21

RESULT 26
ABL50890/c
ID      ABL50890 standard; RNA; 10976 BP.
XX
XX
AC      ABL50890;
XX
XX      23-JUN-2002 (first entry)
XX
XX      Japanese encephalitis virus strain SA14-14-2 polypotein RNA sequence.
DE
XX
XX      Japanese encephalitis virus strain SA14-14-2; polypotein; vaccine; gene;
KW      ss.
XX
XX      Japanese encephalitis virus.
OS
XX
XX      Key          Location/Qualifiers
PH      5'UTR      1..95      Location/Qualifiers
FT      /*tag= a
FT      96..10394
FT      /*tag= b
FT      /product= "polypotein"
FT      mat_peptide 96..476
FT      /*tag= c
FT      /product= "capsid protein"
FT      /note= "C"
FT      477..977
FT      /*tag= d
FT      /product= "premembrane/membrane protein"
FT      /note= "BrM/M"
FT      mat_peptide 978..2477
FT      /*tag= e
FT      /product= "envelope glycoprotein"
FT      /note= "E"
FT      2478..3722
FT      /*tag= f
FT      /product= "nonstructural protein 1"
FT      /note= "NS1"
FT      3723..4214
FT      /*tag= g
FT      /product= "nonstructural protein 2A"
FT      /note= "NS2A"
FT      4215..4607
FT      /*tag= h
FT      /product= "nonstructural protein 2B"
FT      /note= "NS2B"
FT      4608..6464
FT      /*tag= i
FT      /product= "nonstructural protein 3"
FT      /note= "NS3"
FT      6465..7265
FT      /*tag= j
FT      /product= "nonstructural protein 4A"
FT      /note= "NS4A"
FT      7266..10391
FT      /*tag= k
FT      /product= "nonstructural protein 4B"
FT      /note= "NS4B"
FT      10395..10976
FT      /*tag= l
FT      /product= "nonstructural protein 5"
FT      /note= "NS5"
FT      10395..10976
FT      /*tag= m
XX
XX      3'UTR
XX
XX      KR99038070-A.
PN
XX      05-JUN-1999.
PD
```


CC detecting and amplifying a target nucleic acid sequence, for example
 CC flavivirus like West Nile virus, that may be present in a biological
 CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
 CC birds and culex mosquitoes, with humans and horses serving as incidental
 CC hosts. Infection of humans can lead to meningitis or encephalitis. The
 CC invention may allow for accurate and efficient high throughput screening.
 CC The present sequence is that of an oligonucleotide probe which is related
 CC to the invention.

XX SQ Sequence 87 BP; 23 A; 25 C; 26 G; 13 T; 0 U; 0 Other;

Query Match: 79.2%; Score 19; DB 12; Length 87;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GACGGTCTGAGGGCTTAC 24
 |||||
 DB 87 GACGGTCTGAGGGCTTAC 69

RESULT 29
 ADD31012/c
 ID ADD31012 standard; cDNA; 1661 BP.

XX AC ADD31012;

XX DT 15-JAN-2004 (first entry)

XX DE Plant yield-related polynucleotide clone G631.

XX KW db; transcription factor; transgenic plant; growth rate; senescence;
 XX seed germination rate; plant vigor; seedling vigor.

XX OS Arabidopsis thaliana.

XX PN WO2003013227-A2.

XX PD 20-FEB-2003.

XX PF 09-AUG-2002; 2002WO-US025805.

XX PR 09-AUG-2001; 2001US-0310847P.

XX PR 11-NOV-2001; 2001US-0336049P.

XX PR 11-DEC-2001; 2001US-0338692P.

XX PR 14-JUN-2002; 2002US-00171468.

XX PA (MEND-) MENDEL BIOTECHNOLOGY INC.

XX PI Ratcliffe O, Riechmann JL, Adam LJ, Dubell AT, Heard JE;
 XX PI Pilgrim ML, Jiang C, Reuber TL, Creelman RA, Pineda O, Yu G;
 XX PI Broun PE;

XX DR WPI; 2003-248221/24.

XX DR P-PSDB; ADD31013.

XX PT New plant transcription factor polynucleotides and polypeptides, useful
 XX in producing transgenic plants with commercially valuable properties,
 XX PT such as an alteration in a plant growth characteristic, e.g. growth rate
 XX or apomixis.

XX PS Disclosure; SEQ ID NO 1041; 454pp; English.

XX CC The invention relates to a number of isolated Arabidopsis thaliana cDNA
 CC sequences and their encoded proteins which are especially transcription
 CC factor related cDNAs and proteins. The isolated or recombinant plant
 CC transcription factor polynucleotides and polypeptides are useful in
 CC producing transgenic plants with commercially valuable properties, i.e.
 CC modified or altered desirable traits as compared to a reference plant,
 CC such as an alteration in a plant growth characteristic, e.g. growth rate,
 CC germination rate of seeds, vigor of plants and seedlings, or leaf and
 CC flower senescence. Sequence information related to the polynucleotides
 CC and polypeptides can also be used in bioinformatic search methods. The
 CC transgenic plant is useful for growing a progeny plant from a parent

CC plant. This sequence represents one of the cDNAs of the invention.
 XX SQ Sequence 1661 BP; 474 A; 379 C; 344 G; 464 T; 0 U; 0 Other;

Query Match: 73.3%; Score 17.6; DB 10; Length 1661;
 Best Local Similarity 83.3%; Pred. No. 1.8e+02;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTGAGGGCTTAC 24
 |||||
 DB 610 TCCAGTCGGTCTGATGGCTCAC 587

RESULT 30
 ADI43924/c
 ID ADI43924 standard; DNA; 1661 BP.

XX AC ADI43924;

XX DT 22-APR-2004 (first entry)

XX DE Plant transcription factor related polynucleotide #1551.

XX KW transgenic; plant; enhanced tolerance to abiotic stress;
 KW glycosphate tolerance; hormone sensitivity; disease resistance;
 KW sugar sensing; flowering; flower structure; stem bifurcation;
 KW branching pattern; apical dominance; trichome; stem morphology;
 KW root growth; root hair; seed development; cell proliferation;
 KW cell differentiation; premature senescence; necrosis; plant size;
 KW leaf morphology; seed morphology; seed biochemistry; root anthocyanin;
 KW plant anthocyanin; light response; shade avoidance; bioinformatic;
 KW transcription factor; ds.

XX OS Unidentified.

XX PN US2004019927-A1.

XX PD 29-JAN-2004.

XX PF 25-FEB-2003; 2003US-00374780.

XX PR 18-APR-2001; 2001US-00837944.

XX PA (SHER/) SHERMAN B K.

XX PA (RIEC/) RIECHMANN J L.

XX PA (JIAN/) JIANG C.

XX PA (HEAR/) HEARD J E.

XX PA (HAAR/) HAARKE V.

XX PA (CREB/) CREELMAN R A.

XX PA (RATC/) RATCLIFFE O.

XX PA (ADAM/) ADAM L J.

XX PA (REUB/) REUBER T L.

XX PA (KEDD/) KEDDIE J.

XX PA (BROU/) BROUN P E.

XX PA (PILG/) PILGRIM M L.

XX PA (DUBE/) DUBELL A N.

XX PA (PINE/) PINEDA O.

XX PA (YUGG/) YU G.

XX PI Sherman BK, Riechmann JL, Jiang C, Heard JE, Haake V;
 XX PI Creelman RA, Ratcliffe O, Adam LJ, Reuber TL, Keddie J, Broun PE;
 XX PI Pilgrim ML, Dubell AN, Pineda O, Yu G;
 XX WPI; 2004-132245/13.
 XX P-PSDB; ADI43925.

XX CC New transgenic plant comprising a recombinant polynucleotide of any one
 XX PT of more than 500 nucleotide sequences, useful in bioinformatic search
 XX methods.
 XX PS Disclosure; SEQ ID NO 2387; 435pp; English.
 XX CC The invention describes a transgenic plant comprising a recombinant

CC polynucleotide of any one of more than 500 nucleotide sequences fully
 CC defined in the specification or its complement. The method of the
 CC invention can be used to produced a plant having altered traits such as:
 CC enhanced tolerance to abiotic stress; glyphosphate tolerance; hormone
 CC sensitivity; disease resistance; sugar sensing; early or late flowering;
 CC altered flower structure, change in stem bifurcations, altered branching
 CC pattern, reduced apical dominance, reduced trichome density; lack of
 CC trichomes; reduced ectopic trichome development; altered trichome
 CC development; increase in trichome number; altered stem morphology;
 CC increased root growth; increased root hairs; altered seed development;
 CC altered cell proliferation or cell differentiation; rapid development;
 CC premature senescence; increased necrosis; increase in seedling or plant
 CC size; decreased plant size; leaf morphology; seed morphology; seed
 CC biochemistry; increase in root anthocyanins; increase in plant
 CC anthocyanins, or alteration in light response or shade avoidance. The
 CC transgenic plant, polynucleotides and polypeptides are useful in
 CC bioinformatic search methods. This sequence represents a plant
 CC transcription factor related polynucleotide.

SQ Sequence 1661 BP; 474 A; 379 C; 344 G; 464 T; 0 U; 0 Other;
 Query Match 73.3%; Score 17.6; DB 12; Length 1661;
 Best Local Similarity 83.3%; Pred. No. 1.8e+02;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGCGGTTCTGAGGGCTTAC 24
 Db 610 TCCAAATCGGTTCTGAGGCTCAC 587

RESULT 31
 ADI61330/c
 ID ADI61330 standard; cDNA; 1661 BP.
 XX AC ADI61330;
 XX XX
 DT 22-APR-2004 (first entry)
 DE cDNA encoding A. thaliana novel transcription factor (TF) #15.
 XX Plant; transcription factor; TF; plant trait; gene; ss.
 KW Arabidopsis thaliana.
 OS Arabidopsis thaliana.
 XX US2003229915-A1.
 XX PD 11-DEC-2003.
 XX PF 22-NOV-2002; 2002US-00302267.
 XX PR 18-FEB-1999; 99US-0120880P.
 PR 22-FEB-1999; 99US-0121037P.
 PR 11-MAR-1999; 99US-0124278P.
 PR 15-APR-1999; 99US-0129450P.
 PR 20-MAY-1999; 99US-0135134P.
 PR 15-JUL-1999; 99US-0144153P.
 PR 22-OCT-1999; 99US-0161143P.
 PR 01-NOV-1999; 99US-0162556P.
 PR 17-FEB-2000; 2000US-00506720.
 XX (KEDD/) KEDDIE J.
 PA (FROM/) FROMM M.
 PA (HEAR/) HEARD J.
 PA (RIEC/) RIECHMANN J L.
 PA (ADAM/) ADAM L.
 PA (BROU/) BROUN P.
 PA (PINE/) PINEDA O.
 PA (REUB/) REUBER L.
 PA (ZHAN/) ZHANG J.
 PA (YUGG/) YU G.
 PA (JIAN/) JIANG C.
 PA (SAMA/) SAMAHA R.
 PA (PILG/) PILGRIM M.

PA (CREE/) CREELMAN R.
 XX Keddle J, Fromm M, Heard J, Riechmann JL, Adam L, Broun P;
 PI Pineda O, Reuber L, Zhang J, Yu G, Jiang C, Samaha R, Pilgrim M;
 PI Creelman R;
 XX WPI: 2004-052052/05.
 DR P-PSDB; ADI61331.
 XX New polynucleotide, useful in screening for a transcription factor that
 PT modifies a plant trait.
 PS Claim 1; SEQ ID NO 29; 16pp; English.
 XX The present invention relates to the isolation of novel plant
 CC (arabidopsis thaliana) polynucleotide sequences that encode transcription
 CC factors (TFs), and the polypeptide sequences for the TFs. The
 CC polynucleotide sequences are useful in screening for a transcription
 CC factor that modifies a plant trait. Also disclosed is an expression
 CC vector comprising a TF polynucleotide sequence, a host cell comprising
 CC the expression vector, a transgenic plant comprising or ectopically
 CC expressing an isolated TF polynucleotide sequence, a method for screening
 CC for a molecule that modifies a plant trait, a method for producing a
 CC transgenic plant, a method for identifying a sequence homologous to a TF
 CC polynucleotide or polypeptide sequence, and a method for screening for a
 CC transcription factor that modifies a plant trait. The present sequence
 CC encodes a novel A. thaliana TF of the invention. Note: The sequence data
 CC for this patent did not form part of the printed specification. The
 CC complete sequence data for this patent was obtained in electronic format
 CC directly from the USPTO web site at seqdata.uspto.gov.

XX SQ Sequence 1661 BP; 474 A; 379 C; 344 G; 464 T; 0 U; 0 Other;
 Query Match 73.3%; Score 17.6; DB 12; Length 1661;
 Best Local Similarity 83.3%; Pred. No. 1.8e+02;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGCGGTTCTGAGGGCTTAC 24
 Db 610 TCCAAATCGGTTCTGAGGCTCAC 587

RESULT 32
 ADO01998/c
 ID ADO01998 standard; cDNA; 1661 BP.
 XX AC ADO01998;
 XX XX
 DT 01-JUL-2004 (first entry)
 DE Thalecress transcription factor cDNA #206.
 XX Thalecress; transcription factor; ss; gene; plant; transgenic;
 KW abiotic stress; cold tolerance; heat tolerance; drought; osmotic stress;
 KW phosphate limitation; potassium limitation; nitrogen limitation;
 KW hormone sensitivity; disease resistance; sugar sensing; seed germination;
 KW flowering; inflorescence architectural change;
 KW meristem cell differentiation; phyllotaxy; apical dominance;
 KW trichome development; seed development; premature senescence;
 KW delayed senescence; lethality; necrosis; plant size; leaf morphology;
 KW seed morphology; secondary metabolism; light response; shade avoidance.
 XX Arabidopsis thaliana.
 OS Arabidopsis thaliana.
 XX US2004045049-A1.
 XX PD 04-MAR-2004.
 XX PF 10-APR-2003; 2003US-00412699.
 XX PR 13-SEP-1999; 99US-00394519.
 PR 21-JAN-2000; 2000US-00489376.
 PR 17-FEB-2000; 2000US-00506720.

PR 22-MAR-2000; 2000US-00532591.
 PR 22-MAR-2000; 2000US-00533029.
 PR 22-MAR-2000; 2000US-00533030.
 PR 22-MAR-2000; 2000US-00533392.
 PR 22-MAR-2000; 2000US-00533648.
 PR 06-APR-2000; 2000WO-US0009448.
 PR 16-NOV-2000; 2000US-00713394.
 PR 27-MAR-2001; 2001US-00819142.
 PR 17-APR-2001; 2001US-00837444.
 PR 30-JAN-2002; 2002US-00958131.
 PR 14-JUN-2002; 2002US-00171468.
 PR 09-AUG-2002; 2002US-00225066.
 PR 09-AUG-2002; 2002US-00225067.
 PR 09-AUG-2002; 2002US-00225068.
 PR 17-DEC-2002; 2002US-0434166P.
 PR 25-FEB-2003; 2003US-00374780.
 XX
 PA (ZHAN/) ZHANG J.
 PA (FROM/) FROMM M E.
 PA (HEAR/) HEARD J E.
 PA (RIEC/) RIECHMANN J L.
 PA (ADAM/) ADAM L J.
 PA (BROU/) BROUN P E.
 PA (FINE/) PINEDA O.
 PA (REUB/) REUBER T L.
 PA (KEDD/) KEDDIE J S.
 PA (YUGG/) YU G.
 PA (JIAN/) JIANG C.
 PA (SAMA/) SAMAHA R S.
 PA (FILG/) FILGRIM M L.
 PA (CREE/) CREELMAN R A.
 PA (DUBE/) DUBELL A N.
 PA (RATC/) RATCLIFFE O.
 PA (KUMI/) KUMIMOTO R.
 PA (SHER/) SHERMAN B K.
 XX
 PI Zhang J, Fromm ME, Heard JE, Riechmann JL, Adam LJ, Broun PE;
 PI Pineda O, Reuber TL, Keddie JS, Yu G, Jiang C, Samaha RS;
 PI Pilgrim ML, Creelman RA, Dubell AN, Ratcliffe O, Kumimoto R;
 PI Sherman BK;
 XX
 DR WPI; 2004-225755/21.
 DR P-PSDB; ADO01999.
 XX
 PT New transgenic plant, useful in developing phenotypes with altered or
 PT improved characteristics or traits.
 XX
 PS Claim 1; SEQ ID NO 411; 213pp; English.
 XX
 CC The invention relates to a transgenic plant comprises a recombinant
 CC polynucleotide having a polynucleotide sequence or its complementary
 CC sequence comprising a sequence encoding a polypeptide, that initiates
 CC transcription (i.e. a transcription factor) from Arabidopsis, Soybean,
 CC Rice, Rape or Corn, comprising any of the sequences appearing as ADO01588
 CC -ADO03527 or ADO03530-ADO03559. Also included are using a transgenic
 CC plant to grow a progeny plant, an expression cassette (comprising a
 CC constitutive, inducible or tissue-specific promoter and a recombinant
 CC polynucleotide described above), a host cell comprising the expression
 CC cassette, producing a modified plant having a modified trait, identifying
 CC a factor that is modulated by or interacts with a polypeptide encoded by
 CC the polynucleotide sequence and identifying at least one downstream
 CC polynucleotide sequence that is subject to a regulatory effect of any of
 CC the polypeptides encoded by the polynucleotide described above. The
 CC transgenic plant is useful for producing a plant that has an altered
 CC trait e.g. an enhanced tolerance to abiotic stress (increased tolerance
 CC to chilling, germination in cold conditions, freezing tolerance, tolerance
 CC to heat, tolerance to drought, tolerance to osmotic stress, tolerance to
 CC salt, tolerance to phosphate limitation, tolerance to potassium
 CC limitation, decreased sensitivity to nitrogen limitation), altered
 CC hormone sensitivity, reduced sensitivity to abscisic acid, an altered
 CC response to ethylene, disease resistance, altered susceptibility to
 CC Botrytis, altered susceptibility to Fusarium, altered susceptibility to
 CC Erysiphe, altered susceptibility to Pseudomonas syringae, altered

CC susceptibility to Sclerotinia, altered sugar sensing, improved seed
 CC germination and seedling vigor, early flowering, late flowering, extended
 CC period of flowering, an inflorescence architectural change, a change in
 CC stem bifurcations, a lack of a shoot meristem, reduced meristem cell
 CC differentiation, altered phyllotaxy, altered branching pattern, reduced
 CC apical dominance, reduced trichome density, ectopic trichome development,
 CC altered trichome development, altered stem morphology, increased root
 CC growth, increased root hairs, altered seed development, delayed cell
 CC proliferation/cell differentiation, premature senescence, increased
 CC senescence, lethality, increased necrosis, an increase in seedling or
 CC plant size, decreased plant size, a change in leaf morphology, increased
 CC altered leaf development, increased leaf size and mass, glossy leaves,
 CC leaf cell expansion, change in seed morphology, altered seed coloration,
 CC increased seed size, decreased seed size, altered seed shape, change in
 CC leaf biochemistry, increased leaf wax, an alteration in leaf prenyl lipid
 CC content, increased leaf insoluble sugars, decreased leaf insoluble
 CC sugars, increased leaf anthocyanins, an alteration of leaf fatty acid
 CC content, an alteration of leaf glucosinolate content, change in seed
 CC biochemistry, an increase in seed oil content, decrease in seed oil
 CC content, increase in seed fatty acid content, decrease in seed fatty acid
 CC content, increase in seed protein content, decrease in seed protein
 CC content, alteration in seed prenyl lipid content, increase in seed
 CC sterols, upregulation of genes involved in secondary metabolism, increase
 CC in root anthocyanins, increase in plant anthocyanins, and alteration in
 CC light response or shade avoidance. The present sequence encodes a
 CC thalaeal transcription factor of the invention.
 XX
 SQ Sequence 1661 BP; 474 A; 379 C; 344 G; 464 T; 0 U; 0 Other;

Query Match 73.3%; Score 17.6; DB 12; Length 1661;
 Best Local Similarity 83.3%; Pred. No. 1.8e+02;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGACGCGTCTCTGAGGCTTAC 24
 DB 610 TCCAGTCGGTCTGTATGGCTCAC 587

RESULT 33

AAC36549/C

ID AAC36549 standard; DNA; 1823 BP.

XX AAC36549;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 14214.

KW Hybridisation assay; genetic mapping; gene expression control;
 KW protein identification; signal transduction pathway; metabolic pathway;
 KW promoter; termination sequence; ss.

OS Arabidopsis thaliana.

XX EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.

PR 05-MAR-1999; 99US-0123180P.

PR 09-MAR-1999; 99US-0123548P.

PR 23-MAR-1999; 99US-0125788P.

PR 25-MAR-1999; 99US-0126264P.

PR 01-APR-1999; 99US-0126785P.

PR 06-APR-1999; 99US-0127462P.

PR 08-APR-1999; 99US-0128234P.

PR 16-APR-1999; 99US-0128714P.

PR 19-APR-1999; 99US-0130077P.

PR 21-APR-1999; 99US-0130449P.

PR 23-APR-1999; 99US-0130510P.

PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-01322407P.
PR 04-MAY-1999; 99US-01322484P.
PR 05-MAY-1999; 99US-01322486P.
PR 06-MAY-1999; 99US-01322487P.
PR 06-MAY-1999; 99US-01322487P.
PR 07-MAY-1999; 99US-0132263P.
PR 11-MAY-1999; 99US-01334256P.
PR 14-MAY-1999; 99US-01334218P.
PR 14-MAY-1999; 99US-01334219P.
PR 14-MAY-1999; 99US-01334221P.
PR 14-MAY-1999; 99US-01334370P.
PR 18-MAY-1999; 99US-01334768P.
PR 19-MAY-1999; 99US-01334941P.
PR 20-MAY-1999; 99US-01335124P.
PR 21-MAY-1999; 99US-01335353P.
PR 24-MAY-1999; 99US-01335629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 24-JUN-1999; 99US-0140695P.
PR 24-JUN-1999; 99US-0140823P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-01444632P.

PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 05-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 06-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.


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PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161320P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 73.3%; Score 17.6; DB 3; Length 1823;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTTGAGGGCTTAC 24
    ||| ||||| ||||| |||||
Db 673 TCCAGTCGGTCTTGATGGCTCAC 650

RESULT 34
ID AAC35016/c
ID AAC35016 standard; DNA; 1823 BP.
XX
AC AAC35016;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 8703.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 25-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.

99US-0132487P.
99US-0132863P.
99US-0134256P.
99US-0134218P.
99US-0134219P.
99US-0134221P.
99US-0134370P.
99US-0134768P.
99US-0134941P.
99US-0135124P.
99US-0135353P.
99US-0135629P.
99US-0136021P.
99US-0136392P.
99US-0136782P.
99US-0137222P.
99US-0137528P.
99US-0137724P.
99US-0138094P.
99US-0138540P.
99US-0138847P.
99US-0139119P.
99US-0139452P.
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99US-0139457P.
99US-0139458P.
99US-0139459P.
99US-0139460P.
99US-0139461P.
99US-0139462P.
99US-0139463P.
99US-0139750P.
99US-0139763P.
99US-0139817P.
99US-0139899P.
99US-0140353P.
99US-0140354P.
99US-0140695P.
99US-0140823P.
99US-0140991P.
99US-0141287P.
99US-0141842P.
99US-0142154P.
99US-0142055P.
99US-0142390P.
99US-0142803P.
99US-0142920P.
99US-0142977P.
99US-0143542P.
99US-0143624P.
99US-0144005P.
99US-0144085P.
99US-0144086P.
99US-0144325P.
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99US-0144332P.
99US-0144333P.
99US-0144334P.
99US-0144335P.
99US-0144352P.
99US-0144632P.
99US-0144884P.
99US-0144814P.
99US-0145086P.
99US-0145088P.
99US-0145085P.
99US-0145087P.
99US-0145089P.

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PR	22-JUL-1999,	99US-014519229,
PR	23-JUL-1999,	99US-014514549,
PR	23-JUL-1999,	99US-014521818,
PR	23-JUL-1999,	99US-014522449,
PR	23-JUL-1999,	99US-014522449,
PR	26-JUL-1999,	99US-014527618,
PR	27-JUL-1999,	99US-014581313,
PR	27-JUL-1999,	99US-014591899,
PR	27-JUL-1999,	99US-014591899,
PR	28-JUL-1999,	99US-014595118,
PR	28-JUL-1999,	99US-014638618,
PR	02-AUG-1999,	99US-014638888,
PR	02-AUG-1999,	99US-014638889,
PR	03-AUG-1999,	99US-014703889,
PR	04-AUG-1999,	99US-014720449,
PR	04-AUG-1999,	99US-014730249,
PR	05-AUG-1999,	99US-014719218,
PR	05-AUG-1999,	99US-014726018,
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PR	06-AUG-1999,	99US-014741618,
PR	09-AUG-1999,	99US-014749318,
PR	09-AUG-1999,	99US-014793518,
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PR	11-AUG-1999,	99US-014831918,
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PR	13-AUG-1999,	99US-014856518,
PR	13-AUG-1999,	99US-014868418,
PR	16-AUG-1999,	99US-014936818,
PR	17-AUG-1999,	99US-014917518,
PR	18-AUG-1999,	99US-014942618,
PR	20-AUG-1999,	99US-014972218,
PR	20-AUG-1999,	99US-014972318,
PR	20-AUG-1999,	99US-014992918,
PR	23-AUG-1999,	99US-014990218,
PR	23-AUG-1999,	99US-014993018,
PR	23-AUG-1999,	99US-015056618,
PR	26-AUG-1999,	99US-015088418,
PR	27-AUG-1999,	99US-015106518,
PR	27-AUG-1999,	99US-015106618,
PR	27-AUG-1999,	99US-015108018,
PR	30-AUG-1999,	99US-015130318,
PR	31-AUG-1999,	99US-015134388,
PR	01-SEP-1999,	99US-015193018,
PR	07-SEP-1999,	99US-015236318,
PR	10-SEP-1999,	99US-015307018,
PR	13-SEP-1999,	99US-015375818,
PR	16-SEP-1999,	99US-015401818,
PR	16-SEP-1999,	99US-015403918,
PR	20-SEP-1999,	99US-015477918,
PR	22-SEP-1999,	99US-015711718,
PR	05-OCT-1999,	99US-015775318,
PR	06-OCT-1999,	99US-015786518,
PR	07-OCT-1999,	99US-015802918,
PR	08-OCT-1999,	99US-015823218,
PR	12-OCT-1999,	99US-015836918,
PR	14-OCT-1999,	99US-015933118,
PR	13-OCT-1999,	99US-015929318,
PR	13-OCT-1999,	99US-015929418,
PR	14-OCT-1999,	99US-015963818,
PR	18-OCT-1999,	99US-015958418,
PR	21-OCT-1999,	99US-016074118,
PR	21-OCT-1999,	99US-016076718,
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PR	21-OCT-1999,	99US-016077018,
PR	21-OCT-1999,	99US-016081418,

PR	21-OCT-1999;	99US-0160815P.
PR	22-OCT-1999;	99US-0160980P.
PR	22-OCT-1999;	99US-0160981P.
PR	22-OCT-1999;	99US-0160989P.
PR	25-OCT-1999;	99US-0161404P.
PR	25-OCT-1999;	99US-0161405P.
PR	25-OCT-1999;	99US-0161406P.
PR	26-OCT-1999;	99US-0161359P.
PR	26-OCT-1999;	99US-0161360P.
PR	26-OCT-1999;	99US-0161361P.
PR	28-OCT-1999;	99US-0161920P.
PR	28-OCT-1999;	99US-0161932P.
PR	28-OCT-1999;	99US-0161933P.
PR	29-OCT-1999;	99US-0162142P.

Query Match	73.3%;	Score 17
Best Local Similarity	83.3%;	Prod. No.
Matches 20;	Conservative	0; Mismat

Qy	1	TCCGAGACGGTCTTGAGGGCTTAC	24
Db	673	TCCAGTCCGGTCTTGATGGCTCAC	650

RESULT 35
ACN03369/c
ID ACN03369 standard; RNA; 17 BP.
XX AC ACN03369;
XX AC ACN03369;
XX DT 22-APR-2004 (first entry)
XX WNV Inozyme substrate SEQ ID NO 3372.
XX WNV; West Nile Virus; antiinflammatory
XX virucide; neuroprotective; antibacter
XX encephalitis; myocarditis; meningitis
XX liver failure; cancer; cirrhosis; Ham
XX Amberzyme; Zinzyne; ss.
XX OS West Nile Virus.
XX W0200268637-A2.
XX PD 06-SEP-2002.
XX PF 19-OCT-2001; 2001WO-US048350.
XX PR 20-OCT-2000; 2000US-0242411P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (BLAT/) BLATT L.
XX PA (MCSW/) MCSWIGGEN J A.
XX PI Blatt L, Mcswiggen JA;
XX DR WPI; 2002-706994/76.
XX New nucleic acid molecule that modula
XX (WNV), useful for treating a conditio
XX pancreatitis, meningitis, hepatocellu
XX Claim 23; SEQ ID NO 3372; 495pp; Engl
XX The invention relates to nucleic acid
XX of the West Nile Virus (WNV). The nuc
XX treating a condition related to WNV i
XX encephalitis, myocarditis, meningitis
XX liver failure, hepatocellular carcino
XX molecule is selected from the group o
XX Hammerhead, Inozyme, G-cleaver, DNaz
XX nucleic acid molecules further compr
XX least ten 2'-O-methyl modifications.

CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3', inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention

XX SQ Sequence 17 BP; 4 A; 6 C; 4 G; 0 T; 3 U; 0 Other;

Query Match 70.8%; Score 17; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTTCTGAG 17
 Db 17 TCCGAGACGGTTCTGAG 1

RESULT 36

ACN05431/c
 ID ACN05431 standard; RNA; 17 BP.

XX AC ACN05431;

XX DT 22-APR-2004 (first entry)

XX DE WNV DNzyme substrate SEQ ID NO 5434.

XX KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNzyme;
 KW Amberzyme; Zinzyme; ss.

XX OS West Nile Virus.

XX PN WO200268637-A2.

XX PD 06-SEP-2002.

XX PF 19-OCT-2001; 2001WO-US048350.

XX PR 20-OCT-2000; 2000US-0242411P.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PA (BLAT/) BLATT L.

XX PA (MCSW/) MCSWIGGEN J A.

XX PI Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.

XX CC New nucleic acid molecule that modulates replication of West Nile Virus
 PT (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX PS Claim 23; SEQ ID NO 5434; 495pp; English.

XX CC The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNzyme, Amberzyme and Zinzyme. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3', inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention

XX SQ Sequence 17 BP; 3 A; 8 C; 3 G; 0 T; 3 U; 0 Other;

Query Match 70.8%; Score 17; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CGAGACGGTTCTGAGG 19
 Db 17 CGAGACGGTTCTGAGG 1

RESULT 37

ACN07305/c

ID ACN07305 standard; RNA; 17 BP.

XX AC ACN07305;

XX DT 22-APR-2004 (first entry)

XX DE WNV Amberzyme substrate SEQ ID NO 7308.

XX KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNzyme;
 KW Amberzyme; Zinzyme; ss.

XX OS West Nile Virus.

XX PN WO200268637-A2.

XX PD 06-SEP-2002.

XX PF 19-OCT-2001; 2001WO-US048350.

XX PR 20-OCT-2000; 2000US-0242411P.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PA (BLAT/) BLATT L.

XX PA (MCSW/) MCSWIGGEN J A.

XX PI Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.

XX CC New nucleic acid molecule that modulates replication of West Nile Virus
 PT (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX PS Claim 23; SEQ ID NO 7308; 495pp; English.

XX CC The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNzyme, Amberzyme and Zinzyme. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3', inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention

XX SQ Sequence 17 BP; 4 A; 7 C; 3 G; 0 T; 3 U; 0 Other;

Query Match 70.8%; Score 17; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGACGGTTCTGAGGCT 21
 |||||

KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
 KW Amberzyme; Zinzyme; ss.
 XX West Nile Virus.
 OS
 XX WO200268637-A2.
 PN
 XX PD
 XX 06-SEP-2002.
 XX
 XX 19-OCT-2001; 2001WO-US048350.
 XX
 XX 20-OCT-2000; 2000US-0242411P.
 PR
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 XX
 XX Blatt L, Mcswiggen JA;
 PI
 XX WPI; 2002-706994/76.
 DR
 XX
 XX New nucleic acid molecule that modulates replication of West Nile Virus
 PT (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 PT
 XX
 PS Claim 23; SEQ ID NO 3371; 495pp; English.
 XX
 CC The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention
 XX
 SQ Sequence 17 BP; 5 A; 7 C; 3 G; 0 T; 2 U; 0 Other;
 Query Match 70.8%; Score 17; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 GACGGTCTCGAGGCTT 22
 Db 17 GACGGTCTCGAGGCTT 1
 RESULT 41
 ACN12333
 ID ACN12333 standard; RNA; 17 BP.
 XX
 XX ACN12333;
 AC
 DT 22-APR-2004 (first entry)
 XX
 XX WNV minus strand Zinzyme substrate SEQ ID NO 12336.
 DE
 XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
 KW Amberzyme; Zinzyme; ss.
 XX West Nile Virus.
 OS
 XX

PN WO200268637-A2.
 XX
 PD 06-SEP-2002.
 XX
 XX 19-OCT-2001; 2001WO-US048350.
 XX
 XX 20-OCT-2000; 2000US-0242411P.
 PR
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 XX
 XX Blatt L, Mcswiggen JA;
 PI
 XX WPI; 2002-706994/76.
 DR
 XX
 XX New nucleic acid molecule that modulates replication of West Nile Virus
 PT (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 PT
 XX
 PS Claim 23; SEQ ID NO 12336; 495pp; English.
 XX
 CC The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention
 XX
 SQ Sequence 17 BP; 3 A; 4 C; 7 G; 0 T; 3 U; 0 Other;
 Query Match 70.8%; Score 17; DB 6; Length 17;
 Best Local Similarity 82.4%; Pred. No. 1.9e+02;
 Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CCGAGACGGTCTCGAGG 18
 Db 1 CCGAGACGGTCTCGAGG 17
 RESULT 42
 ACN09607
 ID ACN09607 standard; RNA; 17 BP.
 XX
 XX ACN09607;
 AC
 DT 22-APR-2004 (first entry)
 XX
 XX WNV minus strand Inozyme substrate SEQ ID NO 9610.
 DE
 XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
 KW Amberzyme; Zinzyme; ss.
 XX West Nile Virus.
 OS
 XX WO200268637-A2.
 PN
 XX 06-SEP-2002.
 PD
 XX 19-OCT-2001; 2001WO-US048350.
 XX
 XX 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 XX Blatt L, Mcswiggen JA;
 PI
 XX WPI; 2002-706994/76.
 XX New nucleic acid molecule that modulates replication of West Nile Virus
 PT (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 XX Claim 23; SEQ ID NO 9610; 495pp; English.
 XX The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyne. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention
 XX Sequence 17 BP; 2 A; 3 C; 7 G; 0 T; 5 U; 0 Other;
 SQ Query Match 70.8%; Score 17; DB 6; Length 17;
 Best Local Similarity 70.6%; Pred. No. 1.9e+02;
 Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 QY 6 GACGGTTCTGAGGGCTT 22
 DB 1 GACGGUUCUGAGGGCUU 17
 RESULT 43
 ACN03367/c
 ID ACN03367 standard; RNA; 17 BP.
 XX ACN03367;
 XX 22-APR-2004 (first entry)
 XX WNV Inozyme substrate SEQ ID NO 3370.
 XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
 KW Amberzyme; Zinzyne; ss.
 XX West Nile Virus.
 OS WO200268637-A2.
 PN 06-SEP-2002.
 PD 19-OCT-2001; 2001WO-US048350.
 PF 20-OCT-2000; 2000US-0242411P.
 PR (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 XX Blatt L, Mcswiggen JA;
 PI
 XX WPI; 2002-706994/76.
 XX New nucleic acid molecule that modulates replication of West Nile Virus
 PT (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 XX Claim 23; SEQ ID NO 9610; 495pp; English.

DR WPI; 2002-706994/76.
 XX New nucleic acid molecule that modulates replication of West Nile Virus
 PT (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 XX Claim 23; SEQ ID NO 3370; 495pp; English.
 XX The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyne. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention
 XX Sequence 17 BP; 5 A; 6 C; 4 G; 0 T; 2 U; 0 Other;
 SQ Query Match 70.8%; Score 17; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 CGGTTCTGAGGGCTTAC 24
 DB 17 CGGTTCTGAGGGCTTAC 1
 RESULT 44
 ACN07446
 ID ACN07446 standard; RNA; 17 BP.
 XX ACN07446;
 XX 22-APR-2004 (first entry)
 XX WNV minus strand Hammerhead Ribozyme substrate SEQ ID NO 7449.
 XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
 KW Amberzyme; Zinzyne; ss.
 XX West Nile Virus.
 OS WO200268637-A2.
 PN 06-SEP-2002.
 PD 19-OCT-2001; 2001WO-US048350.
 PF 20-OCT-2000; 2000US-0242411P.
 PR (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 XX Blatt L, Mcswiggen JA;
 PI
 XX WPI; 2002-706994/76.
 XX New nucleic acid molecule that modulates replication of West Nile Virus
 PT (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 XX Claim 23; SEQ ID NO 7449; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention

XX Sequence 17 BP; 3 A; 3 C; 8 G; 0 T; 3 U; 0 Other;
 SQ

Query Match 70.8%; Score 17; DB 6; Length 17;
 Best Local Similarity 82.4%; Pred. No. 1.9e+02;
 Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGACGGTCTGAGGGC 20
 |||||:|:|:|:|
 Db 1 GAGACGGUUCUGAGGGC 17

RESULT 45
 ACN07447
 ID ACN07447 standard; RNA; 17 BP.
 XX ACN07447;
 AC ACN07447;
 DT 22-APR-2004 (first entry)
 XX WNV minus strand Hammerhead Ribozyme substrate SEQ ID NO 7450.
 DE WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 XX virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
 KW Amberzyme; Zinzyme; ss.
 XX West Nile Virus.
 OS
 XX WO200268637-A2.
 PN
 XX 06-SEP-2002.
 PD
 XX 19-OCT-2001; 2001WO-US048350.
 PF
 XX 20-OCT-2000; 2000US-0242411P.
 PR
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 XX Blatt L, Mcswiggen JA;
 XX WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus
 CC (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX Claim 23; SEQ ID NO 7450; 495pp; English.
 PS
 XX The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of

CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention

XX Sequence 17 BP; 3 A; 3 C; 7 G; 0 T; 4 U; 0 Other;
 SQ

Query Match 70.8%; Score 17; DB 6; Length 17;
 Best Local Similarity 76.5%; Pred. No. 1.9e+02;
 Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 5 AGACGGTCTGAGGGCT 21
 |||||:|:|:|:|
 Db 1 AGACGGUUCUGAGGGCU 17

RESULT 46
 ACN01377/C
 ID ACN01377 standard; RNA; 17 BP.
 XX ACN01377;
 AC ACN01377;
 DT 22-APR-2004 (first entry)
 XX WNV Hammerhead Ribozyme substrate SEQ ID NO 1367.
 DE WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 XX virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
 KW Amberzyme; Zinzyme; ss.
 XX West Nile Virus.
 OS
 XX WO200268637-A2.
 PN
 XX 06-SEP-2002.
 PD
 XX 19-OCT-2001; 2001WO-US048350.
 PF
 XX 20-OCT-2000; 2000US-0242411P.
 PR
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 XX Blatt L, Mcswiggen JA;
 XX WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus
 CC (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX Claim 23; SEQ ID NO 1367; 495pp; English.
 PS
 XX The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid

CC molecule of the invention
 XX Sequence 17 BP; 5 A; 6 C; 3 G; 0 T; 3 U; 0 Other;
 SQ Query Match 70.8%; Score 17; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACGGTTCTGAGGCTTA 23
 DB 17 ACGGTTCTGAGGCTTA 1

RESULT 47
 ACH18165/c
 ID ACH18165 standard; cDNA; 487 BP.
 XX AC ACH18165;
 XX AC ACH18165;
 XX 13-OCT-2003 (first entry)
 XX Human adult heart cDNA #2479.
 DE Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
 KW genome mapping; biodiversity; genetic disorder.
 XX Homo sapiens.
 OS US2003073623-A1.
 PN 17-APR-2003.
 PD 30-JUL-2001; 2001US-00918995.
 PF 30-JUL-2001; 2001US-00918995.
 PR (DRMA/) DRMANAC R T.
 XX (LABAT/) LABAT I.
 PA (STAC/) STACHE-CRAIN B.
 PA (DICK/) DICKSON M C.
 PA (JONE/) JONES L W.
 XX Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
 XX WPI; 2003-615964/58.
 XX New polynucleotide sequences obtained from various cDNA libraries, useful
 PT as hybridization probes, as oligomers for PCR, for chromosome and gene
 PT mapping, in the recombinant production of protein, or in generating
 PT antisense DNA or RNA.
 XX Claim 1; SEQ ID NO 5377; 44pp; English.

CC The invention relates to an isolated polynucleotide comprising any one of
 CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
 CC determined by the technique of SBH (sequencing by hybridisation). Also
 CC included is a purified polypeptide comprising a sequence corresponding to
 CC a reading frame of the novel polynucleotide. The nucleic acid sequences
 CC are useful in diagnostics as expressed sequence tags (EST) for
 CC identifying expressed genes or for physical mapping of the human genome,
 CC in forensics, in assessing biodiversity, or in identifying mutations
 CC responsible for genetic disorders and other traits. The nucleotide
 CC sequences are also useful as hybridisation probes, as oligomers for PCR,
 CC for chromosome and gene mapping, in the recombinant production of
 CC protein, or in generating antisense DNA or RNA. The purified polypeptide
 CC is useful for generating antibodies specific for it. The present sequence
 CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
 CC for this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=20030073623
 XX Sequence 487 BP; 135 A; 140 C; 87 G; 122 T; 0 U; 3 Other;

Query Match 70.0%; Score 16.8; DB 9; Length 487;
 Best Local Similarity 90.0%; Pred. No. 3.8e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTGAGGCG 20
 DB 47 TCCGAGACGGTTCTGAGGCG 28

RESULT 48
 AAV20871
 ID AAV20871 standard; cDNA; 2799 BP.
 XX AC AAV20871;
 XX 16-JUL-1998 (first entry)
 XX Murine phospholipase D 2 (mPLD2) encoding cDNA.
 DE Phospholipase D; PLD; murine; PLD mediator; autoimmune disease;
 KW rheumatoid arthritis; psoriasis; ulcerative colitis; cancer; mPLD2;
 XX inflammatory disease; wound healing; ds.
 OS Mus sp.
 XX Key Location/Qualifiers
 FT CDS 1..2799
 FT /*tag= a
 FT /product= "murine PLD2 protein"
 XX WO9810076-A2.
 XX 12-MAR-1998.
 XX 06-AUG-1997; 97WO-US013919.
 XX 05-SEP-1996; 96US-0025469P.
 XX (ONYX-) ONYX PHARM INC.
 XX Frohman MA, Morris AJ;
 XX WPI; 1998-193626/17.
 XX P-PSDB; AAW53281.
 XX DNA sequence encoding phospholipase D - useful to identify modulators to
 PT treat auto-immune and inflammatory diseases.
 XX Claim 5; Page 57-58; 70pp; English.

CC This cDNA encodes a murine phospholipase D (PLD) 2 (mPLD2) protein. This
 CC can be used in a method for identifying mediators of PLD, which comprises
 CC transfecting a cell line with an expression vector comprising nucleic
 CC acid sequences encoding a PLD protein and culturing the cell line in
 CC culture medium, where the PLD protein is expressed stably. An effective
 CC amount of a compound sufficient to cause a detectable loss in the
 CC catalytic activity of PLD is added to the culture medium, and the loss in
 CC catalytic activity is detected. The PLD proteins are enzymes having
 CC phosphatidylcholine specific PLD activity. The PLD polypeptides which are
 CC perinuclear membrane associated require PI(4,5)P2 for in vitro activity
 CC and is activated by at least 1 G protein. The PLD polypeptides that are
 CC plasma membrane associated, activates cytoskeletal reorganisation
 CC pathways, require PI(4,5)P2 for in vitro activity and does not require
 CC Rac1m cdc42, RhoA, PKC or ARF1 for activation. A PLD mediator can be used
 CC to treat autoimmune or inflammatory diseases, specifically rheumatoid
 CC arthritis, psoriasis and ulcerative colitis. The mediator can also be
 CC used in wound healing and for treating cancer and other diseases
 CC characterised by pathogenic mitogenicity
 XX Sequence 2799 BP; 639 A; 766 C; 762 G; 632 T; 0 U; 0 Other;

Query Match 70.0%; Score 16.8; DB 2; Length 2799;
 Best Local Similarity 90.0%; Pred. No. 4.8e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCGAGACGGTTCTGAGGGCT 21
|||||
Db 444 CCGAGGAGGTTCTGAGGGCT 463

RESULT 49

ADJ67687
ID ADJ67687 standard; DNA; 2802 BP.

XX AC ADJ67687;

XX DT 20-MAY-2004 (first entry)

XX DE Kif1C DNA #3.

XX KW Kif1C; gene; ds; kinesin-like motor protein;
XX BACILLUS anthracis infection; anthrax; antibacterial.

XX OS Unidentified.

XX PN US2004038222-A1.

XX PD 26-FEB-2004.

XX PF 30-SEP-2002; 2002US-00261175.

XX PR 29-SEP-2001; 2001US-0325864P.

XX PA (DIET/) DIETRICH W F.

XX PI (WATT/) WATTERS J W.

XX PI Dietrich WF, Watters JW;

XX DR WPI; 2004-213930/20.

XX Isolated Kif1C nucleic acids that confer resistance to Bacillus anthracis
PT Lethal Toxin, useful for detecting and conferring resistance to anthrax
PT infections.

XX PS Claim 3; SEQ ID NO 3; 80pp; English.

XX The invention relates to an isolated nucleic acid sequence or fragment
CC coding for a modified Kif1C polypeptide, a kinesin-like motor protein.
CC The invention also relates to a method of protecting a cell against
CC Bacillus anthracis infection, comprising administering the nucleic acid
CC to the cell and a method of treating a mammal affected by anthrax,
CC comprising administering the nucleic acid to the mammal or cells of the
CC mammal. The Kif1C nucleic acids may be used as hybridisation probes to
CC detect the presence of similar sequences in a sample and therefore detect
CC resistance to infection. They may also be used to produce the Kif1C
CC polypeptide which may be used in assays to identify modulators of anthrax
CC infection, a modified susceptible Kif1C amino acid sequence or a
CC functional fragment. This sequence represents a Kif1C nucleic acid of the
XX invention.

XX SQ Sequence 2802 BP; 639 A; 769 C; 761 G; 633 T; 0 U; 0 Other;

Query Match 70.0%; Score 16.8; DB 12; Length 2802;
Best Local Similarity 90.0%; Pred. No. 4.8e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCGAGACGGTTCTGAGGGCT 21
|||||
Db 444 CCGAGGAGGTTCTGAGGGCT 463

RESULT 50

AAV20872

ID AAV20872 standard; cDNA; 3374 BP.

XX AC AAV20872;

XX

DT 16-JUL-1998 (first entry)

XX DE Murine phospholipase D 2 (mPLD2) encoding cDNA.

XX KW Phospholipase D; PLD; murine; PLD mediator; autoimmune disease;
XX rheumatoid arthritis; psoriasis; ulcerative colitis; cancer; mPLD2;
XX inflammatory disease; wound healing; ds.

XX OS Mus sp.

XX FH Key Location/Qualifiers
FT CDS 139..2937
FT /*tag= a
FT /product= "murine PLD2 protein"

XX PN W09810076-A2.

XX PD 12-MAR-1998.

XX PF 06-AUG-1997; 97WO-US013919.

XX PR 05-SEP-1996; 96US-0025469P.

XX PA (ONYX-) ONYX PHARM INC.

XX PI Frohman MA, Morris AJ;

XX DR WPI; 1998-193626/17.

XX DR P-PSDB; AAW53281.

XX DNA sequence encoding phospholipase D - useful to identify modulators to
PT treat auto-immune and inflammatory diseases.

XX PS Claim 5; Page 62-66; 70pp; English.

XX This cDNA encodes a murine phospholipase D (PLD) 2 (mPLD2) protein. This
CC can be used in a method for identifying mediators of PLD, which comprises
CC transfecting a cell line with an expression vector comprising nucleic
CC acid sequences encoding a PLD protein and culturing the cell line in
CC culture medium, where the PLD protein is expressed stably. An effective
CC amount of a compound sufficient to cause a detectable loss in the
CC catalytic activity of PLD is added to the culture medium, and the loss in
CC catalytic activity is detected. The PLD proteins are enzymes having
CC perinuclear membrane associated require PI(4,5)P2 for in vitro activity
CC and is activated by at least 1 G protein. The PLD polypeptides that are
CC plasma membrane associated, activates cytoskeletal reorganisation
CC pathways, require PI(4,5)P2 for in vitro activity and does not require
CC Rac1m cdc42, RhoA, PKC or ARF1 for activation. A PLD mediator can be used
CC to treat autoimmune or inflammatory diseases, specifically rheumatoid
CC arthritis, psoriasis and ulcerative colitis. The mediator can also be
CC used in wound healing and for treating cancer and other diseases
CC characterised by pathogenic mitogenicity

XX SQ Sequence 3374 BP; 753 A; 955 C; 905 G; 760 T; 0 U; 1 Other;

Query Match 70.0%; Score 16.8; DB 2; Length 3374;
Best Local Similarity 90.0%; Pred. No. 4.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCGAGACGGTTCTGAGGGCT 21
|||||
Db 582 CCGAGGAGGTTCTGAGGGCT 601

Search completed: March 25, 2005, 11:15:16
Job time : 269.143 secs

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OM nucleic - nucleic search, using sw model

Run on: March 25, 2005, 10:41:57 ; Search time 1788 Seconds
(without alignments)

510.930 Million cell updates/sec

Title: US-10-688-489-75

Perfect score: 24

Sequence: 1 tcgagacggtttctgagggtttac 24

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18.2	75.8	213	4	BM718194
2	18.2	75.8	501	4	BM344555
3	17.8	74.2	463	2	AW569902
4	17.8	74.2	499	2	BE210385
5	17.8	74.2	538	4	BM520888
6	17.8	74.2	542	6	CA853343
7	17.8	74.2	544	4	BM520767
8	17.8	74.2	545	5	BQ080425
9	17.8	74.2	553	5	BQ080423
10	17.8	74.2	554	5	BM954596
11	17.8	74.2	558	4	BM093047
12	17.8	74.2	591	9	AG239356
13	17.8	74.2	655	2	AW309508
14	17.8	74.2	660	4	BI971255
15	17.8	74.2	715	7	CN156862
16	17.8	74.2	761	4	BI971148
17	17.8	74.2	796	9	CC577625
18	17.8	74.2	843	2	AW349137
19	17.8	74.2	928	4	BG166681
20	17.8	74.2	1028	8	BZ177662
21	17.8	74.2	1058	9	CN803040
22	17.6	73.3	251	1	AA193305
23	17.6	73.3	311	1	AA193764
24	17.6	73.3	380	1	AI986900

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BO292360	PM2-AM008	
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BU467230	603372043	
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CD734101	4047540.1	
BU290274	604166906	
BU360919	603584340	
BU455179	603216541	
CA103359	SCBZHR104	
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BU307797	603533776	
BU456386	603217494	
CA217713	SCRUAD113	
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EX816591	Arabidops	
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AL274226	Tetraodon	
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CD586590	RK037A1G0	
AW163071	au91h09.y	
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EX541881	Leishmani	
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BU233467	603410229	
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CA588569	hab65d12.	
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BQ718395	AGENCOURT	
BZ549211	pac81-60	
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CE206168	tigr-g88-	
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CE218594	tigr-g88-	
CE111389	tigr-g88-	
CE015704	tigr-g88-	
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246	16.4	68.3	636	6	CN881360	CN881360 010427AA5	C 319	16.2	67.5	663	6	CD408676	CD408676 Gm ck3517
247	16.4	68.3	639	1	AU239615	AU239615 AU239615	C 320	16.2	67.5	663	8	BH927892	BH927892 odf24h01
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250	16.4	68.3	745	8	CC368431	CC368431 PUEFF33TD	C 323	16.2	67.5	672	2	BB636114	BB636114 BB636114
251	16.4	68.3	784	9	CNS03AFQ	AL2315151 Tetradon	C 324	16.2	67.5	674	7	CF075905	CF075905 Hd mx17.6
252	16.4	68.3	806	9	CC802540	CC802540 ih31d01.b	C 325	16.2	67.5	679	8	AZ824022	AZ824022 2M0098J24
253	16.4	68.3	879	8	BZ990549	BZ990549 PUGIN43TB	C 326	16.2	67.5	681	4	BJ165269	BJ165269 BJ165269
254	16.4	68.3	926	9	CNS03NV1	AL252658 Tetradon	C 327	16.2	67.5	684	6	CD399629	CD399629 Gm ck2131
255	16.4	68.3	965	9	CC734683	CC734683 OGU867TV	C 328	16.2	67.5	685	2	BE974043	BE974043 601680374
256	16.4	68.3	966	5	EX834218	EX834218 EX834218	C 329	16.2	67.5	690	7	CF544450	CF544450 Hd mx17.6
257	16.4	68.3	978	9	CNS037XG	AL231901 Tetradon	C 330	16.2	67.5	690	7	CV432049	CV432049 56870.1 A
258	16.4	68.3	1138	5	BUS55057	BUS55057 AGENCOURT	C 331	16.2	67.5	694	9	AG136438	AG136438 Pan trogl
259	16.4	68.3	1970	3	CNS044GP	EX827087 Arabidops	C 332	16.2	67.5	695	4	BG973504	BG973504 602842195
260	16.2	67.5	180	8	AF061628	AF061628 AF061628	C 333	16.2	67.5	699	7	CF721155	CF721155 CCNHR43TF
261	16.2	67.5	249	2	BF754757	BF754757 MK0-CT045	C 334	16.2	67.5	703	8	CC358002	CC358002 PUEHT14TD
262	16.2	67.5	271	5	BP137457	BP137457 BP137457	C 335	16.2	67.5	705	9	CL166555	CL166555 104_362_1
263	16.2	67.5	276	5	BQ344806	BQ344806 ILS-NT022	C 336	16.2	67.5	712	2	BE264683	BE264683 601192506
264	16.2	67.5	289	2	BB719604	BB719604 BB719604	C 337	16.2	67.5	719	9	AG326391	AG326391 Mus muscu
265	16.2	67.5	315	1	AV046497	AV046497 AV046497	C 338	16.2	67.5	731	5	BU941141	BU941141 AGENCOURT
266	16.2	67.5	318	7	N85945	N85945 J5660F Huma	C 339	16.2	67.5	743	7	CV105837	CV105837 AGENCOURT
267	16.2	67.5	327	2	BF705846	BF705846 271495 WA	C 340	16.2	67.5	744	9	CL166554	CL166554 104_362_1
268	16.2	67.5	330	1	AI398013	AI398013 NC5M1C12T	C 341	16.2	67.5	745	7	CK326228	CK326228 Hd mx23.0
269	16.2	67.5	332	7	CF836462	CF836462 UCRC803.0	C 342	16.2	67.5	750	5	BU252574	BU252574 603745432
270	16.2	67.5	361	5	BP661230	BP661230 BP661230	C 343	16.2	67.5	756	7	CN978584	CN978584 29421.125
271	16.2	67.5	365	7	CO741783	CO741783 Hd mx23.2	C 344	16.2	67.5	758	8	BZ285161	BZ285161 CH230-385
272	16.2	67.5	380	9	CG833539	CG833539 ZMWBC013	C 345	16.2	67.5	762	9	CC928076	CC928076 ZMWBC053
273	16.2	67.5	386	7	CO579549	CO579549 ILLUMIGEN	C 346	16.2	67.5	764	9	CR794611	CR794611 GROAA12A
274	16.2	67.5	400	8	BZ243089	BZ243089 CH230-362	C 347	16.2	67.5	767	8	BZ077316	BZ077316 1kz45603.
275	16.2	67.5	409	8	AZ503372	AZ503372 IM0343A08	C 348	16.2	67.5	768	6	CB328413	CB328413 UT-R-FSO
276	16.2	67.5	417	1	AA142396	AA142396 ms08d03.r	C 349	16.2	67.5	774	5	BU135280	BU135280 AGENCOURT
277	16.2	67.5	430	2	AW101794	AW101794 sd70e05.Y	C 350	16.2	67.5	776	5	BU842034	BU842034 AGENCOURT
278	16.2	67.5	432	8	BH611219	BH611219 SALK_0304	C 351	16.2	67.5	779	8	BH535812	BH535812 BOHMY45TF
279	16.2	67.5	433	1	AA142414	AA142414 ms08d04.r	C 352	16.2	67.5	783	6	CD813757	CD813757 BN15.0200
280	16.2	67.5	467	8	AQ944329	AQ944329 Sheared D	C 353	16.2	67.5	785	9	CG012872	CG012872 ZUADD21TV
281	16.2	67.5	474	2	BE415363	BE415363 MWL028.E0	C 354	16.2	67.5	787	9	CC537886	CC537886 CH240.417
282	16.2	67.5	492	2	BE210916	BE210916 s055c08.Y	C 355	16.2	67.5	787	9	CC549746	CC549746 CH240.434
283	16.2	67.5	498	2	BF836338	BF836338 RC1-HT097	C 356	16.2	67.5	810	6	CD814702	CD814702 BN15.023PB
284	16.2	67.5	503	4	BG509990	BG509990 ead26b11.	C 357	16.2	67.5	819	8	BZ979888	BZ979888 PUFIO63TB
285	16.2	67.5	508	6	CD395262	CD395262 Gm ck1525	C 358	16.2	67.5	836	8	BZ824487	BZ824487 PUFAP30TB
286	16.2	67.5	527	5	BQ296930	BQ296930 sso36b01.	C 359	16.2	67.5	839	7	CF708922	CF708922 CCAEC62TO
287	16.2	67.5	531	4	BJ159999	BJ159999 BJ159999	C 360	16.2	67.5	843	9	CC595452	CC595452 CH240.397
288	16.2	67.5	533	1	AA496043	AA496043 zv72e02.s	C 361	16.2	67.5	851	7	CF702036	CF702036 CCAC231TO
289	16.2	67.5	533	7	CO741197	CO741197 Hd mx23.1	C 362	16.2	67.5	854	7	CF692015	CF692015 CCANHS74TR
290	16.2	67.5	533	8	AQ778376	AQ778376 HS_3161.B	C 363	16.2	67.5	856	9	CNS0211N	AL117704 Tetradon
291	16.2	67.5	536	1	AI460461	AI460461 sa78g10.Y	C 364	16.2	67.5	857	9	CC676774	CC676774 OSGEG14TV
292	16.2	67.5	536	7	CF075895	CF075895 Hd mx17.6	C 365	16.2	67.5	863	9	CW010325	CW010325 ZMMBLA001
293	16.2	67.5	543	5	BA747155	BA747155 DKFP2686L	C 366	16.2	67.5	868	7	CF708909	CF708909 CCAGQ68TR
294	16.2	67.5	546	7	CN635434	CN635434 116C03.54	C 367	16.2	67.5	870	9	CC971969	CC971969 ZUAE688TH
295	16.2	67.5	553	2	BE610566	BE610566 sq63a04.Y	C 368	16.2	67.5	871	9	CG015132	CG015132 ZUACS78TV
296	16.2	67.5	564	4	BI472115	BI472115 sbh99f07.	C 369	16.2	67.5	880	5	BA459433	BA459433 BX459433
297	16.2	67.5	565	2	AW781890	AW781890 s19h8a03.Y	C 370	16.2	67.5	882	7	CF718681	CF718681 CCADM51TF
298	16.2	67.5	565	4	BI74381	BI74381 BI74381	C 371	16.2	67.5	889	9	CG104403	CG104403 PUFQMA7TD
299	16.2	67.5	566	5	BQ041481	BQ041481 gd22f09.Y	C 372	16.2	67.5	895	9	CG049669	CG049669 PUFXA44TD
300	16.2	67.5	581	6	CD449699	CD449699 Hd mx18.0	C 373	16.2	67.5	900	7	CF677989	CF677989 CCAD551TF
301	16.2	67.5	581	7	CF544544	CF544544 Hd mx17.6	C 374	16.2	67.5	907	7	CF708903	CF708903 CCAGQ68TF
302	16.2	67.5	589	9	CE146227	CE146227 t1gr-g88-	C 375	16.2	67.5	912	4	BI828914	BI828914 603075075
303	16.2	67.5	592	4	BG762856	BG762856 602734788	C 376	16.2	67.5	915	9	ECA576659	AJ576659 Equus cab
304	16.2	67.5	592	7	CF544173	CF544173 Hd mx17.7	C 377	16.2	67.5	918	9	CL071117	CL071117 CH216-120
305	16.2	67.5	593	8	CR022133	CR022133 Reverse s	C 378	16.2	67.5	919	2	BE974853	BE974853 601680912
306	16.2	67.5	594	8	AQ946118	AQ946118 Sheared D	C 379	16.2	67.5	920	7	CF702569	CF702569 CCAC159TO
307	16.2	67.5	597	7	CF075811	CF075811 Hd mx17.6	C 380	16.2	67.5	922	7	CF707286	CF707286 CCANEO7TO
308	16.2	67.5	598	9	CE584964	CE584964 t1gr-g88-	C 381	16.2	67.5	922	9	CNS04CJG	AL284533 Tetradon
309	16.2	67.5	599	7	CK326743	CK326743 Hd mx24.0	C 382	16.2	67.5	933	9	CNS0771L	AL432827 T3 end of
310	16.2	67.5	600	1	AA151689	AA151689 z029a05.s	C 383	16.2	67.5	939	2	BF343178	BF343178 602015827
311	16.2	67.5	605	5	BQ176832	BQ176832 UT-M-DJ2-	C 384	16.2	67.5	942	7	CF702042	CF702042 CCAC231TR
312	16.2	67.5	606	1	AI749573	AI749573 at30f09.x	C 385	16.2	67.5	950	9	CG049668	CG049668 PUFXA44TB
313	16.2	67.5	611	7	CF544591	CF544591 Hd mx17.6	C 386	16.2	67.5	984	5	BX900888	BX900888 BX900888
314	16.2	67.5	625	2	BB658589	BB658589 BB658589	C 387	16.2	67.5	996	8	BZ576964	BZ576964 bsh2_5183
315	16.2	67.5	638	2	AW349552	AW349552 GM210007B	C 388	16.2	67.5	1004	9	CNS04449R	AL273816 Tetradon
316	16.2	67.5	645	9	CG984522	CG984522 CH240_154	C 389	16.2	67.5	1004	9	CL018422	CL018422 CH216-311

Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA
sequence: 90-212, >LINE2 (matched complement)
Seq primer: M13 Reverse

FEATURES

Location/Qualifiers
1. .213

source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-EJ0-ain-m-04-0-UI"
/issue_type="fetal eyes, lens, eye anterior segment, optic nerve, retina, Retina Foveal and Macular, RPE and Choroid"
/dev stage="fetal and adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-EJ0"
/note="Organ: eye; Vector: p77T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-E-EJ0 is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p77T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAAGA; lens, CGATTAGCGA; eye anterior segment, AATGCCGCAT; optic nerve, CCATTAAAGT; retina, CCGCG; Retina Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

ORIGIN

Query Match 75.8%; Score 18.2; DB 4; Length 213;
Best Local Similarity 87.0%; Pred. No. 6.e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CCGAGACGGTCTCGAGGGCTTAC 24
||||| ||||| ||||| ||||| |||||
Db 80 CCGAGACGATTCTGGGGGCATAC 102

RESULT 2

BM344555/c 501 bp mRNA linear EST 23-JAN-2002
LOCUS rr56c05.y1 Globodera rostochiensis J2 pCDNAII Smant v1 Globodera
DEFINITION rostochiensis cDNA 5', mRNA sequence.

ACCESSION BM344555

VERSION BM344555.1 GI:18081470

KEYWORDS EST.

SOURCE Globodera rostochiensis

ORGANISM Globodera rostochiensis

REFERENCE 1 (bases 1 to 501)
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchidae; Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.

AUTHORS

McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

The Washington Univ. Nematode EST Project, 1999

Contact: McCarter JP

TITLE

JOURNAL

COMMENT

The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu
The library was contributed by Dr. Geert Smant of the Laboratory of Nematology at Wageningen University, Wageningen, Netherlands (geert.smant@nema.dpw.wau.nl). DNA Sequencing by: Washington University Genome Sequencing Center
Seq primer: -40RP from Gibco
High quality sequence stop: 479.

FEATURES

Location/Qualifiers
1. .501

source
/organism="Globodera rostochiensis"
/mol_type="mRNA"
/db_xref="taxon:31243"
/dev stage="J2"
/lab_host="DH10B"
/clone_lib="Globodera rostochiensis J2 pCDNAII Smant v1"
/note="Vector: pCDNAII (Invitrogen); Site 1: BstXI; Site 2: EcoRI; The library was donated for sequencing by Geert Smant from Wageningen University, Laboratory of Nematology, The Netherlands."

ORIGIN

Query Match 75.8%; Score 18.2; DB 4; Length 501;
Best Local Similarity 87.0%; Pred. No. 7.e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CCGAGACGGTCTCGAGGGCTTAC 24
||||| ||||| ||||| ||||| |||||
Db 105 CCGAGACGGTCTCGTGGCTTTC 83

RESULT 3

LOCUS

DEFINITION

AW569902 463 bp mRNA linear EST 14-JUL-2004
si83a12.y1 Gm-cl031 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-cl031-1271 5', similar to TR-022616 O22616 ORNITHINE
DECARBOXYLASE. [J] ; mRNA sequence.

ACCESSION AW569902

VERSION AW569902.1 GI:7234566

KEYWORDS EST.

SOURCE Glycine max (soybean)

ORGANISM Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE 1 (bases 1 to 463)

AUTHORS

Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Corvelli, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

Public Soybean EST Project

TITLE

JOURNAL

COMMENT

Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu

When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)

Insert Length: 634 Std Error: 0.00

High quality sequence stop: 396.

FEATURES

Location/Qualifiers

1. .463

/organism="Glycine max"

/mol_type="mRNA"

/cultivar="Williams"

/db_xref="taxon:3847"

```

/clones="GENOME SYSTEMS CLONE ID: Gm-cl031-1271"
/tissue_type="Williams seedlings, minus the cotyledons"
/lab_host="DH10B"
/clone_lib="Gm-cl031"
/notes="Vector: pBluescript II XR; Site 1: EcoRI; Site 2:
XhoI; This cDNA library was constructed from mRNA isolated
from whole 'Williams' seedlings, minus the cotyledons,
which were propagated on paper towels with distilled water
for 5 days, incubated at 40 degrees C for 1 hour. The
cotyledons were removed and the remaining tissue was
flash-frozen in liquid nitrogen. Stratagene's cDNA
Synthesis Kit (catalog number 200401) was used to
synthesize the cDNA. First-strand synthesis was performed
with 5-methyl dCTP, hence the ligated cDNA was
hemimethylated. A modification of Stratagene's
first-strand synthesis primer was used. An 'anchor'
nucleotide (V=A, C, or G) was added to the 3' end of the
primer [GAGAGAGAGAGAGAGAGACTGCTCGAG(T)18V] to anchor
the primer at the 5' end of the poly(A) tract. After
second strand synthesis, the cDNA ends were filled in with
cloned Pfu DNA, ligated to EcoRI adapters and
subsequently phosphorylated. The cDNA was then
precipitated and redissolved in sterile, RNase-,
DNase-free water. The XhoI site within the first-strand
synthesis primer was then restricted by digestion with
XhoI from Promega (40U/ul); all XhoI sites in the cDNA
would be protected by their hemimethylated status. The
cDNA constructs were size-fractionated with a 500 bp
cutoff, using GibcoBRL Life Technologies' cDNA Size
Fractionation column. The column eluent was then
precipitated, redissolved, and ligated into Stratagene's
pBluescript II XR predigested vector (pBluescript II SK(+)
vector that has been digested with EcoRI and XhoI, and
phosphorylated by Stratagene). 100% of the white and blue
colonies appear to contain recombinant plasmids with cDNA
inserts, based on size (n=18 and 5, respectively). This
library was constructed by Dr. Paul Keim and Dr. Virginia
Coryell."

ORIGIN
Query Match 74.2%; Score 17.8; DB 2; Length 463;
Best Local Similarity 90.5%; Pred. No. 1.1e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAGACGGTTCGAGGGCTTAC 24
|||
Db 162 GATACGGTTCGAGGGATTAC 182

RESULT 4
BE210385
LOCUS
DEFINITION
8043b04.y1 Gm-cl039 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-cl039-680 5' similar to SW:DCOR_DATST P50134 ORNITHINE
DECARBOXYLASE ; mRNA sequence.

ACCESSION
BE210385
VERSION
BE210385.1 GI:8826655
KEYWORDS
EST.
SOURCE
Glycine max (soybean)
ORGANISM
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 499)
Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)

REFERENCE
AUTHORS
Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)

TITLE
JOURNAL
COMMENT
Public Soybean EST Project
Washington University School of Medicine

Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
High quality sequence stop: 430.
Location/Qualifiers
1. .499
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Ogden"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl039-680"
/tissue_type="whole seedling without cotyledons"
/lab_host="DH10B"
/clone_lib="Gm-cl039"
/notes="Vector: pBluescriptII SK+; Site 1: EcoRI; Site 2:
XhoI; This cDNA library was constructed from mRNA isolated
from 2 week old seedlings with the cotyledons removed at
the time of harvest. The seedlings for the cultivar Ogden
were grown in a growth chamber using germination paper.
Complementary DNA was synthesized from mRNA using a primer
consisting of a poly(dT) sequence with a XhoI restriction
site. EcoRI adapters were ligated to the blunt-ended cDNA
fragments followed by XhoI digestion. The cDNA fragments
were directionally cloned into the EcoRI-XhoI restriction
site of the pBluescript vector. The ligated cDNA fragments
were transformed into DH10B host cells (Gibco BRL). This
library was constructed by Dr. Randy Shoemaker."

ORIGIN
Query Match 74.2%; Score 17.8; DB 2; Length 499;
Best Local Similarity 90.5%; Pred. No. 1.1e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAGACGGTTCGAGGGCTTAC 24
|||
Db 347 GATACGGTTCGAGGGATTAC 367

RESULT 5
BM520888
LOCUS
DEFINITION
sal31302.y1 Gm-cl059 Glycine soja cDNA clone SOYBEAN CLONE ID:
Gm-cl059-3772 5' similar to SW:DCOR_DATST P50134 ORNITHINE
DECARBOXYLASE ; mRNA sequence.

ACCESSION
BM520888
VERSION
BM520888.1 GI:18692040
KEYWORDS
EST.
SOURCE
Glycine soja
ORGANISM
Glycine soja
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 538)
Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)

REFERENCE
AUTHORS
Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)

TITLE
JOURNAL
COMMENT
Public Soybean EST Project
Washington University School of Medicine

```


4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
Seq primer: -40RP from Gibco
High quality sequence stop: 421.

FEATURES

source Location/Qualifiers

1. .538
/organism="Glycine soja"
/mol_type="mRNA"
/db_xref="taxon:3848"
/clone="SOYBEAN CLONE ID: Gm-cl059-3772"
/tissue_type="Whole seedling, 2 week old, etiolated"
/lab_host="DH10B"
/clone_lib="Gm-cl059"
/notes="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed from mRNA isolated from 2 week old etiolated whole seedlings of PI468916. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI- XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed in the laboratory of Dr. Randy Shoemaker at Iowa state university."

ORIGIN

Query Match 74.2%; Score 17.8; DB 4; Length 538;
Best Local Similarity 90.5%; Pred. No. 1.1e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAGACGGTCTGAGGGCTTAC 24
||| ||||| ||||| |||||
Db 290 GATACGGTCTGAGGGATTAC 310

RESULT 6

CA853343 542 bp mRNA linear EST 01-AUG-2003
LOCUS B07B08.seq cDNA Peking library 12hr SCN3 Glycine max cDNA clone
DEFINITION B07B08 5', mRNA sequence.

ACCESSION CA853343
VERSION CA853343.1 GI:33390136
KEYWORDS EST.

SOURCE

Glycine max (soybean)
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE

1 (bases 1 to 542)
Alkharouf, N.W., Khan, R. and Matthews, B.F.
Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode
Unpublished (2002)

JOURNAL

COMMENT Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg. 006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350, USA

Tel: 301 504 5750

Fax: 301 504 5728

Email: alkharouf@ba.ars.usda.gov.

Location/Qualifiers

FEATURES

source 1. .542
/organism="Glycine max"
/mol_type="mRNA"

/cultivar="Peking"
/db_xref="taxon:3847"
/clone="B07B08"

/tissue_type="Roots"

/dev_stage="Seedlings"

/clone_lib="cDNA Peking library 12hr SCN3"
/notes="Vector: pBluescript SK-; cDNA clones from mRNA extracted from roots of soybean cv. Peking 12 hrs after infection by SCN race 3. These are cloned in pBluescript SK- phagemid."

ORIGIN

Query Match 74.2%; Score 17.8; DB 6; Length 542;

Best Local Similarity 90.5%; Pred. No. 1.1e+03;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAGACGGTCTGAGGGCTTAC 24
||| ||||| ||||| |||||

Db 405 GATACGGTCTGAGGGATTAC 425

RESULT 7

BME20767

LOCUS

DEFINITION

BME20767 544 bp mRNA linear EST 06-JUL-2004
sal30d08.y1 Gm-cl059 Glycine soja cDNA clone SOYBEAN CLONE ID: Gm-cl059-3639 5', similar to SW:DCOR_DATST P50134 ORNITHINE DECARBOXYLASE ;, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Glycine soja
Glycine soja
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE

AUTHORS

1 (bases 1 to 544)
Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
Public Soybean EST Project

TITLE

JOURNAL

COMMENT

Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
Seq primer: -40RP from Gibco
High quality sequence stop: 428.

FEATURES

source

1. .544
/organism="Glycine soja"
/mol_type="mRNA"
/db_xref="taxon:3848"
/clone="SOYBEAN CLONE ID: Gm-cl059-3639"
/tissue_type="Whole seedling, 2 week old, etiolated"
/lab_host="DH10B"
/clone_lib="Gm-cl059"

/notes="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed from mRNA isolated from 2 week old etiolated whole seedlings of PI468916. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA

fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI- XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed in the laboratory of Dr. Randy Shoemaker at Iowa state university."

ORIGIN

Query Match 74.2%; Score 17.8; DB 4; Length 544;
 Best Local Similarity 90.5%; Pred. No. 1.1e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAGACGGTTCTGAGGGCTTAC 24
 |||||
 Db 290 GATACGGTTCTGAGGGATTAC 310
 |||||

RESULT 8

BQ080425
 LOCUS
 DEFINITION
 san33a10.y1 Gm-cl084 Glycine max cDNA clone SOYBEAN CLONE ID:
 Gm-cl084-5420 5' similar to TR:022616 O22616 ORNITHINE
 DECARBOXYLASE. [1] ; mRNA sequence.

ACCESSION

BQ080425
 BQ080425.1 GI:19935398

VERSION

EST.

KEYWORDS

Glycine max (soybean)

SOURCE

Glycine max

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.
 1 (bases 1 to 545)
 Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V.,
 Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
 Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
 Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
 Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
 McCann, R., Waterston, R. and Wilson, R.
 Public Soybean EST Project
 Unpublished (1999)

TITLE

JOURNAL

COMMENT

Contact: Shoemaker R/Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu

When it has been determined, an EST from the other end of this
 clone is listed in the 'Other ESTs on clone' field. This clone is
 available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
 Seq primer: -40RP from Gibco
 High quality sequence stop: 421.

FEATURES

source

1. .545
 Location/Qualifiers
 /organism="Glycine max"
 /mol_type="mRNA"
 /cultivar="Williams 82"
 /db_xref="taxon:3847"
 /clone="SOYBEAN CLONE ID: Gm-cl084-5420"
 /tissue_type="Etiolated hypocotyls (Williams 82)"
 /lab_host="DH10B"
 /clone_lib="Gm-cl084"

/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
 XhoI; The cDNA library was constructed by M. Bhattacharya
 from mRNA isolated from etiolated hypocotyls from the
 cultivar Williams 82. Tissue was inoculated with
 Phytophthora soyae race 1 and tissues were harvested 2 and
 4 hours following infection. The library is the pool of
 these two time points. Complementary DNA was synthesized
 from mRNA using a primer consisting of a poly(dT) sequence
 with a XhoI restriction site. EcoRI adapters were ligated

ORIGIN

Query Match 74.2%; Score 17.8; DB 5; Length 545;
 Best Local Similarity 90.5%; Pred. No. 1.1e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAGACGGTTCTGAGGGCTTAC 24
 |||||
 Db 151 GATACGGTTCTGAGGGATTAC 171
 |||||

RESULT 9

BQ080423
 LOCUS
 DEFINITION
 san33a08.y1 Gm-cl084 Glycine max cDNA clone SOYBEAN CLONE ID:
 Gm-cl084-5416 5' similar to TR:022616 O22616 ORNITHINE
 DECARBOXYLASE. [1] ; mRNA sequence.

ACCESSION

BQ080423
 BQ080423.1 GI:19935393

VERSION

EST.

KEYWORDS

Glycine max (soybean)

SOURCE

Glycine max

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.
 1 (bases 1 to 553)
 Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V.,
 Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
 Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
 Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
 Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
 McCann, R., Waterston, R. and Wilson, R.
 Public Soybean EST Project
 Unpublished (1999)

TITLE

JOURNAL

COMMENT

Contact: Shoemaker R/Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu

When it has been determined, an EST from the other end of this
 clone is listed in the 'Other ESTs on clone' field. This clone is
 available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
 Seq primer: -40RP from Gibco
 High quality sequence stop: 422.

FEATURES

source

1. 553
 Location/Qualifiers
 /organism="Glycine max"
 /mol_type="mRNA"
 /cultivar="Williams 82"
 /db_xref="taxon:3847"
 /clone="SOYBEAN CLONE ID: Gm-cl084-5416"
 /tissue_type="Etiolated hypocotyls (Williams 82)"
 /lab_host="DH10B"
 /clone_lib="Gm-cl084"

/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
 XhoI; The cDNA library was constructed by M. Bhattacharya
 from mRNA isolated from etiolated hypocotyls from the
 cultivar Williams 82. Tissue was inoculated with
 Phytophthora soyae race 1 and tissues were harvested 2 and
 4 hours following infection. The library is the pool of
 these two time points. Complementary DNA was synthesized
 from mRNA using a primer consisting of a poly(dT) sequence

to the blunt-ended cDNA fragments followed by XhoI
 digestion. The cDNA fragments were directionally cloned
 into the EcoRI-XhoI restriction site of the pBluescript
 vector. The ligated cDNA fragments were transformed into
 DH10B host cells (Gibco BRL). This library was constructed
 by M. Bhattacharya in the laboratory of Dr. Randy
 Shoemaker at Iowa State University."

with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed by M. Bhattacharya in the laboratory of Dr. Randy Shoemaker at Iowa State University."

ORIGIN

Query Match 74.2%; Score 17.8; DB 5; Length 553;
Best Local Similarity 90.5%; Pred. No. 1.1e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAGACGGTCTGAGGGCTTAC 24
|||||
DB 151 GATACGGTCTGAGGGATTAC 171

RESULT 10

BM954596
LOCUS
DEFINITION
san08c04.y1 Gm-cl084 Glycine max cDNA clone SOYBEAN CLONE ID:
Gm-cl084-3199 5', similar to TR:O22616 O22616 ORNITHINE
DECARBOXYLASE. [1], mRNA sequence.

ACCESSION

BM954596

VERSION

BM954596.1 GI:19453186

KEYWORDS

EST.

SOURCE

Glycine max (soybean)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

REFERENCE

1 (bases 1 to 554)
Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)

TITLE

JOURNAL

COMMENT

Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
Seq primer: -40RP from Gibco
High quality sequence stop: 421.

FEATURES

source

1..554
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Williams 82"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-cl084-3199"
/tissue_type="Etiolated hypocotyls (Williams 82)"
/lab_host="DH10B"
/clone_lib="Gm-cl084"

/notes="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed by M. Bhattacharya from mRNA isolated from etiolated hypocotyls from the cultivar Williams 82. Tissue was inoculated with Phytophthora soyae race 1, and tissues were harvested 2 and 4 hours following infection. The library is the pool of these two time points. Complementary DNA was synthesized

from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed by M. Bhattacharya in the laboratory of Dr. Randy Shoemaker at Iowa State University."

ORIGIN

Query Match 74.2%; Score 17.8; DB 5; Length 554;
Best Local Similarity 90.5%; Pred. No. 1.1e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAGACGGTCTGAGGGCTTAC 24
|||||
DB 141 GATACGGTCTGAGGGATTAC 161

RESULT 11

BM093047
LOCUS
DEFINITION
sa04d03.y1 Gm-cl065 Glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-cl065-9389 5', similar to SW:DCOR_DATST P50134 ORNITHINE
DECARBOXYLASE ;, mRNA sequence.

ACCESSION

BM093047

VERSION

BM093047.1 GI:17022013

KEYWORDS

EST.

SOURCE

Glycine max (soybean)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

REFERENCE

1 (bases 1 to 558)
Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)

TITLE

JOURNAL

COMMENT

Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
High quality sequence stop: 422.

FEATURES

source

1..558
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Williams"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl065-9389"
/tissue_type="germinating shoots"
/lab_host="DH10B"
/clone_lib="Gm-cl065"

/notes="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed from mRNA isolated from germinating shoots of the cultivar Williams. The seeds were allowed to germinate for 24 hours prior to being cold stressed for 2 days at 4C. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI

SOURCE Glycine max (soybean)
 ORGANISM Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 REFERENCE 1 (bases 1 to 761)
 AUTHORS Vodkin, L., Keim, P., Shoemaker, R., Retzel, E., Khanna, A., Coryell, V., Erpelidg, J., Raph, C., Shoop, E., Pardini, J., Liu, L. and Lewin, H.
 TITLE A Functional Genomics Program for Soybean (NSF 9872565)
 JOURNAL Unpublished (1999)
 COMMENT Other ESTs: BE057453 corresponding to Gm-cl028-8092 (5')
 Contact: Vodkin, L.O., PI, A Functional Genomics Program for Soybean (NSF 9872565)
 Lewin, H. A., Director, Keck Center for Comparative and Functional Genomics
 University of Illinois
 Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA
 Tel: (217) 244-6147
 Fax: (217) 333-4582
 Email: l-vodkin@uiuc.edu
 This clone is available through: Incyte Genomics, 4633 World Parkway Circle St. Louis, Missouri 63134. Phone (800) 430-0030 or (314) 427-3222 FAX: (314) 427-3324. Web site: http://www.incyte.com/reagents/catalog.jsp?page=clones/collaboration/index
 Seq primer: 5'-TTTTTTTTTTTTTTTTTTT(A/C/G)-3'.

FEATURES
 source
 Location/Qualifiers
 1..761
 /organism="Glycine max"
 /mol_type="mRNA"
 /db_xref="taxon:3847"
 /clone="Gm-r1083-4491"
 /clone_lib="Gm-r1083"
 /note="The library Gm-r1083 is a sequence-driven, reracked set of 4,992 clones selected from cDNA libraries from various tissues and stages of development of soybean. It represents 1117 sequences from the progenitor library Gm-cl009 (from mature roots of 2 month old greenhouse grown 'Williams' soybean plants); 820 sequences from the progenitor library Gm-cl013 (from 2 to 3 week old whole plants of Williams); and 3055 sequences from library Gm-cl028 (from 'Supernod' plants whose seedlings were inoculated with Bradyrhizobium japonicum, courtesy of Dr. Gary Stacey). The 5' ESTs of the source clones from the different progenitor libraries was used to select singletons, or a representative of each contig, which were reracked to form library Gm-r1083. The cDNA clones of the end. The contig analysis to select unique genes was performed by the laboratory of Ernest Retzel, Center for Computational Genomics and Bioinformatics, University of Minnesota, http://web.ahc.umn.edu/biodata/nsfsoy/. Reracking was performed by Incyte Genomics, St. Louis, http://www.incyte.com, and 3' sequencing by the Keck Center for Comparative and Functional Genomics, University of Illinois, http://www.lie.uiuc.edu/biotech/keck.html. Note: The corresponding 5' EST from each clone in the Gm-r1083 library is listed in the 'OTHER EST' field. The detailed information on the source library for each clone can also be obtained by referring to the Incyte Genomics clone ID of the original cDNA library that is also listed under 'OTHER EST'."

ORIGIN
 Query Match 74.2%; Score 17.8; DB 4; Length 761;
 Best Local Similarity 90.5%; Pred. No. 1.1e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4 GAGACGGTTCTGAGGGCTTAC 24
 |||||
 Db 373 GATACGGTTCTGAGGGATTAC 353
 |||||

RESULT 17
 CC577625
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

FEATURES
 source

ORIGIN

Query Match 74.2%; Score 17.8; DB 9; Length 796;
 Best Local Similarity 90.5%; Pred. No. 1.1e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 CGAGACGGTTCTGAGGGCTTA 23
 |||||
 Db 621 CGGACGGTTCTGAGGGTTTA 641
 |||||

RESULT 18
 AW349137/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS

CC577625 796 bp DNA linear GSS 18-JUN-2003
 CH240_45603.TARBAC13P2 CHORI-240 Bos taurus genomic clone
 CH240_45603, genomic survey sequence.
 CC577625
 CC577625.1 GI:31921484
 GSS.
 Bos taurus (cow)
 Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
 1 (bases 1 to 796)
 Holt, R., Scott, J., Yang, G., Barber, S., Smalish, D., Prabhu, A.-L., Tsai, M., Cloutier, A., Lee, D., Girm, N., Olson, T., Mayo, M., Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A., Chiu, R., Mathewson, C., Wye, N., Masson, A., Brown-John, M., Jones, S., Schein, J., Marra, M., de Jong, P., Keele, J.W. and Kappes, S.M.
 Bovine BAC End Sequences from Library CHORI-240, PLATES 399 to 478
 Unpublished (2003)
 Other GSSs: CH240_45603.T7
 Contact: Rob Holt
 Sequencing
 The British Columbia Cancer Agency Genome Science Centre
 600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6
 Tel: 604-877-6085
 Fax: 604-877-6276
 Email: rholt@bcgsc.ca
 Clones are derived from the bovine BAC library CHORI-240
 (http://www.chori.org/bacpac/bovine240.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources
 (http://www.chori.org/bacpac/ordering/information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the British Columbia Genome Sciences Centre, Canada.
 Plate: 456 row: 0 column: 3
 Seq primer: SP6
 Class: BAC ends.

Location/Qualifiers
 1..796
 /organism="Bos taurus"
 /mol_type="genomic DNA"
 /strain="breed: Hereford"
 /db_xref="taxon:9913"
 /clone="CH240_45603"
 /sex="Male"
 /cell_type="Blood"
 /clone_lib="CHORI-240"
 /note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI; Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"

Query Match 74.2%; Score 17.8; DB 9; Length 796;
 Best Local Similarity 90.5%; Pred. No. 1.1e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 CGAGACGGTTCTGAGGGCTTA 23
 |||||
 Db 621 CGGACGGTTCTGAGGGTTTA 641
 |||||

RESULT 18
 AW349137
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS

Email: szhao@tigr.org
 Clones are derived from the rat BAC library CHORI-230
 (http://www.chori.org/bacpac/rat230.htm). For BAC library
 availability, please contact Pieter de Jong (pdejong@mail.cho.org).
 Clones may be purchased from BACPAC Resources
 (http://www.chori.org/bacpac/or_ering_information.htm). BAC end
 page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
 Plate: 348 row: J column: 2
 Seq primer: T7
 Class: BAC ends.

FEATURES
 source
 Location/Qualifiers
 1..1028
 /organism="Rattus norvegicus"
 /mol_type="genomic DNA"
 /strain="BN/SENHsd/MCW"
 /db_xref="taxon:10116"
 /clone="CH230-348J2"
 /sex="Female"
 /cell_type="Brain"
 /clone_lib="CHORI-230 Segment 2"
 /note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
 CHORI-230 Rat (BN/SENHsd/MCW) BAC library produced by
 Pieter de Jong"

ORIGIN

Query Match 74.2%; Score 17.8; DB 8; Length 1028;
 Best Local Similarity 90.5%; Pred. No. 1.2e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAGACGGTTCTGAGGCGTTAC 24
 ||||| ||||| ||||| |||||
 Db 207 GAGACAGATCTGAGGCGTTAC 187

RESULT 21

CNS03040
 LOCUS
 DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone
 183122 of library G from Tetraodon nigroviridis, genomic survey
 sequence.

ACCESSION AL221793.1 GI:7880612
 VERSION GSS; genome survey sequence.
 KEYWORDS Tetraodon nigroviridis
 SOURCE Tetraodon nigroviridis
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 Tetraodontoidea; Tetraodontidae; Tetraodon.

REFERENCE

1 Roest Crolius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
 Bernot, A., Fzames, C., Wincker, P., Brottier, P., Quetier, F.,
 Saurin, W., and Weissenbach, J.
 Estimate of human gene number provided by genome-wide analysis
 using Tetraodon nigroviridis DNA sequence
 Nat. Genet. 25 (2), 235-238 (2000)
 JOURNAL MEDLINE 20296633
 PUBMED 10835645

REFERENCE

2 Roest Crolius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C.,
 Fzames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F.,
 Saurin, W., Bernot, A., and Weissenbach, J.
 Characterization and repeat analysis of the compact genome of the
 freshwater pufferfish Tetraodon nigroviridis
 Genome Res. 10 (7), 939-949 (2000)

JOURNAL

MEDLINE 2039837

PUBMED 10899143

REFERENCE 3 (bases 1 to 1058)

AUTHORS

Direct Submission

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

12-APR-2000

Submitted (12-APR-2000)

Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)

COMMENT

This sequence is a single read and was generated as part of a large
 scale clone-end sequencing project of the Tetraodon nigroviridis
 genome. For more information, please take a look at
 http://www.genoscope.cns.fr/Tetraodon.

FEATURES

source

Location/Qualifiers
 1..1058
 /organism="Tetraodon nigroviridis"
 /mol_type="genomic DNA"
 /db_xref="taxon:99883"
 /clone="183L22"
 /clone_lib="G"
 /note="Genoscope sequence ID : COAG183DF11LP1-end : T7"

ORIGIN

Query Match 74.2%; Score 17.8; DB 9; Length 1058;
 Best Local Similarity 90.5%; Pred. No. 1.2e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCCGACGCGTTCTGAGGCGT 21
 ||||| ||||| ||||| |||||
 Db 271 TCCGACACAGTTCTGAGGCGT 291

RESULT 22

CL199305
 LOCUS
 DEFINITION ZMMBBc007101lr ZMMBBc (EcoRI) Zea mays genomic clone ZMMBBc007101l
 3', genomic survey sequence.

ACCESSION CL199305
 VERSION CL199305.1 GI:40711831
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

1 (bases 1 to 257)

AUTHORS Bharti, A.K., Young, S., Kavchok, S., Keizer, G., Bronzino, A.C.,
 Zohovetz, V., Fuks, G., Yu, Y., Wing, R., and Messing, J.

TITLE Sequencing of the maize genome at PGIR (2003c)

JOURNAL Unpublished (2003)

COMMENT Contact: Bharti, A.K.
 Dr Joachim Messing's lab
 The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
 University
 190 Frelinghuysen Road, Piscataway, NJ 08854, USA
 Tel: 732 445 3801
 Fax: 732 445 5735
 Email: bharti@waksman.rutgers.edu

Seq primer: SP6

Class: BAC ends

High quality sequence start: 155.

Location/Qualifiers

1..257

/organism="Zea mays"

/mol_type="genomic DNA"

/cultivar="B73"

/db_xref="taxon:4577"

/clone="ZMMBBc007101l"

/lab_host="E. coli DH10B"

/clone_lib="ZMMBBc (EcoRI)"

/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI"

Query Match 73.3%; Score 17.6; DB 9; Length 257;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGACGCGTTCTGAGGCGTAC 24
 ||||| ||||| ||||| |||||
 Db 23 TACGTGACGCGTTCTGAGGCGTAC 46


```

RESULT 23
AA193764/c
LOCUS
DEFINITION
  rs02f12.r1 Sommer Pristionchus Pristionchus pacificus cDNA clone
  456 5' similar to WP:C06A1.1 CE02114 PROTEIN P97 ;, mRNA sequence.
ACCESSION
  AA193764
VERSION
  AA193764.1 GI:11783443
KEYWORDS
  EST.
SOURCE
  Pristionchus pacificus
ORGANISM
  Pristionchus pacificus
  Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
  Neodiplogasteridae; Pristionchus.
REFERENCE
  1 (bases 1 to 311)
AUTHORS
  McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,
  Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,
  Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,
  Tsagarisvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,
  Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,
  Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
  McCann, R., Waterston, R. and Wilson, R.
  The Washington Univ. Nematode EST Project, 1999
  Unpublished (1999)
TITLE
  The Washington Univ. Nematode EST Project, 1999
JOURNAL
  Unpublished (1999)
COMMENT
  Contact: McCarter JP
  The Washington Univ. Nematode EST Project, 1999
  Washington University School of Medicine
  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
  Tel: 314 286 1800
  Fax: 314 286 1810
  Email: est@watson.wustl.edu
  Contact Dr. Ralf Sommer (sora@mail.mpiib-tuebingen.mpg.de) for
  information about this clone.
  High quality sequence stop: 293.
  Location/Qualifiers
    1..311
    /organism="Pristionchus pacificus"
    /mol_type="mRNA"
    /strain="PS 312"
    /db_xref="taxon:54126"
    /clone="456"
    /sex="predominantly hermaphroditic"
    /dev_stage="mixed stages (embryo to adult)"
    /lab_host="not applicable (host cell line)"
    /clone_lib="Sommer Pristionchus"
    /notes="Vector: Uni-ZAP XR Vector (Stratagene); Site.1: 5'
    EcoRI; Site.2: 3' XhoI; 1st strand cDNA was primed with a
    XhoI - oligo(dT) primer. Double-stranded cDNA was ligated
    to EcoRI adaptors digested with XhoI and cloned into XhoI
    and EcoRI sites. Primary complexity of the library was 10
    in the 7th. The library went through one round of
    amplification."
ORIGIN
  Query Match 73.3%; Score 17.6; DB 1; Length 311;
  Best Local Similarity 83.3%; Pred. No. 1.3e+03;
  Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
  QY 1 TCCGAGACGGTCTGAGGCTTAC 24
  |||||
  Db 44 TCCGAGACGGATCTGCGGCAAAAC 21

RESULT 24
AI986900/c
LOCUS
DEFINITION
  rs19a09.y1 Sommer Pristionchus Pristionchus pacificus cDNA 5'
  similar to WP:C06A1.1 CE02114 TRANSITIONAL ENDOPLASMIC RETICULUM
  ATPASE HOMOLOG 1 ;, mRNA sequence.
ACCESSION
  AI986900
VERSION
  AI986900.1 GI:5815984
KEYWORDS
  EST.
SOURCE
  Pristionchus pacificus
  Pristionchus pacificus
  Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
  Neodiplogasteridae; Pristionchus.
REFERENCE
  1 (bases 1 to 380)
AUTHORS
  McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,
  Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,
  Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,
  Tsagarisvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,
  Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,
  Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
  McCann, R., Waterston, R. and Wilson, R.
  The Washington Univ. Nematode EST Project, 1999
  Unpublished (1999)
TITLE
  The Washington Univ. Nematode EST Project, 1999
JOURNAL
  Unpublished (1999)
COMMENT
  Contact: McCarter JP
  The Washington Univ. Nematode EST Project, 1999
  Washington University School of Medicine
  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
  Tel: 314 286 1800
  Fax: 314 286 1810
  Email: est@watson.wustl.edu
  Contact Dr. Ralf Sommer (sora@mail.mpiib-tuebingen.mpg.de) for
  information about this clone.
  High quality sequence stop: 293.
  Location/Qualifiers
    1..380
    /organism="Pristionchus pacificus"
    /mol_type="mRNA"
    /strain="PS 312"
    /db_xref="taxon:54126"
    /clone="456"
    /sex="predominantly hermaphroditic"
    /dev_stage="mixed stages (embryo to adult)"
    /lab_host="not applicable (host cell line)"
    /clone_lib="Sommer Pristionchus"
    /notes="Vector: Uni-ZAP XR Vector (Stratagene); Site.1: 5'
    EcoRI; Site.2: 3' XhoI; 1st strand cDNA was primed with a
    XhoI - oligo(dT) primer. Double-stranded cDNA was ligated
    to EcoRI adaptors digested with XhoI and cloned into XhoI
    and EcoRI sites. Primary complexity of the library was 10
    in the 7th. The library went through one round of
    amplification."
ORIGIN
  Query Match 73.3%; Score 17.6; DB 1; Length 311;
  Best Local Similarity 83.3%; Pred. No. 1.3e+03;
  Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
  QY 1 TCCGAGACGGTCTGAGGCTTAC 24
  |||||
  Db 44 TCCGAGACGGATCTGCGGCAAAAC 21

```

```

Neodiplogasteridae; Pristionchus.
1 (bases 1 to 380)
AUTHORS
  McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,
  Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,
  Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,
  Tsagarisvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,
  Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,
  Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
  McCann, R., Waterston, R. and Wilson, R.
  The Washington Univ. Nematode EST Project, 1999
  Unpublished (1999)
TITLE
  The Washington Univ. Nematode EST Project, 1999
JOURNAL
  Unpublished (1999)
COMMENT
  Contact: McCarter JP
  The Washington Univ. Nematode EST Project, 1999
  Washington University School of Medicine
  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
  Tel: 314 286 1800
  Fax: 314 286 1810
  Email: est@watson.wustl.edu
  The library was constructed by Dr. Ralf Sommer DNA Sequencing by:
  Washington University Genome Sequencing Center
  Contact Dr. Ralf Sommer (ralf.sommer@tuebingen.mpg.de) for
  information about this clone.
  Seq primer: -40RP from Gibco
  High quality sequence stop: 373.
  Location/Qualifiers
    1..380
    /organism="Pristionchus pacificus"
    /mol_type="mRNA"
    /strain="PS 312"
    /db_xref="taxon:54126"
    /sex="predominantly hermaphroditic"
    /dev_stage="mixed stages (embryo to adult)"
    /lab_host="not applicable (host cell line)"
    /clone_lib="Sommer Pristionchus"
    /notes="Vector: Uni-ZAP XR Vector (Stratagene); Site.1: 5'
    EcoRI; Site.2: 3' XhoI; 1st strand cDNA was primed with a
    XhoI - oligo(dT) primer. Double-stranded cDNA was ligated
    to EcoRI adaptors digested with XhoI and cloned into XhoI
    and EcoRI sites. Primary complexity of the library was 10
    in the 7th. The library went through one round of
    amplification."
ORIGIN
  Query Match 73.3%; Score 17.6; DB 1; Length 380;
  Best Local Similarity 83.3%; Pred. No. 1.3e+03;
  Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
  QY 1 TCCGAGACGGTCTGAGGCTTAC 24
  |||||
  Db 155 TCCGAGACGGATCTGCGGCAAAAC 132

RESULT 25
B26775/c
LOCUS
DEFINITION
  T1C12TR TAMU Arabidopsis thaliana genomic clone T1C12, genomic
  survey sequence.
ACCESSION
  B26775
VERSION
  B26775.1 GI:2512741
KEYWORDS
  GSS.
SOURCE
  Arabidopsis thaliana (thale cress)
  Arabidopsis thaliana
  ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
  1 (bases 1 to 403)
REFERENCE
  1 (bases 1 to 403)
  Rounsley, S.D., Kelley, J.M., Field, C.E., Craven, M.B., Adams, M.D. and
  Venter, J.C.
  Use of a BAC End Sequence Database To Identify Minimal Overlaps for
  Arabidopsis Genomic Sequencing
  Unpublished (1997)
  Other GSSs: T1C12TF
  Contact: Steve Rounsley

```

Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: rounsley@tigr.org
Seq primer: M13 Reverse
Clas: BAC ends
High quality sequence stop: 403.

FEATURES
source
1. .403
Location/Qualifiers

/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Columbia"
/db_xref="taxon:3702"
/clone="T1C12"
/sex="hermaphrodite"
/clone_lib="TAMU"
/note="Vector: BelOBACII; Site 1: HindIII; Site 2:
HindIII; Produced by Rod Wing"

ORIGIN

Query Match 73.3%; Score 17.6; DB 8; Length 403;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 TCCGACGCGTCTGAGGCTTAC 24
|||||
Db 162 TCCAGTCGGTCTGATGCTAC 139

RESULT 26

BQ292360
LOCUS BQ292360 435 bp mRNA linear EST 15-MAY-2002
DEFINITION PM2-AN0089-021200-012-b09 AN0089 Homo sapiens cDNA, mRNA sequence.
ACCESSION BQ292360
VERSION BQ292360.1 GI:20801310
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 435)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=PM2&t2=PM2-AN0089-
021200-012-b09&t3=2000-12-02&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 5
High quality sequence stop: 45.
Location/Qualifiers

FEATURES
source

1. .435
/organism="Homo sapiens"
/mol_type="mRNA"

ORIGIN

Query Match 73.3%; Score 17.6; DB 5; Length 435;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 TCCGACGCGTCTGAGGCTTAC 24
|||||
Db 341 TTCGAGCGCTTGAGGCTTAC 364

RESULT 27

AW097360/c
LOCUS AW097360 465 bp mRNA linear EST 10-MAY-2001
DEFINITION rs42h07.y1 Sommer Pristionchus Pristionchus pacificus cDNA 5'
similar to WP:C41C4.8 CE05402 TRANSITIONAL ENDOPLASMIC RETICULUM
ATPASE HOMOLOG 2 ;, mRNA sequence.

ACCESSION AW097360
VERSION AW097360.1 GI:6067671
KEYWORDS EST.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus

REFERENCE
AUTHORS
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Necodiplogasteridae; Pristionchus.
1 (bases 1 to 465)
McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,
Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,
Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C.,
Tsagarisvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,
Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T.,
Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)

TITLE
JOURNAL
COMMENT
Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

The library was constructed by Dr. Ralf Sommer DNA Sequencing by:
Washington University Genome Sequencing Center
Contact Dr. Ralf Sommer (ralf.sommer@uebingen.mpg.de) for
information about this clone.
Seq primer: -40RP from Gibco
High quality sequence stop: 395.
Location/Qualifiers

FEATURES
source

1. .465
/organism="Pristionchus pacificus"
/mol_type="mRNA"
/strains="PS 312"
/db_xref="taxon:54126"
/sex="predominantly hermaphroditic"
/dev_stages="mixed stages (embryo to adult)"
/lab_host="not applicable (host cell line)"
/clone_lib="Sommer Pristionchus"
/note="Vector: Uni-Zap XR Vector (Stratagene); Site 1: 5'
EcoRI; Site 2: 3' XhoI; 1st strand cDNA was primed with a
XhoI - oligo(dT) primer. Double-stranded cDNA was ligated
to EcoRI adaptors digested with XhoI and cloned into XhoI
and EcoRI sites. Primary complexity of the library was 10
in the 7th. The library went through one round of

/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="AN0089"

/note="Organ: amnion_normal; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN amplification."

Query Match 73.3%; Score 17.6; DB 2; Length 465;
 Best Local Similarity 83.3%; Pred. No. 1.4e+03;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTGAGGGCTTAC 24
 |||||
 Db 436 TCCGAGACGGATCTGGGGCAAC 413

RESULT 28
 BU467230
 LOCUS
 DEFINITION 517 bp mRNA linear EST 30-NOV-2002
 603372043F1 CSQRBN20 Gallus gallus cdna clone CHEST280e12 5', mRNA
 sequence.
 ACCESSION BU467230
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Gallus gallus (chicken)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 517)
 REFERENCE Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
 AUTHORS Pong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
 TITLE A Comprehensive Collection of Chicken cDNAs
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
 MEDLINE
 PUBMED 22335534
 COMMENT Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology
 (UMIST)
 PO Box 88, Manchester, M60 1QD, UK
 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.

FEATURES
 source
 1..517
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="Layer and broiler"
 /db_xref="taxon:9031"
 /clone="CHEST280e12"
 /sex="Male and female"
 /tissue_type="Chondrocytes isolated from growth plate
 cartilage"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="CSQRBN20"
 /notes="Vector: pBluescript II KS(+); Site_1: EcoRI;
 Site_2: NotI; This normalized library was constructed from
 1 million independent clones. cDNA synthesis was initiated
 using an oligo(dT) primer, using methylated C in the first
 strand synthesis reaction. Following this first strand
 reaction, double-stranded cDNA was blunted, ligated to
 NotI adapters, digested with EcoRI, size-selected, and
 cloned into the NotI and EcoRI compatible sites of a
 custom modified MCS of the pBluescript (KS+) vector. The
 library was normalized in 2 rounds using conditions
 adapted from Soares et al., PNAS (1994) 91: 9228-9232 and
 Bonaldo et al., Genome Research 6 (1996): 791, except that
 a significantly longer reannealing hybridization was
 used."

ORIGIN

Query Match 73.3%; Score 17.6; DB 5; Length 517;
 Best Local Similarity 83.3%; Pred. No. 1.4e+03;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTGAGGGCTTAC 24
 |||||
 Db 77 TCCAGGTTGTTCTGAGGGCTTTC 100

RESULT 29
 BU468159
 LOCUS
 DEFINITION 517 bp mRNA linear EST 30-NOV-2002
 603373691F1 CSQRBN20 Gallus gallus cdna clone CHEST284e24 5', mRNA
 sequence.
 ACCESSION BU468159
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Gallus gallus (chicken)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 517)
 REFERENCE Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
 AUTHORS Pong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
 TITLE A Comprehensive Collection of Chicken cDNAs
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
 MEDLINE
 PUBMED 22335534
 COMMENT Contact: Simon Hubbard
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 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.

FEATURES
 source
 1..517
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="Layer and broiler"
 /db_xref="taxon:9031"
 /clone="CHEST284e24"
 /sex="Male and female"
 /tissue_type="Chondrocytes isolated from growth plate
 cartilage"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="CSQRBN20"
 /notes="Vector: pBluescript II KS(+); Site_1: EcoRI;
 Site_2: NotI; This normalized library was constructed from
 1 million independent clones. cDNA synthesis was initiated
 using an oligo(dT) primer, using methylated C in the first
 strand synthesis reaction. Following this first strand
 reaction, double-stranded cDNA was blunted, ligated to
 NotI adapters, digested with EcoRI, size-selected, and
 cloned into the NotI and EcoRI compatible sites of a
 custom modified MCS of the pBluescript (KS+) vector. The
 library was normalized in 2 rounds using conditions
 adapted from Soares et al., PNAS (1994) 91: 9228-9232 and
 Bonaldo et al., Genome Research 6 (1996): 791, except that
 a significantly longer reannealing hybridization was
 used."

Query Match 73.3%; Score 17.6; DB 5; Length 517;
 Best Local Similarity 83.3%; Pred. No. 1.4e+03;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTGAGGGCTTAC 24
 |||||
 Db 77 TCCAGGTTGTTCTGAGGGCTTTC 100

RESULT 30
 AV550336/c

COMMENTS

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```

/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="X1418120ex"
/tissue_type="anterior neuroectoderm"
/dev_stage="late gastrula (stage 12.5)"
/clone_lib="Otsada Talra anterior neuroectoderm (ANE)

```

ORIGIN

Query Match 73.3%; Score 17.6; DB 5; Length 586;
 Best Local Similarity 83.3%; Pred. No. 1.4e+03;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTTCTGAGGGCTTAC 24
 |||||
 Db 578 TCCGTGACGGTTGTGCGGGGTGAC 555

RESULT 33

AQ979046
 LOCUS
 DEFINITION AQ979046 601 bp DNA linear GSS 29-JAN-2000
 genomic survey sequence.
 ACCESSION AQ979046
 VERSION
 KEYWORDS
 SOURCE GSS.
 ORGANISM Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 601)
 AUTHORS Zhao,S., Nieman,W., Feldblyum,T., Malek,J., Shatsman,S.,
 Akinret,B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de
 Jong,P. and Fraser,C.M.
 Mouse BAC End Sequences from Library RPCI-23
 Other_GSSs: RPCI-23-341H6.TJ
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the mouse BAC library RPCI-23. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>)
 or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
 Plate: 341 row: H column: 6
 Seq primer: T7
 Class: BAC ends.

FEATURES

source
 Location/Qualifiers
 1..601
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPCI-23-341H6"
 /sex="Female"
 /lab_host="DH10B"
 /clone_lib="RPCI-23"
 /notes="Organ: Kidney/Brain; Vector: pBACe3.6; Site 1:
 EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney_and/or
 brain genomic DNA was isolated and partially digested
 with a combination of EcoRI and EcoRI Methyase. Site
 selected DNA was cloned into the pBACe3.6 vector at the
 EcoRI sites. The ligation products were transformed into
 DH10B electrocompetent cells (BRL Life Technologies)."

ORIGIN

Query Match 73.3%; Score 17.6; DB 8; Length 601;
 Best Local Similarity 83.3%; Pred. No. 1.4e+03;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTTCTGAGGGCTTAC 24
 |||||
 Db 288 TCAGAGACTGTTCTGAGGGCAGAC 311

ORIGIN

Query Match 73.3%; Score 17.6; DB 8; Length 601;
 Best Local Similarity 83.3%; Pred. No. 1.4e+03;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTTCTGAGGGCTTAC 24
 |||||
 Db 288 TCAGAGACTGTTCTGAGGGCAGAC 311

RESULT 34

CD734101
 LOCUS
 DEFINITION CD734101 612 bp mRNA linear EST 26-JUN-2003
 clone lGAL_19123 5', mRNA sequence.
 ACCESSION CD734101
 VERSION
 KEYWORDS
 SOURCE EST.
 ORGANISM Gallus gallus (chicken)

ACCESSION

CD734101

VERSION

KEYWORDS

SOURCE

ORGANISM

Gallus gallus (chicken)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.

REFERENCE

1 (bases 1 to 612)

AUTHORS

Min.W., Lillehoj,H.S., Ashwell,C.M., Matukumalli,L.K., van

Tassel,C. and Han,J.Y.

Chicken intestinal lymphocyte EST database as a resource for the

analysis of mucosal immune function

Unpublished (2003)

Contact: Hyun S. Lillehoj

Animal Parasite Diseases Laboratory

Animal and Natural Resources Institute, USDA

Bldg-1043, BARC-East, Beltsville, MD 20705, USA

Tel: 3015048771

Fax: 3015045103

Email: hlilleho@anri.barc.usda.gov

Single pass sequencing. Bases called and trimmed with phred

0.000925 using options -trim_alt -trim_fasta. Vector identified

by cross_match using options -minmatch 12 -minscore 18

Plate: 19 row: I column: 23

Seq primer: ATTTAGTGACACTATAG

High quality sequence stop: 612.

FEATURES

Location/Qualifiers

1..612

/organism="Gallus gallus"

/mol_type="mRNA"

/strain="white leghorn SC"

/db_xref="taxon:9031"

/clone="lGAL_19123"

/sex="mixed"

/tissue_type="Gut"

/cell_type="Lymphocyte"

/dev_stage="Adult"

/lab_host="EMDH10B"

/clone_lib="lGAL - Chicken Intestinal Lymphocyte"

/note="Organ: Intestine; Vector: pCMV-SPORT6; Site 1:

SalI; Site 2: NotI; Normalized library from chicken gut

infected with coccidia duodenum and middle gut."

ORIGIN

Query Match 73.3%; Score 17.6; DB 6; Length 612;

Best Local Similarity 83.3%; Pred. No. 1.4e+03;

Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTTCTGAGGGCTTAC 24

|||||

Db 516 TCCAGAGTGTCTGAGGGCTTTC 539

|||||

BU290274

604166906F1 CSEQCHN55 Gallus gallus

642 bp mRNA linear EST 27-NOV-2002

sequence.

ACCESSION BU290274

VERSION BU290274.1 GI:25739730

KEYWORDS

SOURCE

ORGANISM

Gallus gallus (chicken)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 642)
 AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
 Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
 TITLE A Comprehensive Collection of Chicken cDNAs
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
 MEDLINE 22335534
 PUBMED 12445392
 COMMENT Contact: Simon Hubbard
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 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.

FEATURES
 source
 1..642
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="Compton Line 151"
 /db_xref="taxon:9031"
 /clone="CHEST102712"
 /sex="Female"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="CSEQCHN55"
 /notes="Organ: kidney + adrenal; Vector: pBluescript II
 KS(+); Site_1: EcoRI; Site_2: NotI; This normalized
 cDNA was constructed from 1 million independent clones.
 cDNA synthesis was initiated using an oligo(dT) primer,
 using methylated C in the first strand synthesis reaction.
 Following this first strand reaction, double-stranded cDNA
 was blunted, ligated to NotI adapters, digested with
 EcoRI, size-selected, and cloned into the NotI and EcoRI
 compatible sites of a custom modified MCS of the
 pBluescript (KS+) vector. The library was normalized in 2
 rounds using conditions adapted from Soares et al., PNAS
 (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
 (1996): 791, except that a significantly longer
 reannealing hybridization was used."

ORIGIN

Query Match 73.3%; Score 17.6; DB 5; Length 642;
 Best Local Similarity 83.3%; Pred. No. 1.4e+03;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 TCCGAGACGTTCTGAGGCGTTAC 24
 Db 492 TCCAGGTGTTCTGAGGCGTTTC 515

ORIGIN

Query Match 73.3%; Score 17.6; DB 5; Length 642;
 Best Local Similarity 83.3%; Pred. No. 1.4e+03;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 TCCGAGACGTTCTGAGGCGTTAC 24
 Db 492 TCCAGGTGTTCTGAGGCGTTTC 515

ORIGIN

RESULT 36
 BU360919
 LOCUS 603584340F1 CSEQCHN72 Gallus gallus CDNA clone CHEST53809 5', mRNA
 DEFINITION
 ACCESSION BU360919
 VERSION BU360919.1 GI:25868920
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 664)

REFERENCE
 AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
 Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
 TITLE A Comprehensive Collection of Chicken cDNAs
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
 MEDLINE 22335534
 PUBMED 12445392
 COMMENT Contact: Simon Hubbard
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FEATURES
 source

1..664
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="Compton Line 151"
 /db_xref="taxon:9031"
 /clone="CHEST53809"
 /sex="Female"
 /tissue_type="Cerebrum"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="CSEQCHN72"
 /notes="Organ: brain; Vector: pBluescript II KS(+); Site_1:
 EcoRI; Site_2: NotI; This normalized library was
 constructed from 1 million independent clones. cDNA
 synthesis was initiated using an oligo(dT) primer, using
 methylated C in the first strand synthesis reaction.
 Following this first strand reaction, double-stranded cDNA
 was blunted, ligated to NotI adapters, digested with
 EcoRI, size-selected, and cloned into the NotI and EcoRI
 compatible sites of a custom modified MCS of the
 pBluescript (KS+) vector. The library was normalized in 2
 rounds using conditions adapted from Soares et al., PNAS
 (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
 (1996): 791, except that a significantly longer
 reannealing hybridization was used."

ORIGIN

Query Match 73.3%; Score 17.6; DB 5; Length 664;
 Best Local Similarity 83.3%; Pred. No. 1.4e+03;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 TCCGAGACGTTCTGAGGCGTTAC 24
 Db 415 TCCAGGTGTTCTGAGGCGTTTC 438

ORIGIN

RESULT 37
 BU455179
 LOCUS 603216541F1 CSEQCHN14 Gallus gallus CDNA clone CHEST204a11 5', mRNA
 DEFINITION
 ACCESSION BU455179
 VERSION BU455179.1 GI:25944490
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 674)

REFERENCE
 AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
 Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
 TITLE A Comprehensive Collection of Chicken cDNAs
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
 MEDLINE 22335534
 PUBMED 12445392
 COMMENT Contact: Simon Hubbard
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 University of Manchester Institute of Science and Technology
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 Tel: 01612008930
 Fax: 01612360409
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FEATURES
 source

1..674
 Location/Qualifiers

ORIGIN reannealing hybridization was used."

Query Match 73.3%; Score 17.6; DB 5; Length 710;
 Best Local Similarity 83.3%; Pred. No. 1.4e+03;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTCTGAGGCGTTAC 24
 |||||
 Db 277 TCCAGGTGGTCTGAGGCGTTTC 300

RESULT 40
 LOCUS BU233904 743 bp mRNA linear EST 26-NOV-2002
 DEFINITION 603410086F1 CSEQCHN24 Gallus gallus cDNA clone CHEST325121 5', mRNA sequence.

ACCESSION BU233904
 VERSION BU233904.1 GI:25477968
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus

REFERENCE 1 (bases 1 to 743)
 AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Pong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
 TITLE A Comprehensive Collection of Chicken cDNAs
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
 MEDLINE 22335534
 PUBMED 12445392

COMMENT Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology (UMIST)
 PO Box 88, Manchester, M60 1QD, UK
 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.

FEATURES source

1. .743
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="White Leghorn, Hisex"
 /db_xref="taxon:9031"
 /clone="CHEST325121"
 /dev_stage="22"
 /lab_host="DH10B"
 /clone_lib="CSEQCHN24"
 /note="Organ: heads; Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

ORIGIN

Query Match 73.3%; Score 17.6; DB 5; Length 743;
 Best Local Similarity 83.3%; Pred. No. 1.4e+03;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTCTGAGGCGTTAC 24
 |||||
 Db 315 TCCAGGTGGTCTGAGGCGTTTC 338

RESULT 41
 LOCUS BU307797

DEFINITION 603539776F1 CSEQCHN60 Gallus gallus cDNA clone CHEST507g19 5', mRNA sequence.

ACCESSION BU307797
 VERSION BU307797.1 GI:25815798
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus

REFERENCE 1 (bases 1 to 770)
 AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Pong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
 TITLE A Comprehensive Collection of Chicken cDNAs
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
 MEDLINE 22335534
 PUBMED 12445392

COMMENT Contact: Simon Hubbard
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 Email: Simon.Hubbard@umist.ac.uk.

FEATURES source

1. .770
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="Compton Line 151"
 /db_xref="taxon:9031"
 /clone="CHEST507g19"
 /sex="Female"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="CSEQCHN60"
 /note="Organ: heart; Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

ORIGIN

Query Match 73.3%; Score 17.6; DB 5; Length 770;
 Best Local Similarity 83.3%; Pred. No. 1.4e+03;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTCTGAGGCGTTAC 24
 |||||
 Db 337 TCCAGGTGGTCTGAGGCGTTTC 360

RESULT 42
 LOCUS BU456386

DEFINITION 603217494F1 CSEQCHN14 Gallus gallus cDNA clone CHEST208k24 5', mRNA sequence.

ACCESSION BU456386
 VERSION BU456386.1 GI:25945697

KEYWORDS SOURCE ORGANISM

EST.
Gallus gallus (chicken)
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

REFERENCE

AUTHORS
Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

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Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

FEATURES

source

1..781
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Layer"
/db_xref="taxon:9031"
/clone="CHEST206K24"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSEQOREN14"
/notes="Organ: ovary; Vector: pBluescript II KS(+); Site_1:
EcoRI; Site_2: NotI; This nonnormalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methyated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

ORIGIN

Query Match 73.3%; Score 17.6; DB 5; Length 781;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy

1 TCCGAGCGGTTCTGAGGCTTAC 24

Db

379 TCCGAGGTGTTCTGAGGCTTTC 402

RESULT 43

CA217713

LOCUS
CA217713 786 bp mRNA linear EST 25-SEP-2003
DEFINITION
SCRUAD1133E05.b AD1 Saccharum officinarum cDNA clone SCRUD1133E05
3', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Saccharum officinarum
Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
complex.

REFERENCE

AUTHORS

Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.

TITLE JOURNAL COMMENT

The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 133 row: E column: 05
Seq primer: SP6 Promoter primer.

FEATURES

source

1..786
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCRUD1133E05"
/lab_host="DH10B"
/clone_lib="AD1"
/notes="Organ: seedlings inoculated with Gluconacetobacter
diazotrophicans; Vector: pSport1; Site_1: SalI; Site_2:
NotI; An unidirectional cDNA library generated from
seedlings inoculated with Gluconacetobacter
diazotrophicans]. cDNA was prepared from polyA+ mRNA using
SuperScript Plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CL-2B 40cm-columns and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at http://sucest.lad.ic.unicamp.br/public"

ORIGIN

Query Match 73.3%; Score 17.6; DB 6; Length 786;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy

1 TCCGAGCGGTTCTGAGGCTTAC 24

Db

638 TCCGGACGGTACTCGAGGCTTAC 661

RESULT 44

BU268001

LOCUS
BU268001 789 bp mRNA linear EST 26-NOV-2002
DEFINITION
603817361F1 CSEQCHN52 Gallus gallus cDNA clone CHEST81316 5', mRNA
sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Gallus gallus (chicken)
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

REFERENCE

AUTHORS

Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)

JOURNAL

MEDLINE

PUBMED

COMMENT

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(UMIST)
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Tel: 01612008930
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FEATURES

Location/Qualifiers

```

source
1. .789
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hisex"
/db_xref="taxon:9031"
/clone="CHEST813116"
/dev_stage="22"
/lab_host="DH10B"
/clone_lib="CSEQCHN52"
/note="Organ: limbs; Vector: pBluescript II KS(+); Site_1:
EcoRI; Site 2: NotI; This normalized library was
constructed from 1 million independent clones' cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

ORIGIN
Query Match      73.3%; Score 17.6; DB 5; Length 789;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCGTGAGGCTTAC 24
    ||||| ||||| ||||| ||||| |||||
Db 407 TCCAGAGTGGTTCGTGAGGCTTC 430

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RESULT 45
BH503335/c
LOCUS
DEFINITION
BH503335
BOHGY11TR BOHG Brassica oleracea genomic clone BOHGY11, genomic
survey sequence.
ACCESSION
BH503335
VERSION
BH503335.1 GI:17711432
KEYWORDS
GSS.
SOURCE
Brassica oleracea
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 801)
Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other GSSs: BOHGY11TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
source
1. .801
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
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genomic DNA inserted into pHOS1 using BstXI linkers"

ORIGIN

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Query Match      73.3%; Score 17.6; DB 8; Length 801;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCGTGAGGCTTAC 24
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Db 762 TCCGAGAGGTTATGAGGGTTGAC 739

RESULT 46
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LOCUS
DEFINITION
BU356670
603473324F1 CSEQCHN70 Gallus gallus cDNA clone CHEST35305 5', mRNA
sequence.
ACCESSION
BU356670
VERSION
BU356670.1 GI:25864671
KEYWORDS
EST.
SOURCE
Gallus gallus (chicken)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE
1 (bases 1 to 806)
Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
A Comprehensive Collection of Chicken cDNAs
Curt. Biol. 12 (22), 1965-1969 (2002)
22335534
12445392
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
1. .806
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hisex"
/db_xref="taxon:9031"
/clone="CHEST35305"
/dev_stage="36"
/lab_host="DH10B"
/clone_lib="CSEQCHN70"
/note="Organ: hearts; Vector: pBluescript II KS(+);
Site 1: EcoRI; Site 2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

FEATURES
source
1. .806
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hisex"
/db_xref="taxon:9031"
/clone="CHEST35305"
/dev_stage="36"
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/clone_lib="CSEQCHN70"
/note="Organ: hearts; Vector: pBluescript II KS(+);
Site 1: EcoRI; Site 2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

ORIGIN
Query Match      73.3%; Score 17.6; DB 5; Length 806;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCGTGAGGCTTAC 24
    ||||| ||||| ||||| ||||| |||||
Db 451 TCCAGAGTGGTTCGTGAGGCTTC 474

RESULT 47

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CL747554	CL747554	894 bp	DNA	linear	GSS 27-JUL-2004
LOCUS	OR_BBa0112K21.f OR_BBa Oryza rufipogon genomic clone OR_BBa0112K21				
DEFINITION	5', genomic survey sequence.				
ACCESSION	CL747554				
VERSION	CL747554.1	GI:50690865			
KEYWORDS	GSS.				
SOURCE	Oryza rufipogon				
ORGANISM	Oryza rufipogon				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.				
REFERENCE	1 (bases 1 to 894)				
AUTHORS	Kim,H., Yu,X., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.				
TITLE	ONAP Project				
JOURNAL	Unpublished (2004)				
COMMENT	Contact: Rod A. Wing Arizona Genomics Institute University of Arizona Forbes Building Room 303, Tucson, AZ 85721-0036, USA Tel: 520 626 9595 Fax: 520 621 1259 Email: http://genome.arizona.edu				
	PCR Primers				
	FORWARD: TAA TAC GAC TCA CTA TAG GG				
	BACKWARD: CAC TCA TTA GGC ACC CCA				
	Insert Length: 161 Std Error: 0.00				
	Plate: 0112 row: K Column: 21				
	Seq primer: TAA TAC GAC TCA CTA TAG GG				
	Class: BAC ends.				
FEATURES	Location/Qualifiers				
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	/mol_type="genomic DNA"				
	/db_xref="taxon:4529"				
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	/tissue_type="young leaves"				
	/lab_host="DH10B-T1 phage resistant"				
	/clone_lib="OR_BBa"				
	/note="Vector: pAG1BAC1; Site_1: HindIII; Site_2: HindIII"				
ORIGIN					
Query Match	73.3%	Score 17.6;	DB 9;	Length 894;	
Best Local Similarity	83.3%;	Pred. No. 1.4e+03;			
Matches	20;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;
QY	1 TCCGAGACGGTTCGAGGGCTTAC 24				
	501 TCCGTGACGAATCTGAGGGCTTGC 524				
Db					
RESULT 48					
B12912/c					
LOCUS	B12912	896 bp	DNA	linear	GSS 14-MAY-1997
DEFINITION	T1C12-Sp6.1 TAMU Arabidopsis thaliana genomic clone T1C12, genomic survey sequence.				
ACCESSION	B12912				
VERSION	B12912.1	GI:2094044			
KEYWORDS	GSS.				
SOURCE	Arabidopsis thaliana (thale cress)				
ORGANISM	Arabidopsis thaliana				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.				
REFERENCE	1 (bases 1 to 896)				
AUTHORS	Feng,J., Dewar,K., Buehler,E., Kim,C., Li,Y., Shinn,P., Sun,H. and Ecker,J.				
TITLE	BAC End Sequences at ATGC				
JOURNAL	Unpublished (1997)				
COMMENT	Other GSSs: T1C12-T7, T1C12-Sp6 Contact: Ecker J. Arabidopsis Thaliana Genome Center				

RESULT 50
CNSUAD0F/c
LOCUS
DEFINITION
CNSUAD0F 1773 bp mRNA linear HTC 06-FEB-2004
Arabidopsis thaliana Full-length cDNA Complete sequence from clone
GSLTPGH22ZF06 of Hormone Treated Callus of strain col-0 of
Arabidopsis thaliana (thale cress).
BX816012
BX816012.1 GI:42473422
HTC; GSLT cDNA.
SOURCE
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
1 (bases 1 to 1773)
Castelli,V., Aury,J.M., Jaillon,O., Wincker,F., Clepet,C.,
Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V.,
Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.
Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
Annotation
Unpublished
2 (bases 1 to 1773)
Genoscope.
Direct Submission
Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out
full-length libraries construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.
URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences). 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
length
http://www.genoscope.cns.fr/cgi-bin/ggb?source=Arabidopsis.
FEATURES
source
1..1773
/organism="Arabidopsis thaliana"
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/strain="Col-0"
/db_xref="taxon:3702"
/clone="GSLTPGH22ZF06"
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ORIGIN
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Best Local Similarity 83.3%; Pred.No. 1.5e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Dy 1 TCCGACGGTTCGTAGGCTTAC 24
||| ||||| ||||| |||||
Db 627 TCCAGTCGTTCTGATGGCTAC 604
Search completed: March 25, 2005, 12:33:59
Job time : 1850 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 25, 2005, 10:59:21 ; Search time 78.2857 Seconds
(without alignments)

501.632 Million cell updates/sec

Title: US-10-688-489-75

Perfect score: 24

Sequence: 1 tcgcagcgggtcttgagggtttac 24

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 segs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

Issued Patents NA.*

1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*

2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*

3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*

4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*

5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*

6: /cgn2_6/ptodata/1/ina/backfileseq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16.8	70.0	2799	3	US-08-368-752B-5
2	16.8	70.0	2799	3	US-09-536-224-5
3	16.6	69.2	601	4	US-09-949-016-157466
4	16.6	69.2	601	4	US-09-949-016-157573
5	16.6	69.2	601	4	US-09-949-016-157873
6	16.6	69.2	126176	4	US-09-949-016-16137
7	16.6	69.2	126176	4	US-09-949-016-16138
8	16.6	69.2	153866	4	US-09-949-016-16919
9	16.6	69.2	156698	4	US-09-949-016-16038
10	16.6	69.2	767677	4	US-09-949-016-12147
11	16.6	69.2	767677	4	US-09-949-016-17361
12	16.6	69.2	4403765	3	US-09-103-840A-2
13	16.6	69.2	4411529	3	US-09-103-840A-1
14	16.2	67.5	921	4	US-09-107-532A-2264
15	16.2	67.5	1815	4	US-09-832-496-1
16	16.2	67.5	1815	4	US-09-832-616-1
17	16.2	67.5	21721	4	US-09-369-939A-41
18	16.2	67.5	22976	4	US-09-369-939A-19
19	16.2	67.5	23187	4	US-09-499-522-1
20	16	66.7	522	4	US-09-252-991A-8519
21	16	66.7	579	4	US-09-270-767-12997
22	16	66.7	1113	4	US-09-352-991A-8445
23	16	66.7	1850	4	US-09-799-451-367
24	16	66.7	2409	4	US-09-252-991A-8479
25	16	66.7	7240	4	US-09-695-795A-1
26	15.8	65.8	37	1	US-08-199-507B-21
27	15.8	65.8	37	1	US-08-441-828-21

28	15.8	65.8	601	4	US-09-949-016-192257	Sequence 192257,
29	15.8	65.8	1621	1	US-08-292-688A-10	Sequence 10, Appl
30	15.8	1795		2	US-08-791-849A-12	Sequence 12, Appl
31	15.8	55031		4	US-09-949-016-17389	Sequence 17389, A
32	15.8	90776		4	US-09-949-016-17230	Sequence 17230, A
33	15.8	122772		4	US-09-949-016-14132	Sequence 14132, A
34	15.8	767677		4	US-09-949-016-12147	Sequence 12147, A
35	15.8	767677		4	US-09-949-016-17361	Sequence 17361, A
36	15.6	601		4	US-09-949-016-45837	Sequence 45837, A
37	15.6	601		4	US-09-949-016-45859	Sequence 45859, A
38	15.6	948		4	US-09-489-039A-1034	Sequence 1034, Ap
39	15.6	1341		4	US-09-248-796A-6062	Sequence 6062, Ap
40	15.6	2121		4	US-09-902-540-8806	Sequence 8806, Ap
41	15.6	2332		4	US-09-949-016-253	Sequence 253, App
42	15.6	2332		4	US-09-949-016-5522	Sequence 5522, Ap
43	15.6	3595		4	US-09-949-016-408	Sequence 408, App
44	15.6	3607		4	US-09-563-269-17	Sequence 17, Appl
45	15.6	3943		3	US-08-506-296B-27	Sequence 27, Appl
46	15.6	4041		4	US-09-949-016-1305	Sequence 1305, Ap
47	15.6	4041		4	US-09-949-016-1306	Sequence 1306, Ap
48	15.6	4078		4	US-09-016-434-1152	Sequence 1152, Ap
49	15.6	4546		4	US-09-949-016-4140	Sequence 4140, Ap
50	15.6	4553		4	US-09-023-655-975	Sequence 975, App
51	15.6	4553		4	US-09-949-016-726	Sequence 726, App
52	15.6	5319		2	US-08-861-464-7	Sequence 7, Appli
53	15.6	5319		3	US-08-396-001-7	Sequence 7, Appli
54	15.6	5319		3	US-09-323-433A-7	Sequence 7, Appli
55	15.6	5319		4	US-09-826-752-7	Sequence 7, Appli
56	15.6	10096		4	US-09-902-540-935	Sequence 935, App
57	15.6	15659		4	US-09-949-016-16053	Sequence 16053, A
58	15.6	16924		4	US-09-949-016-13720	Sequence 13720, A
59	15.6	18318		1	US-08-414-926A-6	Sequence 6, Appli
60	15.6	18318		2	US-08-926-922-6	Sequence 6, Appli
61	15.6	18318		3	US-09-253-682-6	Sequence 6, Appli
62	15.6	18318		3	US-09-527-657-6	Sequence 6, Appli
63	15.6	18318		4	US-09-892-100-6	Sequence 6, Appli
64	15.6	60304		4	US-09-949-016-11995	Sequence 11995, A
65	15.6	60304		4	US-09-949-016-17264	Sequence 17264, A
66	15.6	63183		4	US-09-949-016-13047	Sequence 13047, A
67	15.6	63183		4	US-09-949-016-13048	Sequence 13048, A
68	15.6	229354		4	US-09-705-400-64	Sequence 64, Appl
69	15.6	325034		4	US-09-949-016-14957	Sequence 14957, A
70	15.6	389504		4	US-09-949-016-11774	Sequence 11774, A
71	15.4	64.2	73853	4	US-09-949-016-12029	Sequence 12029, A
72	15.4	64.2	134987	4	US-09-949-016-15348	Sequence 15348, A
73	15.4	64.2	134987	4	US-09-949-016-15349	Sequence 15349, A
74	15.4	64.2	134987	4	US-09-949-016-15350	Sequence 15350, A
75	15.4	64.2	134987	4	US-09-949-016-15507	Sequence 15507, A
76	15.4	64.2	134987	4	US-09-949-016-15508	Sequence 15508, A
77	15.4	64.2	134987	4	US-09-949-016-15509	Sequence 15509, A
78	15.2	63.3	147	4	US-09-513-999C-22084	Sequence 22084, A
79	15.2	63.3	221	4	US-09-513-999C-20238	Sequence 20238, A
80	15.2	63.3	601	4	US-09-949-016-21395	Sequence 21395, A
81	15.2	63.3	601	4	US-09-949-016-21396	Sequence 21396, A
82	15.2	63.3	601	4	US-09-949-016-26139	Sequence 26139, A
83	15.2	63.3	601	4	US-09-949-016-128275	Sequence 128275, A
84	15.2	63.3	601	4	US-09-949-016-190884	Sequence 190884, A
85	15.2	63.3	601	4	US-09-949-016-190885	Sequence 190885, A
86	15.2	63.3	1035	4	US-09-540-236-1142	Sequence 1142, Ap
87	15.2	63.3	1368	4	US-09-489-039A-5652	Sequence 5652, Ap
88	15.2	63.3	1492	4	US-09-369-247-23	Sequence 23, Appl
89	15.2	63.3	1611	4	US-09-808-701A-13	Sequence 13, Appl
90	15.2	63.3	2213	4	US-09-620-312D-1038	Sequence 1038, Ap
91	15.2	63.3	2478	3	US-08-485-355B-47	Sequence 47, Appl
92	15.2	63.3	2478	3	US-08-485-355B-49	Sequence 49, Appl
93	15.2	63.3	2478	3	US-09-194-613-1	Sequence 1, Appli
94	15.2	63.3	2782	4	US-08-485-355B-51	Sequence 51, Appl
95	15.2	63.3	2782	4	US-09-949-016-5457	Sequence 5457, Ap
96	15.2	63.3	2797	3	US-09-240-639-3	Sequence 3, Appli
97	15.2	63.3	2797	4	US-09-908-510A-3	Sequence 3, Appli
98	15.2	63.3	2797	4	US-09-905-744B-3	Sequence 3, Appli
99	15.2	63.3	2797	4	US-10-107-660-3	Sequence 3, Appli
100	15.2	63.3	2797	4	US-10-107-576-3	Sequence 3, Appli

C 101	15.2	63.3	2797	4	US-09-905-732B-3	Sequence 3, Appli	174	14.8	61.7	601	4	US-09-949-016-156680	Sequence 156680,
C 102	15.2	63.3	2797	4	US-09-923-304-3	Sequence 3, Appli	175	14.8	61.7	758	4	US-09-976-594-101	Sequence 101, App
C 103	15.2	63.3	2797	4	US-09-949-016-178	Sequence 178, App	176	14.8	61.7	1437	4	US-09-894-844-90	Sequence 90, Appl
C 104	15.2	63.3	2797	4	US-09-905-743B-3	Sequence 3, Appli	177	14.8	61.7	1693	1	US-08-292-688A-13	Sequence 13, Appl
C 105	15.2	63.3	3611	3	US-09-336-643A-9	Sequence 9, Appli	178	14.8	61.7	1693	1	US-08-292-688A-14	Sequence 14, Appl
C 106	15.2	63.3	3611	3	US-09-949-016-3632	Sequence 3632, Ap	179	14.8	61.7	1729	1	US-09-620-312D-1016	Sequence 1016, Ap
C 107	15.2	63.3	13782	4	US-09-949-016-14992	Sequence 14992, A	180	14.8	61.7	12460	4	US-09-949-016-13009	Sequence 13009, A
C 108	15.2	63.3	13782	4	US-09-811-825A-3	Sequence 3, Appli	181	14.8	61.7	38961	4	US-09-949-016-12143	Sequence 12143, A
C 109	15.2	63.3	18554	4	US-09-949-016-15750	Sequence 15750, A	182	14.8	61.7	38961	4	US-09-949-016-14474	Sequence 14474, A
C 110	15.2	63.3	20444	4	US-09-596-002-16	Sequence 16, Appl	183	14.8	61.7	73818	4	US-09-949-016-16822	Sequence 16822, A
C 111	15.2	63.3	22407	4	US-09-949-016-11920	Sequence 11920, A	184	14.8	61.7	194889	4	US-09-949-016-15654	Sequence 15654, A
C 112	15.2	63.3	45539	4	US-09-949-016-17199	Sequence 17199, A	185	14.8	61.7	231129	4	US-09-949-016-16110	Sequence 16110, A
C 113	15.2	63.3	45463	4	US-09-949-016-14781	Sequence 14781, A	186	14.8	61.7	266293	4	US-09-949-016-11934	Sequence 11934, A
C 114	15.2	63.3	59252	4	US-09-949-016-12150	Sequence 12150, A	187	14.6	60.8	71	1	US-08-148-910-10	Sequence 10, Appl
C 115	15.2	63.3	59252	4	US-09-949-016-15374	Sequence 15374, A	188	14.6	60.8	71	1	US-08-448-937A-10	Sequence 10, Appl
C 116	15.2	63.3	276687	4	US-09-949-016-13840	Sequence 13840, A	189	14.6	60.8	235	4	US-09-513-999C-12048	Sequence 12048, A
C 117	15	62.5	258	4	US-09-313-294A-2060	Sequence 2060, Ap	190	14.6	60.8	341	4	US-09-513-999C-3453	Sequence 3453, Ap
C 118	15	62.5	524	4	US-09-270-767-4427	Sequence 4427, Ap	191	14.6	60.8	349	4	US-09-621-976-7870	Sequence 7870, Ap
C 119	15	62.5	524	4	US-09-270-767-19709	Sequence 19709, A	192	14.6	60.8	366	4	US-09-424-840B-29	Sequence 29, Appl
C 120	15	62.5	601	4	US-09-949-016-46408	Sequence 46408, A	193	14.6	60.8	366	4	US-09-949-016-90142	Sequence 90142, A
C 121	15	62.5	601	4	US-09-949-016-63051	Sequence 63051, A	194	14.6	60.8	464	4	US-09-949-016-90168	Sequence 90168, A
C 122	15	62.5	601	4	US-09-949-016-63052	Sequence 63052, A	195	14.6	60.8	465	4	US-09-949-016-90141	Sequence 90141, A
C 123	15	62.5	601	4	US-09-949-016-168647	Sequence 168647, A	196	14.6	60.8	465	4	US-09-949-016-90167	Sequence 90167, A
C 124	15	62.5	601	4	US-09-949-016-183481	Sequence 183481, A	197	14.6	60.8	486	4	US-09-702-705-877	Sequence 877, App
C 125	15	62.5	744	4	US-09-489-039A-4338	Sequence 4338, Ap	198	14.6	60.8	486	4	US-09-736-457-877	Sequence 877, App
C 126	15	62.5	744	4	US-09-543-681A-156	Sequence 156, App	199	14.6	60.8	486	4	US-09-614-124B-877	Sequence 877, App
C 127	15	62.5	897	3	US-09-058-389A-17	Sequence 17, Appl	200	14.6	60.8	486	4	US-09-671-325-877	Sequence 877, App
C 128	15	62.5	897	3	US-09-611-781-17	Sequence 17, Appl	201	14.6	60.8	486	4	US-09-658-824-877	Sequence 877, App
C 129	15	62.5	1035	4	US-09-489-039A-4287	Sequence 4287, Ap	202	14.6	60.8	491	4	US-09-513-999C-23735	Sequence 23735, A
C 130	15	62.5	1272	3	US-09-058-389A-7	Sequence 7, Appli	203	14.6	60.8	503	4	US-09-621-976-10616	Sequence 10616, A
C 131	15	62.5	1272	3	US-09-611-781-7	Sequence 7, Appli	204	14.6	60.8	512	4	US-09-621-976-10625	Sequence 10625, A
C 132	15	62.5	1738	2	US-08-932-376A-1	Sequence 1, Appli	205	14.6	60.8	518	4	US-09-621-976-2942	Sequence 2942, Ap
C 133	15	62.5	1847	3	US-09-058-389A-9	Sequence 9, Appli	206	14.6	60.8	519	4	US-09-621-976-2942	Sequence 2942, Ap
C 134	15	62.5	1847	3	US-09-611-781-9	Sequence 9, Appli	207	14.6	60.8	535	4	US-09-242-999-23	Sequence 23, Appl
C 135	15	62.5	1963	4	US-09-620-312D-596	Sequence 596, App	208	14.6	60.8	588	3	US-09-227-357-114	Sequence 114, App
C 136	15	62.5	2220	2	US-08-932-376A-3	Sequence 3, Appli	209	14.6	60.8	601	4	US-09-949-016-27228	Sequence 27228, A
C 137	15	62.5	6101	4	US-09-949-016-1376	Sequence 1376, Ap	210	14.6	60.8	601	4	US-09-949-016-30639	Sequence 30639, A
C 138	15	62.5	6354	3	US-09-058-389A-5	Sequence 5, Appli	211	14.6	60.8	601	4	US-09-949-016-50453	Sequence 50453, A
C 139	15	62.5	6354	3	US-09-611-781-5	Sequence 5, Appli	212	14.6	60.8	601	4	US-09-949-016-73142	Sequence 73142, A
C 140	15	62.5	6384	4	US-09-949-016-12165	Sequence 12165, A	213	14.6	60.8	601	4	US-09-949-016-81278	Sequence 81278, A
C 141	15	62.5	6384	4	US-09-949-016-13581	Sequence 13581, A	214	14.6	60.8	601	4	US-09-949-016-90139	Sequence 90139, A
C 142	15	62.5	7017	4	US-09-949-016-67	Sequence 67, Appl	215	14.6	60.8	601	4	US-09-949-016-90140	Sequence 90140, A
C 143	15	62.5	9990	4	US-09-949-016-15542	Sequence 15542, A	216	14.6	60.8	601	4	US-09-949-016-90165	Sequence 90165, A
C 144	15	62.5	12023	4	US-09-634-238-405	Sequence 405, App	217	14.6	60.8	601	4	US-09-949-016-90166	Sequence 90166, A
C 145	15	62.5	12359	4	US-09-949-016-17004	Sequence 17004, A	218	14.6	60.8	601	4	US-09-949-016-102925	Sequence 102925, A
C 146	15	62.5	12366	4	US-09-949-016-13082	Sequence 13082, A	219	14.6	60.8	601	4	US-09-949-016-102926	Sequence 102926, A
C 147	15	62.5	22131	4	US-09-949-016-15391	Sequence 15391, A	220	14.6	60.8	601	4	US-09-949-016-105796	Sequence 105796, A
C 148	15	62.5	22131	4	US-09-949-016-15392	Sequence 15392, A	221	14.6	60.8	601	4	US-09-949-016-105797	Sequence 105797, A
C 149	15	62.5	27180	4	US-09-949-016-15392	Sequence 15392, A	222	14.6	60.8	601	4	US-09-949-016-145130	Sequence 145130, A
C 150	15	62.5	27180	4	US-09-949-016-15392	Sequence 15392, A	223	14.6	60.8	601	4	US-09-949-016-145131	Sequence 145131, A
C 151	15	62.5	30364	4	US-09-949-016-14587	Sequence 14587, A	224	14.6	60.8	601	4	US-09-949-016-186488	Sequence 186488, A
C 152	15	62.5	30364	4	US-09-949-016-15620	Sequence 15620, A	225	14.6	60.8	601	4	US-09-949-016-203566	Sequence 203566, A
C 153	15	62.5	32155	4	US-09-949-016-16497	Sequence 16497, A	226	14.6	60.8	601	4	US-09-949-016-203567	Sequence 203567, A
C 154	15	62.5	32155	4	US-08-311-731A-1	Sequence 1, Appli	227	14.6	60.8	615	4	US-09-461-325-122	Sequence 452, App
C 155	15	62.5	41618	4	US-09-949-016-14356	Sequence 14356, A	228	14.6	60.8	615	4	US-09-461-325-122	Sequence 122, App
C 156	15	62.5	41618	4	US-09-949-016-14681	Sequence 14681, A	229	14.6	60.8	615	4	US-10-112-542-122	Sequence 122, App
C 157	15	62.5	47493	4	US-09-949-016-13241	Sequence 13241, A	230	14.6	60.8	615	4	US-10-112-542-122	Sequence 122, App
C 158	15	62.5	58439	4	US-09-949-016-13565	Sequence 13565, A	231	14.6	60.8	615	4	US-09-949-016-4373	Sequence 4373, Ap
C 159	15	62.5	98439	4	US-09-949-016-13597	Sequence 13597, A	232	14.6	60.8	615	4	US-09-807-802A-8	Sequence 8, Appli
C 160	15	62.5	107800	4	US-09-949-016-13118	Sequence 13118, A	233	14.6	60.8	1200	4	US-09-234-332-4	Sequence 4, Appli
C 161	15	62.5	116425	4	US-09-949-016-11809	Sequence 11809, A	234	14.6	60.8	1635	3	US-09-702-703-1798	Sequence 1798, Ap
C 162	15	62.5	176373	3	US-09-128-153-17	Sequence 17, Appl	235	14.6	60.8	1635	3	US-09-736-457-1798	Sequence 1798, Ap
C 163	15	62.5	264358	4	US-09-949-016-15725	Sequence 15725, A	236	14.6	60.8	1716	4	US-09-671-325-1798	Sequence 44, Appl
C 164	15	62.5	373182	4	US-09-949-016-17371	Sequence 17371, A	237	14.6	60.8	1716	4	US-09-674-677-6	Sequence 6, Appli
C 165	15	62.5	373694	4	US-09-949-016-12062	Sequence 12062, A	238	14.6	60.8	1872	4	US-09-807-802A-4	Sequence 4, Appli
C 166	15	62.5	462589	4	US-09-949-016-12900	Sequence 12900, A	239	14.6	60.8	2132	3	US-09-552-322-1	Sequence 1, Appli
C 167	15	62.5	476044	4	US-09-949-016-13412	Sequence 13412, A	240	14.6	60.8	2150	4	US-09-461-325-76	Sequence 76, Appl
C 168	15	62.5	1230025	4	US-09-198-452A-1	Sequence 1, Appli	241	14.6	60.8	2150	4	US-10-012-542-76	Sequence 76, Appl
C 169	15	62.5	1230230	4	US-09-438-185A-1	Sequence 1, Appli	242	14.6	60.8	2150	4	US-10-115-123-76	Sequence 76, Appl
C 170	15	62.5	4403765	3	US-09-103-840A-2	Sequence 2, Appli	243	14.6	60.8	3116	4	US-08-149-103-2	Sequence 2, Appli
C 171	14.8	61.7	207	4	US-09-513-999C-10938	Sequence 10938, A	244	14.6	60.8				
C 172	14.8	61.7	593	4	US-09-517-431E-10	Sequence 10, Appl	245	14.6	60.8				
C 173	14.8	61.7	601	4	US-09-949-016-138761	Sequence 138761, A	246	14.6	60.8				

TELECOMMUNICATION INFORMATION:

TELEPHONE: 510-222-9700
TELEFAX: 510-222-9758
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2799 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2799
US-08-968-752B-5

Query Match 70.0%; Score 16.8; DB 3; Length 2799;
Best Local Similarity 90.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCGAGACGGTCTCTGAGGGCT 21
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Db 444 CCGAGGAGGTTCTGAGGGCT 463

RESULT 2

US-09-536-224-5
Sequence 5, Application US/09536224
Patent No. 6379665
GENERAL INFORMATION:
APPLICANT: Frohman, Michael A.
APPLICANT: Morris, Andrew
TITLE OF INVENTION: No. 6379665el Phospholipase D Polypeptide and
TITLE OF INVENTION: DNA Sequences
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: ONYX Pharmaceuticals, Inc.
STREET: 3031 Research Drive
CITY: Richmond
STATE: California
COUNTRY: USA
ZIP: 94806

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/536,224
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/968,752
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Giotta, Gregory J.
REGISTRATION NUMBER: 32,028
REFERENCE/DOCKET NUMBER: ONYX2004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-222-9700
TELEFAX: 510-222-9758
INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 2799 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS

LOCATION: 1..2799
US-09-536-224-5

Query Match 70.0%; Score 16.8; DB 3; Length 2799;
Best Local Similarity 90.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCGAGACGGTCTCTGAGGGCT 21
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Db 444 CCGAGGAGGTTCTGAGGGCT 463

RESULT 3

US-09-949-016-157466
Sequence 157466, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 157466
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-157466

Query Match 69.2%; Score 16.6; DB 4; Length 601;
Best Local Similarity 82.6%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCTGAGGGCTTA 23
||||| |||||||
Db 273 TCAGAGATGATTTTGAGGGCTTA 295

RESULT 4

US-09-949-016-157573
Sequence 157573, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 157573
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-157573

Query Match 69.2%; Score 16.6; DB 4; Length 601;
Best Local Similarity 82.6%; Pred. No. 1.2e+02;


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RESULT 13
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103.840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match      69.2%; Score 16.6; DB 3; Length 4411529;
Best Local Similarity 82.6%; Pred. No. 2.3e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCGAGGGCTTA 23
Db 2394408 TCCGAGACGGTCCGGCGGCGATA 2394386

RESULT 14
US-09-107-532A-2264
; Sequence 2284, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; CORRESPONDENCE ADDRESS:
; ADDRESS: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 2264:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 921 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
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; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...921
; SEQUENCE DESCRIPTION: SEQ ID NO: 2264:
US-09-107-532A-2264

Query Match      67.5%; Score 16.2; DB 4; Length 921;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GAGACGGTTCGAGGGCTTAC 24
Db 533 GAGACGGTTATGACGGCTTCC 553

RESULT 15
US-09-832-496-1
; Sequence 1, Application US/09832496
; Patent No. 6503508
; GENERAL INFORMATION:
; APPLICANT: Danielisen, Steffen
; APPLICANT: Schneider, Palle
; TITLE OF INVENTION: Polypeptides having haloperoxidase activity
; FILE REFERENCE: 10042.200-US
; CURRENT APPLICATION NUMBER: US/09/832,496
; CURRENT FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1815
; TYPE: DNA
; ORGANISM: Dreschlera hartleibii
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) .. (1815)
US-09-832-496-1

Query Match      67.5%; Score 16.2; DB 4; Length 1815;
Best Local Similarity 85.7%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CGAGACGGTTCGAGGGCTTA 23
Db 1606 CGTGAGGGTTGTGAGGGCTTA 1626

RESULT 16
US-09-832-616-1
; Sequence 1, Application US/09832616
; Patent No. 6506586
; GENERAL INFORMATION:
; APPLICANT: Danielisen, Steffen
; APPLICANT: Schneider, Palle
; TITLE OF INVENTION: Nucleic acids encoding polypeptides having haloperoxidase activit
; FILE REFERENCE: 10175.200-US
; CURRENT APPLICATION NUMBER: US/09/832,616
; CURRENT FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1815
; TYPE: DNA
; ORGANISM: Dreschlera hartleibii
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) .. (1815)
US-09-832-616-1
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Query Match      67.5%; Score 16.2; DB 4; Length 1815;
Best Local Similarity 85.7%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CGAGACGGTCTCTAGGGCTTA 23
Db 1606 CGTGAGGGTTGTGAGGGCTTA 1626

RESULT 17
US-09-269-939A-41/c
; Sequence 41, Application US/09269939A
; Patent No. 6635431
; GENERAL INFORMATION:
; APPLICANT: Bihain, Bernard
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Yen-Potin, Frances
; TITLE OF INVENTION: LSR Receptor, Its Activity, Its Cloning and Its Application To
; TITLE OF INVENTION: The Diagnosis Prevention And/or Treatment of Obesity and
; TITLE OF INVENTION: Related Risks or Complications
; FILE REFERENCE: GENSET-035APC
; CURRENT APPLICATION NUMBER: US/09/269,939A
; CURRENT FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: FR 97/10088
; PRIOR FILING DATE: 1997-08-06
; PRIOR APPLICATION NUMBER: FR 98/05032
; PRIOR FILING DATE: 1998-04-22
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent.pm
; SEQ ID NO 41
; LENGTH: 21721
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1898..2253
; NAME/KEY: exon
; LOCATION: 3438..3782
; NAME/KEY: exon
; LOCATION: 12064..12183
; NAME/KEY: exon
; LOCATION: 15049..15105
; NAME/KEY: exon
; LOCATION: 15670..15816
; NAME/KEY: exon
; LOCATION: 19486..19659
; NAME/KEY: exon
; LOCATION: 19806..19865
; NAME/KEY: exon
; LOCATION: 19963..20094
; NAME/KEY: exon
; LOCATION: 20236..20864
; NAME/KEY: exon
; LOCATION: 20954..21094
; NAME/KEY: Misc_Feature
; LOCATION: 715
; OTHER INFORMATION: diverging nucleotide, G in ref genbank:AC002128
; NAME/KEY: Misc_Feature
; LOCATION: 1229
; OTHER INFORMATION: diverging insertion, G in ref genbank:AC002128
; NAME/KEY: Misc_Feature
; LOCATION: 3676
; OTHER INFORMATION: diverging nucleotide, T in ref genbank:AC002128
; NAME/KEY: Misc_Feature
; LOCATION: 5039
; OTHER INFORMATION: diverging deletion, G in ref genbank:AD000684
; LOCATION: 5118
; OTHER INFORMATION: diverging nucleotide, C in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 7337
; OTHER INFORMATION: diverging deletion, C in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 8294
; OTHER INFORMATION: diverging nucleotide, G in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 8604
; OTHER INFORMATION: diverging nucleotide, C in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 8928
; OTHER INFORMATION: diverging nucleotide, A in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 9021
; OTHER INFORMATION: diverging nucleotide, G in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 9851
; OTHER INFORMATION: diverging insertion, GAATGAAA in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 9878
; OTHER INFORMATION: diverging nucleotide, C in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 11478
; OTHER INFORMATION: diverging nucleotide, T in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 11577
; OTHER INFORMATION: diverging deletion, C in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 11779
; OTHER INFORMATION: diverging nucleotide, T in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 13411
; OTHER INFORMATION: diverging deletion, T in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 13538
; OTHER INFORMATION: diverging nucleotide, G in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 13896
; OTHER INFORMATION: diverging nucleotide, G in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 14912
; OTHER INFORMATION: diverging nucleotide, A in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 16732
; OTHER INFORMATION: diverging nucleotide, C in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 17169
; OTHER INFORMATION: diverging nucleotide, G in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 18946
; OTHER INFORMATION: diverging deletion, G in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 19474
; OTHER INFORMATION: diverging nucleotide, G in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 20500
; OTHER INFORMATION: diverging deletion, G in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 20501
; OTHER INFORMATION: diverging deletion, G in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 20502
; OTHER INFORMATION: diverging deletion, A in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 21270
; OTHER INFORMATION: diverging nucleotide, G in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 21356
; OTHER INFORMATION: diverging insertion, T in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 21476
; OTHER INFORMATION: diverging nucleotide, A in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 21588
; OTHER INFORMATION: diverging insertion, C in ref genbank:AD000684
; NAME/KEY: Misc_Feature
```

```

; LOCATION: 21601
; OTHER INFORMATION: diverging deletion, T in ref genbank:AD000684
; NAME/KEY: Misc Feature
; LOCATION: 21635
; OTHER INFORMATION: diverging insertion, G in ref genbank:AD000684
; NAME/KEY: Misc Feature
; LOCATION: 19963..19965
; OTHER INFORMATION: Potential variant splicing site AAG
; NAME/KEY: Misc Feature
; LOCATION: 1..21721
; OTHER INFORMATION: n= a,g,c or t
US-09-269-939A-41

```

Query Match: 67.5%; Score 16.2; DB 4; Length 21721;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0;

QY 1 TCCGAGACGGTTC TGAGGGCT 21
||| || | ||| ||| ||| |||
Db 14809 TCCAGGGGGTTCTGAGGGCT 14789

RESULT 18
US-09-269-939A-19/c
; Sequence 19, Application US/09269939A
; Patent No. 6635431
; GENERAL INFORMATION:

/ INFORMATION:
 / APPLICANT: Bihain, Bernard
 / APPLICANT: Bougueleret, Lydie
 / APPLICANT: Yen-Potin, Frances
 / TITLE OF INVENTION: LSR Receptor, Its Activity, Its Cloning and Its Application To
 / TITLE OF INVENTION: The Diagnosis Prevention And/or Treatment of Obesity and
 / TITLE OF INVENTION: Related Risks or Complications
 / FILE REFERENCE: GENSET.035APC
 / CURRENT APPLICATION NUMBER: US/09/269,939A
 / CURRENT FILING DATE: 1999-05-28
 / PRIOR APPLICATION NUMBER: FR 97/10088
 / PRIOR FILING DATE: 1997-08-06
 / PRIOR APPLICATION NUMBER: FR 98/05032
 / PRIOR FILING DATE: 1998-04-22
 / NUMBER OF SEQ ID NOS: 41
 / SOFTWARE: Patent.pm

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; SOFTWARE: FACSIMILE.PRM
; SEQ ID NO 19
; LENGTH: 22976

```

LENGTH: 22376
TYPE: DNA

ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: exon

; LOCATION: 1898..2253

; NAME/KEY: exon

; LOCATION: 3437..3781

; NAME/KEY: exon

; LOCATION: 12065..12184

; NAME/KEY: exon

; LOCATION: 15045..15101

```

; NAME/KEY: exon
LOCATION: 1500 15013

```

```

; LOCATION: 15666..15812
: NAME/KEY: 0x00

```

```

; NAME/KEY: exon
: LOCATION: 19479 19553

```

```

; LOCATION: 19479..19652
; NAME/KEY: exon

```

```

; NAME/KEY: exon
; LOCATION: 19799..19858

```

```

LOCATION: 19799..19858
NAME/KEY: exon

```

NAME/ KEY: exon
LOCATION: 19956..20087

```
LOCATION: 19936..20087
NAME/KEY: exon
```

LOCATION: 20229..20854

NAME/KEY: exon

LOCATION: 20944..21094

NAME/KEY: Misc_Feature

LOCATION: 19956..19958

;; OTHER INFORMATION: Pote

US-09-269-939A-19

Quincy: Match

Query Match

Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels

Qy 1 TCCGAGACGGTTCGAGGGCT 21
Db 14805 TCCGAGGGGTTCGAGGGCT 14785

RESULT 19
US-09-499-522-1/c
; Sequence 1, Application US/09499522
; Patent No. 6479238
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bihain, Bernard
; TITLE OF INVENTION: POLYMORPHIC MARKERS OF THE LSR GENE
; FILE REFERENCE: GENSET.0531AUS

```

/ CURRENT APPLICATION NUMBER: US 09/499,522
/ CURRENT FILING DATE: 2000-02-10
/ EARLIER APPLICATION NUMBER: US 60/119,592
/ EARLIER FILING DATE: 1999-02-10
/ EARLIER APPLICATION NUMBER: US 60/144,784
/ EARLIER FILING DATE: 1999-07-20
/ NUMBER OF SEQ ID NOS: 20
/ SOFTWARE: Patent.pm
/ SEQ ID NO 1
/ LENGTH: 23187

```

```

/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 2001..2356
/ OTHER INFORMATION: exon1
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 3540..3884
/ OTHER INFORMATION: exon2
/

```

```

;
; FEATURE:
; NAME/KEY: exon
; LOCATION: 12163..12282
; OTHER INFORMATION: exon3
; FEATURE:
; NAME/KEY: exon
; LOCATION: 15144..15200
; OTHER INFORMATION: exon4
; FEATURE:
; NAME/KEY: exon

```

```

; LOCATION: 15765..15911
; OTHER INFORMATION: exon5
;
; FEATURE:
;
; NAME/KEY: exon
; LOCATION: 19579..19752
; OTHER INFORMATION: exon6
;
; FEATURE:
;
; NAME/KEY: exon
; LOCATION: 19899..19958
; OTHER INFORMATION: exon7
;

```

```

, FEATURE:
, NAME/KEY: exon
, LOCATION: 20056..20187
, OTHER INFORMATION: exon8
, FEATURE:
, NAME/KEY: exon
, LOCATION: 20329..20957
, OTHER INFORMATION: exon9
, FEATURE:
, NAME/KEY: exon

```

```

; LOCATION: 21047..21187
; OTHER INFORMATION: exon10
;
; FEATURE:
; NAME/KEY: polyA_signal
; LOCATION: 21168..21173
;

```

```

OTHER INFORMATION: AATAAA
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..2000
OTHER INFORMATION: potential 5'regulatory region
FEATURE:
NAME/KEY: misc feature
LOCATION: 22324..23187
OTHER INFORMATION: homology with USP2 gene in ref: emb1 Y07661
FEATURE:
NAME/KEY: primer bind
LOCATION: 523..544
OTHER INFORMATION: upstream amplification primer 17-2
FEATURE:
NAME/KEY: primer bind
LOCATION: 1047..1068
OTHER INFORMATION: downstream amplification primer 17-2, complement
FEATURE:
NAME/KEY: primer bind
LOCATION: 946..963
OTHER INFORMATION: upstream amplification primer 99-4576
FEATURE:
NAME/KEY: primer bind
LOCATION: 1385..1402
OTHER INFORMATION: downstream amplification primer 99-4576, complement
FEATURE:
NAME/KEY: primer bind
LOCATION: 1096..1115
OTHER INFORMATION: upstream amplification primer 9-19
FEATURE:
NAME/KEY: primer bind
LOCATION: 1616..1635
OTHER INFORMATION: downstream amplification primer 9-19, complement
FEATURE:
NAME/KEY: primer bind
LOCATION: 1602..1621
OTHER INFORMATION: upstream amplification primer 9-20
FEATURE:
NAME/KEY: primer bind
LOCATION: 2074..2093
OTHER INFORMATION: downstream amplification primer 9-20, complement
FEATURE:
NAME/KEY: primer bind
LOCATION: 2036..2053
OTHER INFORMATION: upstream amplification primer 99-4557
FEATURE:
NAME/KEY: primer bind
LOCATION: 2583..2580
OTHER INFORMATION: downstream amplification primer 99-4557, complement
FEATURE:
NAME/KEY: primer bind
LOCATION: 2084..2102
OTHER INFORMATION: upstream amplification primer 9-1
FEATURE:
NAME/KEY: primer bind
LOCATION: 2483..2500
OTHER INFORMATION: downstream amplification primer 9-1, complement
FEATURE:
NAME/KEY: primer bind
LOCATION: 2470..2489
OTHER INFORMATION: upstream amplification primer 9-21, complement
FEATURE:
NAME/KEY: primer bind
LOCATION: 2062..2081
OTHER INFORMATION: downstream amplification primer 9-21
FEATURE:
NAME/KEY: primer bind
LOCATION: 3455..3474
OTHER INFORMATION: upstream amplification primer 9-3
FEATURE:
NAME/KEY: primer bind
LOCATION: 3882..3901
OTHER INFORMATION: downstream amplification primer 9-3, complement

```

```

FEATURE:
NAME/KEY: primer bind
LOCATION: 3775..3792
OTHER INFORMATION: upstream amplification primer 99-4558
FEATURE:
NAME/KEY: primer bind
LOCATION: 4336..4356
OTHER INFORMATION: downstream amplification primer 99-4558, complement
FEATURE:
NAME/KEY: primer bind
LOCATION: 4902..4920
OTHER INFORMATION: upstream amplification primer 99-14419, complement
FEATURE:
NAME/KEY: primer bind
LOCATION: 4444..4463
OTHER INFORMATION: downstream amplification primer 99-14419
FEATURE:
NAME/KEY: primer bind
LOCATION: 6638..6655
OTHER INFORMATION: upstream amplification primer 99-4577
FEATURE:
NAME/KEY: primer bind
LOCATION: 7072..7089
OTHER INFORMATION: downstream amplification primer 99-4577, complement
FEATURE:
NAME/KEY: primer bind
LOCATION: 7995..8012
OTHER INFORMATION: upstream amplification primer 99-4559
FEATURE:
NAME/KEY: primer bind
LOCATION: 8576..8593
OTHER INFORMATION: downstream amplification primer 99-4559, complement
FEATURE:
NAME/KEY: primer bind
LOCATION: 9622..9639
OTHER INFORMATION: upstream amplification primer 99-3148
FEATURE:
NAME/KEY: primer bind
LOCATION: 10023..10040
OTHER INFORMATION: downstream amplification primer 99-3148, complement
FEATURE:
NAME/KEY: primer bind
LOCATION: 9964..9981
OTHER INFORMATION: upstream amplification primer 99-4560
FEATURE:
NAME/KEY: primer bind
LOCATION: 10546..10563
OTHER INFORMATION: downstream amplification primer 99-4560, complement
FEATURE:
NAME/KEY: primer bind
LOCATION: 10996..11015
OTHER INFORMATION: upstream amplification primer 99-14411, complement
FEATURE:
NAME/KEY: primer bind
LOCATION: 10492..10512
OTHER INFORMATION: downstream amplification primer 99-14411
FEATURE:
NAME/KEY: primer bind
LOCATION: 11972..11990
OTHER INFORMATION: upstream amplification primer 99-4561
FEATURE:
NAME/KEY: primer bind
LOCATION: 12481..12501
OTHER INFORMATION: downstream amplification primer 99-4561, complement

```

Query Match 67.5%; Score 16.2; DB 4; Length 23187;
 Best Local Similarity 85.7%; Pred. No. 2.9e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTCTGAGGGCT 21
 ||||| ||||| ||||| ||||| |||||

Db 14904 TCCAGGGGGTCTGAGGGCT 14884

```
RESULT 20
US-09-252-991A-8519
; Sequence 8519, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8519
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8519

Query Match      66.7%; Score 16; DB 4; Length 522;
Best Local Similarity 79.2%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCGTGAGGGCTTAC 24
Db 425 TCCGAGACGGTTCGTGAGGGCTTGC 448

RESULT 21
US-09-270-767-12997
; Sequence 12997, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12997
; LENGTH: 579
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-12997

Query Match      66.7%; Score 16; DB 4; Length 579;
Best Local Similarity 79.2%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCGTGAGGGCTTAC 24
Db 195 TCCGAGACGGTTCGTGAGGGCTTTC 218

RESULT 22
US-09-252-991A-8445
; Sequence 8445, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
```

```
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8445
; LENGTH: 1113
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8445

Query Match      66.7%; Score 16; DB 4; Length 1113;
Best Local Similarity 79.2%; Pred. No. 2.6e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCGTGAGGGCTTAC 24
Db 103 TCCGAGACGGTTCGTGAGGGCTTGC 126

RESULT 23
US-09-799-451-367
; Sequence 367, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Kyle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yunqing
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; FILE REFERENCE: Polypeptides
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pt FL_genes Version 2.0
; SEQ ID NO 367
; LENGTH: 1850
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (274)..(1236)
US-09-799-451-367

Query Match      66.7%; Score 16; DB 4; Length 1850;
Best Local Similarity 79.2%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCGTGAGGGCTTAC 24
Db 587 TCCGAGCCTTTCGTGAGGGCTTTC 610

RESULT 24
US-09-252-991A-8479
; Sequence 8479, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
```


ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/199,507B
FILING DATE: 22 FEBRUARY 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX13
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-199-507B-21

Query Match 65.8%; Score 15.8; DB 1; Length 37;
Best Local Similarity 89.5%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels

QY 2 CCAGACGGTCTCAGGGC 20
DB 20 CCAGACGGTCTCAGGGC 2

RESULT 27

US-08-441-828-21/c
Sequence 21, Application US/08441828
Patent No. 5734034
GENERAL INFORMATION:
APPLICANT: JAVASENA, S. AND GOLD, L.
TITLE OF INVENTION: NUCLEIC ACID LIGAND INHIBITORS
TITLE OF INVENTION: OF HUMAN NEUTROPHIL ELASTASE
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB
MEDIUM TYPE: storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,828
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/199,507

```

; FILING DATE: 22 FEBRUARY 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX113
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-441-828-21

Query Match 65.8%; Score 15.8; DB 1; Length 37;
Best Local Similarity 89.5%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCGAGACGGTTCAGGGC 20
Db 20 CCGAGACGGTTCAGGGC 2

RESULT 28
US-09-949-016-192257
; Sequence 192257, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 192257
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-192257

Query Match 65.8%; Score 15.8; DB 4; Length 601;
Best Local Similarity 89.5%; Pred. No. 3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 AGACGGTTCAGGGCTTA 23
Db 126 AGACGGCTCAGGGGCTTA 144

RESULT 29
US-08-292-688A-10
; Sequence 10, Application US/08292688A
; Patent No. 5814493
; GENERAL INFORMATION:
; APPLICANT: ROBERTSON, Donald L.
; APPLICANT: FISHER, Kuhia L.
; TITLE OF INVENTION: VIRUSES AND EXPRESSION VECTORS

```

```

; TITLE OF INVENTION: CONTAINING LTR SIZE VARIANTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,688A
; FILING DATE: 18-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Radio, Susan M.
; REGISTRATION NUMBER: 40,373
; REFERENCE/DOCKET NUMBER: 004535-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1621 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-292-688A-10

Query Match 65.8%; Score 15.8; DB 1; Length 1621;
Best Local Similarity 89.5%; Pred. No. 3.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 AGACGGTTCAGGGCTTA 23
Db 980 AGACGGTTCAGGGCTTA 998

RESULT 30
US-08-791-849A-12
; Sequence 12, Application US/08791849A
; Patent No. 5914449
; GENERAL INFORMATION:
; APPLICANT: Makoto MURASE et al.
; TITLE OF INVENTION: Method for Increasing Storage
; CAPACITY OF PLANT SEEDS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,849A
; FILING DATE: January 30, 1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.

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REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1795 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: soybean (Glycine max)
US-08-791-849A-12

Query Match 65.8%; Score 15.8; DB 2; Length 1795;
Best Local Similarity 89.5%; Pred. No. 3.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCGAGACGGTCTGAGGCG 20
|||||
DB 177 CCGAGAGCTCTGAGGCG 195

RESULT 31
US-09-949-016-17389/c
Sequence 17389, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17389
LENGTH: 55031
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...((55031)
OTHER INFORMATION: n = A, T, C or G
US-09-949-016-17389

Query Match 65.8%; Score 15.8; DB 4; Length 55031;
Best Local Similarity 89.5%; Pred. No. 5.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAGACGGTCTGAGGCGTT 22
|||||
DB 52159 GAGACGCTCTGAGGCGTT 52141

RESULT 32
US-09-949-016-17230/c
Sequence 17230, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17230
LENGTH: 90776
TYPE: DNA
ORGANISM: Human
US-09-949-016-17230

Query Match 65.8%; Score 15.8; DB 4; Length 90776;
Best Local Similarity 89.5%; Pred. No. 5.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 AGACGGTCTGAGGCGCTTA 23
|||||
DB 45462 AGACGGCTCTGAGGCGCTA 45444

RESULT 33
US-09-949-016-14132
Sequence 14132, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14132
LENGTH: 122772
TYPE: DNA
ORGANISM: Human
US-09-949-016-14132

Query Match 65.8%; Score 15.8; DB 4; Length 122772;
Best Local Similarity 89.5%; Pred. No. 5.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CGAGACGGTCTGAGGCGT 21
|||||
DB 76088 CGAGACGTTCTGAGGCT 76106

RESULT 34
US-09-949-016-12147
Sequence 12147, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20

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; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12147
; LENGTH: 767677
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(767677)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12147

Query Match      65.8%; Score 15.8; DB 4; Length 767677;
Best Local Similarity 89.5%; Pred. No. 6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCGAGACGGTTCGAGGCC 20
Db 240204 CCGAGATGGTTCGAGTGC 240222

RESULT 35
US-09-949-016-17361
; Sequence 17361, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17361
; LENGTH: 767677
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(767677)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17361

Query Match      65.8%; Score 15.8; DB 4; Length 767677;
Best Local Similarity 89.5%; Pred. No. 6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCGAGACGGTTCGAGGCC 20
Db 240204 CCGAGATGGTTCGAGTGC 240222

RESULT 36
US-09-949-016-45837
; Sequence 45837, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
```

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; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45837
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-45837

Query Match      65.0%; Score 15.6; DB 4; Length 601;
Best Local Similarity 81.8%; Pred. No. 3.8e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCGGAGACGGTTCGAGGGCTT 22
Db 96 TCGGAGAGGGGCGCTGAGGGCTT 117

RESULT 37
US-09-949-016-45859
; Sequence 45859, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45859
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-45859

Query Match      65.0%; Score 15.6; DB 4; Length 601;
Best Local Similarity 81.8%; Pred. No. 3.8e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCGGAGACGGTTCGAGGGCTT 22
Db 96 TCGGAGAGGGGCGCTGAGGGCTT 117

RESULT 38
US-09-489-039A-1034
; Sequence 1034, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 1034
```

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; LENGTH: 948
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-1034

Query Match      65.0%; Score 15.6; DB 4; Length 948;
Best Local Similarity 81.8%; Pred. No. 4.4e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      3 CGAGACGGTCTCGAGGCTTAC 24
      ||||| ||||| ||||| ||||| |||||
Db      780 CGAGCGCGTCTCGAGGCTTAC 801

RESULT 39
US-09-248-796A-6062
; Sequence 8062, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 6062
; LENGTH: 1341
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-6062

Query Match      65.0%; Score 15.6; DB 4; Length 1341;
Best Local Similarity 81.8%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      3 CGAGACGGTCTCGAGGCTTAC 24
      ||||| ||||| ||||| ||||| |||||
Db      669 CCAGCGCGTCTCGACAGCTTAC 690

RESULT 40
US-09-902-540-8806/c
; Sequence 8806, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 8806
; LENGTH: 2121
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-8806

Query Match      65.0%; Score 15.6; DB 4; Length 2121;
Best Local Similarity 81.8%; Pred. No. 4.4e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 TCCGAGACGGTCTCGAGGCTT 22
      ||||| ||||| ||||| ||||| |||||

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Db      737 TCCGGGCGGTCTCGAGGCTT 716

RESULT 41
US-09-949-016-253/c
; Sequence 253, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 253
; LENGTH: 2332
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-253

Query Match      65.0%; Score 15.6; DB 4; Length 2332;
Best Local Similarity 81.8%; Pred. No. 4.4e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 CCGAGACGGTCTCGAGGCTTA 23
      ||||| ||||| ||||| ||||| |||||
Db      1016 CCAGGACGGTCTCCGGGCTTA 995

RESULT 42
US-09-949-016-5522/c
; Sequence 5522, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5522
; LENGTH: 2332
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5522

Query Match      65.0%; Score 15.6; DB 4; Length 2332;
Best Local Similarity 81.8%; Pred. No. 4.4e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 CCGAGACGGTCTCGAGGCTTA 23
      ||||| ||||| ||||| ||||| |||||
Db      1016 CCAGGACGGTCTCCGGGCTTA 995

RESULT 43
US-09-949-016-408/c

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; Sequence 408, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 408
; LENGTH: 3595
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-408

Query Match 65.0%; Score 15.6; DB 4; Length 3595;
Best Local Similarity 81.8%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 CGAGACGGTCTGAGGCGTTAC 24
Db 2924 CAAGAGCGTCTGAGGCGTTAC 2903

RESULT 44
US-09-563-269-17/c
; Sequence 17, Application US/09563269
; Patent No. 6555655
; GENERAL INFORMATION:
; APPLICANT: RUPAR, MARK J.
; APPLICANT: DONOVAN, WILLIAM P.
; APPLICANT: CHU, CHIH-REI
; APPLICANT: PEASE, ELIZABETH
; APPLICANT: TAN, YUPING
; APPLICANT: SLANEY, ANNETTE C.
; APPLICANT: BAUM, JAMES A.
; APPLICANT: MALVAR, THOMAS M.
; TITLE OF INVENTION: COLEOPTERAN-TOXIC POLYPEPTIDE COMPOSITIONS AND INSECT
; RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: MEC0164
; CURRENT APPLICATION NUMBER: US/09/563,269
; CURRENT FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 3607
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-09-563-269-17

Query Match 65.0%; Score 15.6; DB 4; Length 3607;
Best Local Similarity 81.8%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTGAGGCGTT 22
Db 3547 TTCTAGACGCTTCTGAGGCGATT 3526

RESULT 45
US-08-506-296B-27
; Sequence 27, Application US/08506296B
; Patent No. 6313265
; GENERAL INFORMATION:
; APPLICANT: Phillips, Greg

; APPLICANT: Cunningham, Bruce A.
; APPLICANT: Crossin, Kathryn L.
; TITLE OF INVENTION: NEURITE OUTGROWTH-PROMOTING POLYPEPTIDES
; CONTAINING FIBRONECTIN TYPE III REPEATS AND METHODS OF USE
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute
; STREET: 10550 No. 6313265th Torrey Pines Road, TPC-8
; CITY: La Jolla
; STATE: California
; COUNTRY: U.S.
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/506,296B
; FILING DATE: 24-JUL-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 488.0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 554-2937
; TELEFAX: (619) 554-6312
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3943 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 33..3839
US-08-506-296B-27

Query Match 65.0%; Score 15.6; DB 3; Length 3943;
Best Local Similarity 81.8%; Pred. No. 4.7e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTGAGGCGTT 22
Db 3325 TCCGAGTTGGTCTGAGGCGCT 3346

RESULT 46
US-09-949-016-1305
; Sequence 1305, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1305
; LENGTH: 4041
; TYPE: DNA

```
; ORGANISM: Human
US-09-949-016-1305

Query Match          65.0%; Score 15.6; DB 4; Length 4041;
Best Local Similarity 81.8%; Pred. No. 4.7e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCTGAGGGCTT 22
    ||||| ||||| ||||| |||||
Db 1768 TCCGAGAGGGCGCTTGAGGGCTT 1789

RESULT 47
US-09-949-016-1306
; Sequence 1306, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1306
; LENGTH: 4041
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1306

Query Match          65.0%; Score 15.6; DB 4; Length 4041;
Best Local Similarity 81.8%; Pred. No. 4.7e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCTGAGGGCTT 22
    ||||| ||||| ||||| |||||
Db 1768 TCCGAGAGGGCGCTTGAGGGCTT 1789

RESULT 48
US-09-016-434-1152/c
; Sequence 1152, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1152:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4078 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1524091
US-09-016-434-1152

Query Match          65.0%; Score 15.6; DB 4; Length 4078;
Best Local Similarity 81.8%; Pred. No. 4.7e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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; Sequence 4140, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4140
; LENGTH: 4546
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4140

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Best Local Similarity 81.8%; Pred. No. 4.8e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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; Sequence 975, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
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; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 975:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4553 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1524091
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US-09-023-655-975

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Best Local Similarity 81.8%; Pred. NO. 4.8e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 25, 2005, 11:41:26 ; Search time 277.714 Seconds
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Title: US-10-688-489-75
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Searched: 5552208 seqs, 2979665951 residues

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Listing first 500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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					Sequence 75, Appl
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					Sequence 2, Appl
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					Sequence 73, Appl
					Sequence 84, Appl
					Sequence 72, Appl
					Sequence 71, Appl
					Sequence 5, Appl

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Sequence 2, Appli	US-10-699-550-2	18
Sequence 66, Appl	US-10-679-520A-66	19
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Sequence 101, App	US-10-688-489-101	18
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Sequence 41, Appl	US-09-967-768A-116	9
Sequence 19, Appl	US-10-052-482-31	17
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Sequence 31, Appl	US-10-126-022-5	17
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142	15.6	65.0	757	13	US-10-027-632-169459	Sequence 169459, A	c 215	15.6	65.0	4886	17	US-10-379-632-44	Sequence 44, Appli
143	15.6	65.0	757	17	US-10-027-632-169459	Sequence 169459, A	c 216	15.6	65.0	4906	17	US-10-379-632-64	Sequence 64, Appli
144	15.6	65.0	757	17	US-10-027-632-169459	Sequence 169459, A	c 217	15.6	65.0	4911	17	US-10-379-632-34	Sequence 34, Appli
145	15.6	65.0	896	13	US-10-027-632-126347	Sequence 126347, A	c 218	15.6	65.0	4927	17	US-10-379-632-39	Sequence 39, Appli
146	15.6	65.0	896	13	US-10-027-632-126347	Sequence 126347, A	c 219	15.6	65.0	4944	17	US-10-379-632-3	Sequence 3, Appli
147	15.6	65.0	896	13	US-10-027-632-126347	Sequence 126347, A	c 220	15.6	65.0	4967	17	US-10-379-632-49	Sequence 49, Appli
148	15.6	65.0	896	17	US-10-027-632-126347	Sequence 126347, A	c 221	15.6	65.0	4976	17	US-10-379-632-21	Sequence 21, Appli
149	15.6	65.0	938	9	US-09-867-550-1629	Sequence 1629, Ap	c 222	15.6	65.0	4979	17	US-10-379-632-37	Sequence 37, Appli
150	15.6	65.0	1077	17	US-10-243-552-701	Sequence 701, App	c 223	15.6	65.0	4981	17	US-10-379-632-81	Sequence 81, Appli
151	15.6	65.0	1287	18	US-10-411-910A-190	Sequence 190, App	c 224	15.6	65.0	4988	17	US-10-379-632-41	Sequence 41, Appli
152	15.6	65.0	1335	18	US-10-437-963-26436	Sequence 26436, A	c 225	15.6	65.0	4992	17	US-10-379-632-7	Sequence 7, Appli
153	15.6	65.0	1569	17	US-10-424-599-18161	Sequence 18161, A	c 226	15.6	65.0	4997	17	US-10-379-632-5	Sequence 5, Appli
154	15.6	65.0	1620	18	US-10-619-189-75	Sequence 75, Appli	c 227	15.6	65.0	5008	17	US-10-379-632-33	Sequence 33, Appli
155	15.6	65.0	1624	18	US-10-437-963-2228	Sequence 2228, Ap	c 228	15.6	65.0	5062	17	US-10-379-632-78	Sequence 78, Appli
156	15.6	65.0	1778	17	US-10-273-287-15	Sequence 15, Appli	c 229	15.6	65.0	5069	17	US-10-379-632-25	Sequence 25, Appli
157	15.6	65.0	1814	17	US-10-273-287-15	Sequence 15, Appli	c 230	15.6	65.0	5073	17	US-10-379-632-10	Sequence 10, Appli

231	15.6	65.0	5076	17	US-10-379-632-36	Sequence 36, Appl	304	15.4	64.2	3015	18	US-10-437-963-41677	Sequence 41677, A
232	15.6	65.0	5078	17	US-10-379-632-69	Sequence 69, Appl	c 305	15.4	64.2	92076	18	US-10-322-281-465	Sequence 465, App
233	15.6	65.0	5083	17	US-10-379-632-75	Sequence 75, Appl	306	15.2	63.3	60	10	US-09-908-973-15491	Sequence 15491, A
234	15.6	65.0	5088	17	US-10-379-632-43	Sequence 43, Appl	307	15.2	63.3	201	18	US-10-719-993-3740	Sequence 3740, Ap
235	15.6	65.0	5094	17	US-10-379-632-4	Sequence 4, Appl	308	15.2	63.3	201	18	US-10-719-993-3742	Sequence 3742, Ap
236	15.6	65.0	5137	17	US-10-379-632-28	Sequence 28, Appl	309	15.2	63.3	201	18	US-10-719-993-3744	Sequence 3744, Ap
237	15.6	65.0	5146	17	US-10-379-632-2	Sequence 2, Appl	c 310	15.2	63.3	226	18	US-10-425-115-1487	Sequence 1487, Ap
238	15.6	65.0	5164	17	US-10-379-632-72	Sequence 72, Appl	311	15.2	63.3	251	16	US-10-029-386-19036	Sequence 19036, A
239	15.6	65.0	5169	17	US-10-379-632-47	Sequence 47, Appl	312	15.2	63.3	343	17	US-10-424-599-116755	Sequence 116755,
240	15.6	65.0	5175	17	US-10-379-632-68	Sequence 68, Appl	313	15.2	63.3	344	9	US-09-878-134-220	Sequence 220, App
241	15.6	65.0	5183	17	US-10-379-632-80	Sequence 80, Appl	314	15.2	63.3	375	13	US-10-040-739-1462	Sequence 1462, Ap
242	15.6	65.0	5185	17	US-10-379-632-42	Sequence 42, Appl	c 315	15.2	63.3	441	11	US-09-864-408A-5553	Sequence 5553, Ap
243	15.6	65.0	5190	17	US-10-379-632-30	Sequence 30, Appl	316	15.2	63.3	442	10	US-09-918-995-37829	Sequence 37829, A
244	15.6	65.0	5232	17	US-10-379-632-32	Sequence 32, Appl	c 317	15.2	63.3	457	17	US-10-282-122A-11452	Sequence 11452, A
245	15.6	65.0	5243	17	US-10-379-632-1	Sequence 1, Appl	c 318	15.2	63.3	459	10	US-09-918-995-16808	Sequence 16808, A
246	15.6	65.0	5264	17	US-10-379-632-77	Sequence 77, Appl	c 319	15.2	63.3	468	10	US-09-918-995-25966	Sequence 25966, A
247	15.6	65.0	5271	17	US-10-379-632-24	Sequence 24, Appl	c 320	15.2	63.3	489	10	US-09-918-993-3278	Sequence 3278, Ap
248	15.6	65.0	5280	17	US-10-379-632-79	Sequence 79, Appl	321	15.2	63.3	502	19	US-10-696-639-2327	Sequence 2327, Ap
249	15.6	65.0	5285	17	US-10-379-632-74	Sequence 74, Appl	c 322	15.2	63.3	507	19	US-10-696-639-2998	Sequence 2998, Ap
250	15.6	65.0	5287	17	US-10-379-632-29	Sequence 29, Appl	c 323	15.2	63.3	513	9	US-09-864-761-12432	Sequence 12432, A
251	15.6	65.0	5319	9	US-09-826-752-7	Sequence 7, Appl	324	15.2	63.3	533	18	US-10-437-963-82686	Sequence 82686, A
252	15.6	65.0	5319	11	US-09-968-007A-360	Sequence 360, Appl	325	15.2	63.3	539	19	US-10-696-639-2093	Sequence 2093, Ap
253	15.6	65.0	5319	19	US-10-912-434-7	Sequence 7, Appl	326	15.2	63.3	555	16	US-10-029-386-5280	Sequence 5280, Ap
254	15.6	65.0	5339	17	US-10-379-632-27	Sequence 27, Appl	327	15.2	63.3	567	16	US-10-029-386-10175	Sequence 10175, A
255	15.6	65.0	5359	14	US-10-197-666A-139	Sequence 139, Appl	328	15.2	63.3	576	9	US-09-758-593A-3	Sequence 3, Appl
256	15.6	65.0	5361	17	US-10-379-632-76	Sequence 76, Appl	329	15.2	63.3	576	15	US-10-328-704-3	Sequence 3, Appl
257	15.6	65.0	5366	17	US-10-379-632-46	Sequence 46, Appl	330	15.2	63.3	581	13	US-10-027-632-203288	Sequence 203288,
258	15.6	65.0	5368	17	US-10-379-632-23	Sequence 23, Appl	331	15.2	63.3	581	13	US-10-027-632-203289	Sequence 203289,
259	15.6	65.0	5382	17	US-10-379-632-73	Sequence 73, Appl	332	15.2	63.3	581	17	US-10-027-632-203288	Sequence 203288,
260	15.6	65.0	5390	18	US-10-684-422-241	Sequence 241, App	333	15.2	63.3	591	17	US-10-027-632-203289	Sequence 203289,
261	15.6	65.0	5434	17	US-10-379-632-31	Sequence 31, Appl	334	15.2	63.3	618	13	US-10-027-632-277149	Sequence 277149,
262	15.6	65.0	5436	17	US-10-379-632-26	Sequence 26, Appl	335	15.2	63.3	618	17	US-10-027-632-277149	Sequence 277149,
263	15.6	65.0	5463	17	US-10-379-632-48	Sequence 48, Appl	336	15.2	63.3	672	9	US-09-764-864-110	Sequence 110, App
264	15.6	65.0	5531	17	US-10-379-632-20	Sequence 20, Appl	337	15.2	63.3	678	17	US-10-240-425-967	Sequence 967, App
265	15.6	65.0	5782	18	US-10-437-963-26437	Sequence 26437, A	c 338	15.2	63.3	702	13	US-10-027-632-34070	Sequence 34070, A
266	15.6	65.0	5909	18	US-10-602-494-142	Sequence 142, App	c 339	15.2	63.3	702	13	US-10-027-632-34071	Sequence 34071, A
267	15.6	65.0	5984	17	US-10-379-632-45	Sequence 45, Appl	c 340	15.2	63.3	702	13	US-10-027-632-34070	Sequence 34071, A
268	15.6	65.0	6136	17	US-10-275-287-57	Sequence 57, Appl	c 341	15.2	63.3	702	17	US-10-027-632-34071	Sequence 34071, A
269	15.6	65.0	6138	17	US-10-275-287-4	Sequence 4, Appl	342	15.2	63.3	722	18	US-10-425-115-36512	Sequence 36512, A
270	15.6	65.0	6141	17	US-10-275-287-3	Sequence 3, Appl	343	15.2	63.3	829	13	US-10-027-632-167931	Sequence 167931,
271	15.6	65.0	7032	9	US-09-764-847-1429	Sequence 1429, Ap	344	15.2	63.3	829	17	US-10-027-632-167931	Sequence 167931,
272	15.6	65.0	7032	14	US-10-092-154-1429	Sequence 1429, Ap	345	15.2	63.3	876	13	US-10-027-632-135124	Sequence 135124,
273	15.6	65.0	7646	17	US-10-275-287-1	Sequence 1, Appl	346	15.2	63.3	876	13	US-10-027-632-135125	Sequence 135125,
274	15.6	65.0	7650	17	US-10-275-287-56	Sequence 56, Appl	c 347	15.2	63.3	876	13	US-10-027-632-135124	Sequence 135124,
275	15.6	65.0	11990	9	US-09-969-708-569	Sequence 569, App	348	15.2	63.3	876	17	US-10-027-632-135125	Sequence 135125,
276	15.6	65.0	11990	10	US-09-873-367C-161	Sequence 161, App	c 349	15.2	63.3	933	13	US-10-027-632-121365	Sequence 121365,
277	15.6	65.0	11990	17	US-10-240-425-1326	Sequence 1326, Ap	c 350	15.2	63.3	933	17	US-10-027-632-121365	Sequence 121365,
278	15.6	65.0	15549	17	US-10-275-287-58	Sequence 58, Appl	c 351	15.2	63.3	969	9	US-09-938-842A-2446	Sequence 2446, Ap
279	15.6	65.0	16570	17	US-10-275-287-2	Sequence 2, Appl	c 352	15.2	63.3	969	11	US-09-938-842A-2446	Sequence 2446, Ap
280	15.6	65.0	18318	16	US-10-394-848-6	Sequence 6, Appl	353	15.2	63.3	1002	16	US-10-204-456-1	Sequence 1, Appl
281	15.6	65.0	18876	17	US-10-329-079-42	Sequence 42, Appl	354	15.2	63.3	1026	15	US-10-156-761-1549	Sequence 1549, Ap
282	15.6	65.0	25473	18	US-10-719-993-7034	Sequence 7034, Ap	355	15.2	63.3	1148	18	US-10-719-993-245	Sequence 245, App
283	15.6	65.0	26180	19	US-10-741-600-17763	Sequence 17763, A	356	15.2	63.3	1158	9	US-09-880-192-48	Sequence 48, Appl
284	15.6	65.0	61944	16	US-10-329-079-34	Sequence 34, Appl	357	15.2	63.3	1158	9	US-09-758-593A-2	Sequence 2, Appl
285	15.6	65.0	185695	14	US-10-020-141-11	Sequence 11, Appl	358	15.2	63.3	1158	15	US-10-328-704-2	Sequence 48, Appl
286	15.6	65.0	185695	14	US-10-017-721-1	Sequence 1, Appl	359	15.2	63.3	1158	16	US-10-427-348-48	Sequence 246, App
287	15.6	65.0	219352	18	US-10-322-281-45	Sequence 45, Appl	360	15.2	63.3	1159	18	US-10-719-993-246	Sequence 246, App
288	15.6	65.0	400660	18	US-10-388-838-68	Sequence 68, Appl	c 361	15.2	63.3	1260	18	US-10-739-930-59	Sequence 59, Appl
289	15.6	65.0	2256846	18	US-10-470-585-1	Sequence 1, Appl	362	15.2	63.3	1392	17	US-10-369-493-3373	Sequence 35373, A
290	15.4	64.2	660	13	US-10-027-632-131659	Sequence 131659,	363	15.2	63.3	1416	17	US-10-719-993-244	Sequence 244, App
291	15.4	64.2	660	13	US-10-027-632-131660	Sequence 131660,	c 364	15.2	63.3	1416	17	US-10-282-122A-20170	Sequence 20170, A
292	15.4	64.2	660	17	US-10-027-632-131659	Sequence 131659,	365	15.2	63.3	1452	17	US-10-094-749-1245	Sequence 1245, Ap
293	15.4	64.2	660	17	US-10-027-632-131660	Sequence 131660,	366	15.2	63.3	1475	18	US-10-723-860-5560	Sequence 5560, Ap
294	15.4	64.2	840	13	US-10-027-632-166031	Sequence 166031,	367	15.2	63.3	1475	18	US-10-723-860-6074	Sequence 6074, Ap
295	15.4	64.2	840	13	US-10-027-632-166032	Sequence 166032,	c 368	15.2	63.3	1492	14	US-10-062-548-23	Sequence 23, Appl
296	15.4	64.2	840	17	US-10-027-632-166031	Sequence 166031,	c 369	15.2	63.3	1492	19	US-10-918-446-23	Sequence 23, Appl
297	15.4	64.2	840	13	US-10-027-632-166032	Sequence 166032,	370	15.2	63.3	1508	17	US-10-108-260A-967	Sequence 967, App
298	15.4	64.2	913	13	US-10-027-632-153508	Sequence 153508,	371	15.2	63.3	1590	18	US-10-739-930-4996	Sequence 4996, Ap
299	15.4	64.2	913	13	US-10-027-632-153509	Sequence 153509,	c 372	15.2	63.3	1611	9	US-09-808-701-13	Sequence 13, Appl
300	15.4	64.2	913	17	US-10-027-632-153508	Sequence 153508,	c 373	15.2	63.3	1611	14	US-10-233-131-13	Sequence 13, Appl
301	15.4	64.2	913	17	US-10-027-632-153509	Sequence 153509,	c 374	15.2	63.3	1619	10	US-09-873-367C-329	Sequence 329, App
302	15.4	64.2	1119	18	US-10-425-115-67486	Sequence 67486, A	c 375	15.2	63.3	1633	17	US-10-369-493-27750	Sequence 27750, A
303	15.4	64.2	1937	18	US-10-357-930-24785	Sequence 24785, A	c 376	15.2	63.3	1665	10	US-09-946-374-159	Sequence 159, App

C 377	15.2	63.3	1665	13	US-10-006-867-85	Sequence 85, Appl	C 450	15.2	63.3	1665	14	US-10-184-623-285	Sequence 285, App
C 378	15.2	63.3	1665	13	US-10-052-586-285	Sequence 285, App	C 451	15.2	63.3	1665	14	US-10-184-635-285	Sequence 285, App
C 379	15.2	63.3	1665	13	US-10-063-547-85	Sequence 85, Appl	C 452	15.2	63.3	1665	14	US-10-184-637-285	Sequence 285, App
C 380	15.2	63.3	1665	13	US-10-063-551-85	Sequence 85, Appl	C 453	15.2	63.3	1665	14	US-10-184-646-285	Sequence 285, App
C 381	15.2	63.3	1665	14	US-10-174-590-285	Sequence 285, App	C 454	15.2	63.3	1665	14	US-10-184-647-285	Sequence 285, App
C 382	15.2	63.3	1665	14	US-10-176-758-285	Sequence 285, App	C 455	15.2	63.3	1665	14	US-10-184-652-285	Sequence 285, App
C 383	15.2	63.3	1665	14	US-10-175-737-285	Sequence 285, App	C 456	15.2	63.3	1665	14	US-10-187-594-285	Sequence 285, App
C 384	15.2	63.3	1665	14	US-10-063-616-85	Sequence 85, Appl	C 457	15.2	63.3	1665	14	US-10-187-596-285	Sequence 285, App
C 385	15.2	63.3	1665	14	US-10-174-581-285	Sequence 285, App	C 458	15.2	63.3	1665	14	US-10-187-745-285	Sequence 285, App
C 386	15.2	63.3	1665	14	US-10-176-483-285	Sequence 285, App	C 459	15.2	63.3	1665	14	US-10-187-885-285	Sequence 285, App
C 387	15.2	63.3	1665	14	US-10-176-749-285	Sequence 285, App	C 460	15.2	63.3	1665	14	US-10-187-886-285	Sequence 285, App
C 388	15.2	63.3	1665	14	US-10-176-914-285	Sequence 285, App	C 461	15.2	63.3	1665	14	US-10-193-484-285	Sequence 285, App
C 389	15.2	63.3	1665	14	US-10-176-915-285	Sequence 285, App	C 462	15.2	63.3	1665	14	US-10-196-756-285	Sequence 285, App
C 390	15.2	63.3	1665	14	US-10-063-569-85	Sequence 85, Appl	C 463	15.2	63.3	1665	14	US-10-176-751-285	Sequence 285, App
C 391	15.2	63.3	1665	14	US-10-063-511-85	Sequence 85, Appl	C 464	15.2	63.3	1665	14	US-10-176-990-285	Sequence 285, App
C 392	15.2	63.3	1665	14	US-10-063-512-85	Sequence 85, Appl	C 465	15.2	63.3	1665	14	US-10-176-990-285	Sequence 285, App
C 393	15.2	63.3	1665	14	US-10-173-706-285	Sequence 285, App	C 466	15.2	63.3	1665	14	US-10-180-541-285	Sequence 285, App
C 394	15.2	63.3	1665	14	US-10-175-738-285	Sequence 285, App	C 467	15.2	63.3	1665	14	US-10-180-542-285	Sequence 285, App
C 395	15.2	63.3	1665	14	US-10-175-752-285	Sequence 285, App	C 468	15.2	63.3	1665	14	US-10-180-548-285	Sequence 285, App
C 396	15.2	63.3	1665	14	US-10-176-482-285	Sequence 285, App	C 469	15.2	63.3	1665	14	US-10-180-551-285	Sequence 285, App
C 397	15.2	63.3	1665	14	US-10-176-913-285	Sequence 285, App	C 470	15.2	63.3	1665	14	US-10-180-998-285	Sequence 285, App
C 398	15.2	63.3	1665	14	US-10-176-913-285	Sequence 285, App	C 471	15.2	63.3	1665	14	US-10-180-999-285	Sequence 285, App
C 399	15.2	63.3	1665	14	US-10-180-552-285	Sequence 285, App	C 472	15.2	63.3	1665	14	US-10-183-013-285	Sequence 285, App
C 400	15.2	63.3	1665	14	US-10-180-552-285	Sequence 285, App	C 473	15.2	63.3	1665	14	US-10-184-612-285	Sequence 285, App
C 401	15.2	63.3	1665	14	US-10-063-502-85	Sequence 85, Appl	C 474	15.2	63.3	1665	14	US-10-184-612-285	Sequence 285, App
C 402	15.2	63.3	1665	14	US-10-173-700-285	Sequence 285, App	C 475	15.2	63.3	1665	14	US-10-184-616-285	Sequence 285, App
C 403	15.2	63.3	1665	14	US-10-174-572-285	Sequence 285, App	C 476	15.2	63.3	1665	14	US-10-184-617-285	Sequence 285, App
C 404	15.2	63.3	1665	14	US-10-174-579-285	Sequence 285, App	C 477	15.2	63.3	1665	14	US-10-184-622-285	Sequence 285, App
C 405	15.2	63.3	1665	14	US-10-174-582-285	Sequence 285, App	C 478	15.2	63.3	1665	14	US-10-184-628-285	Sequence 285, App
C 406	15.2	63.3	1665	14	US-10-174-582-285	Sequence 285, App	C 479	15.2	63.3	1665	14	US-10-184-629-285	Sequence 285, App
C 407	15.2	63.3	1665	14	US-10-175-739-285	Sequence 285, App	C 480	15.2	63.3	1665	14	US-10-184-630-285	Sequence 285, App
C 408	15.2	63.3	1665	14	US-10-175-739-285	Sequence 285, App	C 481	15.2	63.3	1665	14	US-10-184-631-285	Sequence 285, App
C 409	15.2	63.3	1665	14	US-10-175-740-285	Sequence 285, App	C 482	15.2	63.3	1665	14	US-10-184-632-285	Sequence 285, App
C 410	15.2	63.3	1665	14	US-10-175-740-285	Sequence 285, App	C 483	15.2	63.3	1665	14	US-10-184-636-285	Sequence 285, App
C 411	15.2	63.3	1665	14	US-10-176-488-285	Sequence 285, App	C 484	15.2	63.3	1665	14	US-10-184-640-285	Sequence 285, App
C 412	15.2	63.3	1665	14	US-10-176-492-285	Sequence 285, App	C 485	15.2	63.3	1665	14	US-10-184-650-285	Sequence 285, App
C 413	15.2	63.3	1665	14	US-10-176-747-285	Sequence 285, App	C 486	15.2	63.3	1665	14	US-10-184-651-285	Sequence 285, App
C 414	15.2	63.3	1665	14	US-10-176-747-285	Sequence 285, App	C 487	15.2	63.3	1665	14	US-10-187-588-285	Sequence 285, App
C 415	15.2	63.3	1665	14	US-10-176-750-285	Sequence 285, App	C 488	15.2	63.3	1665	14	US-10-187-597-285	Sequence 285, App
C 416	15.2	63.3	1665	14	US-10-176-985-285	Sequence 285, App	C 489	15.2	63.3	1665	14	US-10-187-598-285	Sequence 285, App
C 417	15.2	63.3	1665	14	US-10-176-987-285	Sequence 285, App	C 490	15.2	63.3	1665	14	US-10-187-600-285	Sequence 285, App
C 418	15.2	63.3	1665	14	US-10-176-992-285	Sequence 285, App	C 491	15.2	63.3	1665	14	US-10-187-601-285	Sequence 285, App
C 419	15.2	63.3	1665	14	US-10-176-992-285	Sequence 285, App	C 492	15.2	63.3	1665	14	US-10-187-602-285	Sequence 285, App
C 420	15.2	63.3	1665	14	US-10-184-658-285	Sequence 285, App	C 493	15.2	63.3	1665	14	US-10-187-603-285	Sequence 285, App
C 421	15.2	63.3	1665	14	US-10-176-991-285	Sequence 285, App	C 494	15.2	63.3	1665	14	US-10-187-741-285	Sequence 285, App
C 422	15.2	63.3	1665	14	US-10-063-549-85	Sequence 85, Appl	C 495	15.2	63.3	1665	14	US-10-187-743-285	Sequence 285, App
C 423	15.2	63.3	1665	14	US-10-173-692-285	Sequence 285, App	C 496	15.2	63.3	1665	14	US-10-187-746-285	Sequence 285, App
C 424	15.2	63.3	1665	14	US-10-173-692-285	Sequence 285, App	C 497	15.2	63.3	1665	14	US-10-187-747-285	Sequence 285, App
C 425	15.2	63.3	1665	14	US-10-174-576-285	Sequence 285, App	C 498	15.2	63.3	1665	14	US-10-187-751-285	Sequence 285, App
C 426	15.2	63.3	1665	14	US-10-174-585-285	Sequence 285, App	C 499	15.2	63.3	1665	14	US-10-187-753-285	Sequence 285, App
C 427	15.2	63.3	1665	14	US-10-174-586-285	Sequence 285, App	C 500	15.2	63.3	1665	14	US-10-187-754-285	Sequence 285, App
C 428	15.2	63.3	1665	14	US-10-175-747-285	Sequence 285, App							
C 429	15.2	63.3	1665	14	US-10-176-481-285	Sequence 285, App							
C 430	15.2	63.3	1665	14	US-10-176-485-285	Sequence 285, App							
C 431	15.2	63.3	1665	14	US-10-176-487-285	Sequence 285, App							
C 432	15.2	63.3	1665	14	US-10-176-493-285	Sequence 285, App							
C 433	15.2	63.3	1665	14	US-10-176-756-285	Sequence 285, App							
C 434	15.2	63.3	1665	14	US-10-176-911-285	Sequence 285, App							
C 435	15.2	63.3	1665	14	US-10-176-919-285	Sequence 285, App							
C 436	15.2	63.3	1665	14	US-10-176-925-285	Sequence 285, App							
C 437	15.2	63.3	1665	14	US-10-176-925-285	Sequence 285, App							
C 438	15.2	63.3	1665	14	US-10-180-549-285	Sequence 285, App							
C 439	15.2	63.3	1665	14	US-10-180-550-285	Sequence 285, App							
C 440	15.2	63.3	1665	14	US-10-180-543-285	Sequence 285, App							
C 441	15.2	63.3	1665	14	US-10-180-544-285	Sequence 285, App							
C 442	15.2	63.3	1665	14	US-10-180-546-285	Sequence 285, App							
C 443	15.2	63.3	1665	14	US-10-180-547-285	Sequence 285, App							
C 444	15.2	63.3	1665	14	US-10-180-549-285	Sequence 285, App							
C 445	15.2	63.3	1665	14	US-10-180-555-285	Sequence 285, App							
C 446	15.2	63.3	1665	14	US-10-180-559-285	Sequence 285, App							
C 447	15.2	63.3	1665	14	US-10-181-000-285	Sequence 285, App							
C 448	15.2	63.3	1665	14	US-10-183-010-285	Sequence 285, App							
C 449	15.2	63.3	1665	14	US-10-183-012-285	Sequence 285, App							
C 450	15.2	63.3	1665	14	US-10-184-614-285	Sequence 285, App							

ALIGNMENTS

RESULT 1

US-10-688-489-74
; Sequence 74, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Pollner, Jeffrey M.
; APPLICANT: Linnen, Jeffrey B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE OF INVENTION: West Nile Virus
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16

; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 24
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-74

Query Match 100.0%; Score 24; DB 18; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCTGAGGGCTTAC 24
|||||
Db 1 TCCGAGACGGTCTCTGAGGGCTTAC 24

RESULT 2
US-10-688-489-75
; Sequence 75, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; TITLE OF INVENTION: West Nile Virus
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 75
; LENGTH: 24
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-75

Query Match 100.0%; Score 24; DB 18; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCTGAGGGCTTAC 24
|||||
Db 1 TCCGAGACGGTCTCTGAGGGCTTAC 24

RESULT 3
US-10-815-480-1/c
; Sequence 1, Application US/10815480
; Publication No. US20040229261A1
; GENERAL INFORMATION:
; APPLICANT: Young, Karen K. Y.
; APPLICANT: Roche Molecular Systems, Inc.
; TITLE OF INVENTION: Compositions and Methods for Detecting Certain
; TITLE OF INVENTION: Flaviviruses, Including Members of the Japanese
; TITLE OF INVENTION: Encephalitis Virus Serogroup
; FILE REFERENCE: 022101-000230US
; CURRENT APPLICATION NUMBER: US/10/815,480
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US 60/459,491

; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/552,454
; PRIOR FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: US 60/555,530
; PRIOR FILING DATE: 2004-03-22
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:region of
; OTHER INFORMATION: conserved sequence in 3' untranslated region of
; OTHER INFORMATION: the genomes of flaviviruses
US-10-815-480-1

Query Match 100.0%; Score 24; DB 18; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCTGAGGGCTTAC 24
|||||
Db 24 TCCGAGACGGTCTCTGAGGGCTTAC 1

RESULT 4
US-10-815-480-2
; Sequence 2, Application US/10815480
; Publication No. US20040229261A1
; GENERAL INFORMATION:
; APPLICANT: Young, Karen K. Y.
; APPLICANT: Roche Molecular Systems, Inc.
; TITLE OF INVENTION: Compositions and Methods for Detecting Certain
; TITLE OF INVENTION: Flaviviruses, Including Members of the Japanese
; FILE REFERENCE: 022101-000230US
; CURRENT APPLICATION NUMBER: US/10/815,480
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US 60/459,491
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/552,454
; PRIOR FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: US 60/555,530
; PRIOR FILING DATE: 2004-03-22
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:complement to
; OTHER INFORMATION: SEQ ID NO:1
US-10-815-480-2

Query Match 100.0%; Score 24; DB 18; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCTGAGGGCTTAC 24
|||||
Db 2 TCCGAGACGGTCTCTGAGGGCTTAC 25

RESULT 5
US-10-815-480-7/c
; Sequence 7, Application US/10815480
; Publication No. US20040229261A1
; GENERAL INFORMATION:
; APPLICANT: Young, Karen K. Y.
; APPLICANT: Roche Molecular Systems, Inc.
; TITLE OF INVENTION: Compositions and Methods for Detecting Certain

```

; TITLE OF INVENTION: Flaviviruses, Including Members of the Japanese
; TITLE OF INVENTION: Encephalitis Virus Serogroup
; FILE REFERENCE: 022101-0002300S
; CURRENT APPLICATION NUMBER: US/10/815,480
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US 60/459,491
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/552,454
; PRIOR FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: US 60/555,530
; PRIOR FILING DATE: 2004-03-22
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Koutango virus
; OTHER INFORMATION: Primer 1
US-10-815-480-7

```

```

Query Match      100.0%; Score 24; DB 18; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 TCCGAGACGGTCTCGAGGGCTTAC 24
    |||||
Db 24 TCCGAGACGGTCTCGAGGGCTTAC 1

```

```

RESULT 6
US-10-815-480-8/c
; Sequence 8, Application US/10815480
; Publication No. US20040229261A1
; GENERAL INFORMATION:
; APPLICANT: Young, Karen K. Y.
; APPLICANT: Roche Molecular Systems, Inc.
; TITLE OF INVENTION: Compositions and Methods for Detecting Certain
; TITLE OF INVENTION: Flaviviruses, Including Members of the Japanese
; FILE REFERENCE: 022101-0002300S
; CURRENT APPLICATION NUMBER: US/10/815,480
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US 60/459,491
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/552,454
; PRIOR FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: US 60/555,530
; PRIOR FILING DATE: 2004-03-22
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Example Primer
; OTHER INFORMATION: 1
US-10-815-480-8

```

```

Query Match      100.0%; Score 24; DB 18; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 TCCGAGACGGTCTCGAGGGCTTAC 24
    |||||
Db 24 TCCGAGACGGTCTCGAGGGCTTAC 1

```

```

RESULT 7
US-10-688-489-73
; Sequence 73, Application US/10688489

```

```

; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; TITLE OF INVENTION: West Nile Virus
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 73
; LENGTH: 48
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-73

```

```

Query Match      100.0%; Score 24; DB 18; Length 48;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 TCCGAGACGGTCTCGAGGGCTTAC 24
    |||||
Db 1 TCCGAGACGGTCTCGAGGGCTTAC 24

```

```

RESULT 8
US-10-688-489-84
; Sequence 84, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; TITLE OF INVENTION: West Nile Virus
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 84
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(27)
; OTHER INFORMATION: T7 promoter sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (28)...(51)
; OTHER INFORMATION: WNV-complementary sequence
US-10-688-489-84

```

```

Query Match      100.0%; Score 24; DB 18; Length 51;

```

Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCGAGGGCTTAC 24
Db 28 TCCGAGACGGTCTCGAGGGCTTAC 51

RESULT 9

US-10-688-489-72
; Sequence 72, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 72
; LENGTH: 70
; TYPE: DNA
; ORGANISM: West Nile virus
US-10-688-489-72

Query Match 100.0%; Score 24; DB 18; Length 70;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCGAGGGCTTAC 24
Db 1 TCCGAGACGGTCTCGAGGGCTTAC 24

RESULT 10

US-10-815-480-71/c
; Sequence 71, Application US/10815480
; Publication No. US20040229261A1
; GENERAL INFORMATION:
; APPLICANT: Young, Karen K. Y.
; APPLICANT: Roche Molecular Systems, Inc.
; TITLE OF INVENTION: Compositions and Methods for Detecting Certain
; TITLE OF INVENTION: Flaviviruses, Including Members of the Japanese
; TITLE OF INVENTION: Encephalitis Virus Serogroup
; FILE REFERENCE: 022101-000230US
; CURRENT APPLICATION NUMBER: US/10/815,480
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US 60/459,491
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/552,454
; PRIOR FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: US 60/555,530
; PRIOR FILING DATE: 2004-03-22
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 71
; LENGTH: 98
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:region of

; OTHER INFORMATION: conserved sequence in 3' untranslated region of
; OTHER INFORMATION: the genome of flavivirus AF196835
US-10-815-480-71

Query Match 100.0%; Score 24; DB 18; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCGAGGGCTTAC 24
Db 68 TCCGAGACGGTCTCGAGGGCTTAC 45

RESULT 11

US-10-361-002-5/c
; Sequence 5, Application US/10361002
; Publication No. US20040170954A1
; GENERAL INFORMATION:
; APPLICANT: Clearant, Inc.
; APPLICANT: McKenney, Keith
; APPLICANT: Gillmeister, Lidja
; APPLICANT: Marlowe, Kristina
; APPLICANT: Armistead, David
; TITLE OF INVENTION: Pathogen Inactivation Assay
; FILE REFERENCE: CI-0043
; CURRENT APPLICATION NUMBER: US/10/361,002
; CURRENT FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 10945
; TYPE: DNA
; ORGANISM: West Nile virus
US-10-361-002-5

Query Match 100.0%; Score 24; DB 18; Length 10945;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCGAGGGCTTAC 24
Db 10587 TCCGAGACGGTCTCGAGGGCTTAC 10564

RESULT 12

US-10-361-004-5/c
; Sequence 5, Application US/10361004
; Publication No. US20040170981A1
; GENERAL INFORMATION:
; APPLICANT: Clearant, Inc.
; APPLICANT: McKenney, Keith
; APPLICANT: Gillmeister, Lidja
; APPLICANT: Marlowe, Kristina
; APPLICANT: Armistead, David
; TITLE OF INVENTION: Real-Time Polymerase Chain Reaction Using Large Target Amplicons
; FILE REFERENCE: CI-0042
; CURRENT APPLICATION NUMBER: US/10/361,004
; CURRENT FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 10945
; TYPE: DNA
; ORGANISM: West Nile virus
US-10-361-004-5

Query Match 100.0%; Score 24; DB 18; Length 10945;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCGAGGGCTTAC 24
Db 10587 TCCGAGACGGTCTCGAGGGCTTAC 10564

RESULT 13
US-10-699-550-1/c
; Sequence 1, Application US/10699550
; Publication No. US20040197769A1
; GENERAL INFORMATION:
; APPLICANT: WONG, SUSAN J.
; APPLICANT: SHI, PEI-YONG
; TITLE OF INVENTION: DIAGNOSTIC TEST FOR WEST NILE VIRUS
; FILE REFERENCE: 454311-2232.1
; CURRENT APPLICATION NUMBER: US/10/699,550
; PRIOR FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: 60/476,513
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/422,755
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: PCT/US02/09036
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: 60/402,860
; PRIOR FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/281,947
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/275,025
; PRIOR FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 10975
; TYPE: DNA
; ORGANISM: West Nile virus
US-10-699-550-1

Query Match 100.0%; Score 24; DB 18; Length 10975;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCGAGGGCTTAC 24
Db 10611 TCCGAGACGGTTCGAGGGCTTAC 10588

RESULT 14
US-10-699-550-2/c
; Sequence 2, Application US/10699550
; Publication No. US20040197769A1
; GENERAL INFORMATION:
; APPLICANT: WONG, SUSAN J.
; APPLICANT: SHI, PEI-YONG
; TITLE OF INVENTION: DIAGNOSTIC TEST FOR WEST NILE VIRUS
; FILE REFERENCE: 454311-2232.1
; CURRENT APPLICATION NUMBER: US/10/699,550
; PRIOR FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: 60/476,513
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/422,755
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: PCT/US02/09036
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: 60/402,860
; PRIOR FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/281,947
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/275,025
; PRIOR FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 11029
; TYPE: DNA
; ORGANISM: West Nile virus
US-10-699-550-2

Query Match 100.0%; Score 24; DB 18; Length 11029;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCGAGGGCTTAC 24
Db 10629 TCCGAGACGGTTCGAGGGCTTAC 10606

RESULT 15
US-10-679-520A-66/c
; Sequence 66, Application US/10679520A
; Publication No. US20050031641A1
; GENERAL INFORMATION:
; APPLICANT: AUDONNET, SHEENA MAY
; APPLICANT: LOODNET, JEAN-CHRISTOPHE FRANCIS
; APPLICANT: MINKE, JULES MAARTEN
; TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST WEST NILE VIRUS
; FILE REFERENCE: 574313-3161.4
; CURRENT APPLICATION NUMBER: US/10/679,520A
; PRIOR FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: 10/374,953
; PRIOR FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: 10/116,298
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/281,923
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: PCT/FR02/01200
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: FR 01/04737
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 66
; LENGTH: 11029
; TYPE: DNA
; ORGANISM: West Nile virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (97)..(10395)
US-10-679-520A-66

Query Match 100.0%; Score 24; DB 19; Length 11029;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCGAGGGCTTAC 24
Db 10629 TCCGAGACGGTTCGAGGGCTTAC 10606

RESULT 16
US-10-706-892-1/c
; Sequence 1, Application US/10706892
; Publication No. US20050058987A1
; GENERAL INFORMATION:
; APPLICANT: SHI, PEI-YONG
; TITLE OF INVENTION: SCREENING FOR WEST NILE VIRUS ANTIVIRAL THERAPY
; FILE REFERENCE: 454311-2231.1
; CURRENT APPLICATION NUMBER: US/10/706,892
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/427,117
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 11029
; TYPE: DNA
; ORGANISM: West Nile virus
US-10-706-892-1

Query Match 100.0%; Score 24; DB 19; Length 11029;
Best Local Similarity 100.0%; Pred. No. 0.05;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCTGAGGGCTTAC 24
|||||
Db 10629 TCCGAGACGGTCTCTGAGGGCTTAC 10606

RESULT 17

US-10-688-489-76
; Sequence 76, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 76
; LENGTH: 23
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-76

Query Match 95.8%; Score 23; DB 18; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCTGAGGGCTTA 23
|||||
Db 1 TCCGAGACGGTCTCTGAGGGCTTA 23

RESULT 18

US-10-688-489-85
; Sequence 85, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 85
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; NAME/KEY: misc.feature
; LOCATION: (1)...(27)
; OTHER INFORMATION: T7 promoter sequence
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (28)...(50)
; OTHER INFORMATION: WNV-complementary sequence
US-10-688-489-85

Query Match 95.8%; Score 23; DB 18; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCTGAGGGCTTA 23
|||||
Db 28 TCCGAGACGGTCTCTGAGGGCTTA 50

RESULT 19

US-10-706-892-2/c
; Sequence 2, Application US/10706892
; Publication No. US20050058987A1
; GENERAL INFORMATION:
; APPLICANT: SHI, PEI-YONG
; TITLE OF INVENTION: SCREENING FOR WEST NILE VIRUS ANTIVIRAL THERAPY
; FILE REFERENCE: 454311-2231.1
; CURRENT APPLICATION NUMBER: US/10/706,892
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/427,117
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 11029
; TYPE: DNA
; ORGANISM: West Nile virus
US-10-706-892-2

Query Match 93.3%; Score 22.4; DB 19; Length 11029;
Best Local Similarity 95.8%; Pred. No. 0.31;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCTGAGGGCTTAC 24
|||||
Db 10629 TCCGAGACGGTCTCTGAGGGCTTAC 10606

RESULT 20

US-10-688-489-77
; Sequence 77, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 77
; LENGTH: 22
; TYPE: DNA

```
; ORGANISM: West Nile Virus
US-10-688-489-77

Query Match          91.7%; Score 22; DB 18; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCGAGGGCTT 22
    |||||
Db 1 TCCGAGACGGTTCGAGGGCTT 22

RESULT 21
US-10-688-489-86
; Sequence 86, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GPI40-04.UT
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: US/10/688,489
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 86
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(27)
; OTHER INFORMATION: T7 promoter sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (28)..(49)
; OTHER INFORMATION: WNV-complementary sequence
US-10-688-489-86

Query Match          91.7%; Score 22; DB 18; Length 49;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCGAGGGCTT 22
    |||||
Db 28 TCCGAGACGGTTCGAGGGCTT 49

RESULT 22
US-10-688-489-149
; Sequence 149, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GPI40-04.UT
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: US/10/688,489
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 116
; LENGTH: 19
; TYPE: DNA
; ORGANISM: West Nile Virus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(19)
; OTHER INFORMATION: 2'-OME nucleotide analogs
US-10-688-489-116

Query Match          79.2%; Score 19; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GACGGTTCGAGGGCTTAC 24
    |||||
Db 19 GACGGTTCGAGGGCTTAC 1

RESULT 24
US-10-688-489-101/c
; Sequence 101, Application US/10688489
; Publication No. US20040259108A1
```

```
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 149
; LENGTH: 23
; TYPE: RNA
; ORGANISM: West Nile Virus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(23)
; OTHER INFORMATION: 2'-OME nucleotide analogs
US-10-688-489-149

Query Match          87.5%; Score 21; DB 18; Length 23;
Best Local Similarity 76.2%; Pred. No. 1.7;
Matches 16; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGACGGTTCGAGGGCTTAC 24
    |||||
Db 1 GAGACGGTTCGAGGGCTTAC 21

RESULT 23
US-10-688-489-116/c
; Sequence 116, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GPI40-04.UT
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 116
; LENGTH: 19
; TYPE: DNA
; ORGANISM: West Nile Virus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(19)
; OTHER INFORMATION: 2'-OME nucleotide analogs
US-10-688-489-116

Query Match          79.2%; Score 19; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GACGGTTCGAGGGCTTAC 24
    |||||
Db 19 GACGGTTCGAGGGCTTAC 1

RESULT 24
US-10-688-489-101/c
; Sequence 101, Application US/10688489
; Publication No. US20040259108A1
```

GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; TITLE OF INVENTION: West Nile Virus
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; PRIOR FILING DATE: 2003-10-16
; PRIOR FILING DATE: 2002-10-16
; PRIOR FILING DATE: 2002-11-25
; PRIOR FILING DATE: 2002-11-25
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 101
; LENGTH: 87
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-101

Query Match 79.2%; Score 19; DB 18; Length 87;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GACGGTCTGAGGCTTAC 24
DB 87 GACGGTCTGAGGCTTAC 69
|||||

RESULT 25
US-10-425-114-6462
; Sequence 6462, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 6462
; LENGTH: 434
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700565822_FLI
US-10-425-114-6462

Query Match 74.2%; Score 17.8; DB 17; Length 434;
Best Local Similarity 90.5%; Pred. No. 62;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GACACGGTCTGAGGCTTAC 24
DB 29 GATACGGTCTGAGGGATTAC 49
|||||

RESULT 26
US-10-424-599-28488
; Sequence 28488, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 28488
; LENGTH: 1831
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_125726C.1
US-10-424-599-28488

Query Match 74.2%; Score 17.8; DB 17; Length 1831;
Best Local Similarity 90.5%; Pred. No. 61;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GACACGGTCTGAGGCTTAC 24
DB 1202 GATACGGTCTGAGGGATTAC 1222
|||||

RESULT 27
US-10-225-066A-1045/c
; Sequence 1045, Application US/10225066A
; Publication No. US20030226173A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: RATCLIFFE, Oliver
; APPLICANT: RIESCHMANN, Jose Luis
; APPLICANT: ADAM, Luc J
; APPLICANT: DUBELL, Arnold T
; APPLICANT: HEARD, Jacqueline E
; APPLICANT: PILGRIM, Marsha L
; APPLICANT: JIANG, Cai-Zhong
; APPLICANT: REUBER, T. Lynne
; APPLICANT: CREELMAN, Robert A
; APPLICANT: PINEDA, Omalra
; APPLICANT: YU, Guo-Liang
; APPLICANT: BROUN, Pierre E
; TITLE OF INVENTION: Yield-Related Polynucleotides and Polypeptides in Plants
; FILE REFERENCE: MEI0036-2 US
; CURRENT APPLICATION NUMBER: US/10/225,066A
; CURRENT FILING DATE: 2002-08-09
; PRIOR FILING DATE: 2002-08-09
; PRIOR FILING DATE: 2001-04-18
; PRIOR FILING DATE: 2001-04-18
; PRIOR FILING DATE: 2001-08-09
; PRIOR FILING DATE: 2001-08-09
; PRIOR FILING DATE: 2001-12-05
; PRIOR FILING DATE: 2001-12-05
; PRIOR FILING DATE: 2001-12-11
; PRIOR FILING DATE: 2001-12-11
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 1122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1045
; LENGTH: 1661
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-225-066A-1045

Query Match 73.3%; Score 17.6; DB 17; Length 1661;
Best Local Similarity 83.3%; Pred. No. 76;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGACACGGTCTGAGGCTTAC 24
|||||

Db 610 TCCAAGTCGGTTCGTGAGGCTTAC 587

RESULT 28

US-10-302-267-29/c
; Sequence 29, Application US/10302267
; Publication No. US20030229915A1
; GENERAL INFORMATION:

; APPLICANT: Keddle, James
; APPLICANT: Fromm, Michael
; APPLICANT: Heard, Jacqueline
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Adam, Luc
; APPLICANT: Broun, Pierre
; APPLICANT: Pineda, Omaira
; APPLICANT: Reuber, Lynne
; APPLICANT: Zhang, James
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Samaha, Raymond
; APPLICANT: Pilgrim, Marsha
; APPLICANT: Creelman, Robert

; TITLE OF INVENTION: PLANT GENE SEQUENCES II

; FILE REFERENCE: MBI-0007

; CURRENT APPLICATION NUMBER: US/10/302,267

; CURRENT FILING DATE: 2002-11-22

; PRIOR APPLICATION NUMBER: US/09/506,720

; PRIOR FILING DATE: 2000-02-17

; PRIOR APPLICATION NUMBER: 60/120,880

; PRIOR FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: 60/121,037

; PRIOR FILING DATE: 1999-02-22

; PRIOR APPLICATION NUMBER: 60/124,278

; PRIOR FILING DATE: 1999-03-11

; PRIOR APPLICATION NUMBER: 60/129,450

; PRIOR FILING DATE: 1999-04-15

; PRIOR APPLICATION NUMBER: 60/135,134

; PRIOR FILING DATE: 1999-05-20

; PRIOR APPLICATION NUMBER: 60/144,153

; PRIOR FILING DATE: 1999-07-15

; PRIOR APPLICATION NUMBER: 60/161,143

; PRIOR FILING DATE: 1999-10-22

; PRIOR APPLICATION NUMBER: 60/162,656

; PRIOR FILING DATE: 1999-11-01

; NUMBER OF SEQ ID NOS: 218

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 29

; LENGTH: 1661

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (190)..(1458)

; OTHER INFORMATION: G631

US-10-302-267-29

Query Match 73.3%; Score 17.6; DB 17; Length 1661;

Best Local Similarity 83.3%; Pred. No. 76;

Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCGTGAGGCTTAC 24

Db 610 TCCAAGTCGGTTCGTGAGGCTTAC 587

RESULT 29

US-10-374-780A-2387/c

; Sequence 2387, Application US/10374780A

; Publication No. US20040019927A1

; GENERAL INFORMATION:

; APPLICANT: Sherman, Bradley K

; APPLICANT: Riechmann, Jose Luis

; APPLICANT: Jiang, Cai-Zhong

; APPLICANT: Heard, Jacqueline E
; APPLICANT: Haake, Volker
; APPLICANT: Creelman, Robert A
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Adam, Luc J
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Keddle, James
; APPLICANT: Broun, Pierre E
; APPLICANT: Pilgrim, Marsha L
; APPLICANT: Dubell III, Arnold T
; APPLICANT: Pineda, Omaira
; APPLICANT: Yu, Guo-Liang

; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS

; FILE REFERENCE: MBI-0047 CIP

; CURRENT APPLICATION NUMBER: US/10/374,780A

; CURRENT FILING DATE: 2003-02-25

; PRIOR APPLICATION NUMBER: 09/837,944

; PRIOR FILING DATE: 2001-04-18

; PRIOR APPLICATION NUMBER: 60/310,847

; PRIOR FILING DATE: 2001-08-09

; PRIOR APPLICATION NUMBER: 09/934,455

; PRIOR FILING DATE: 2001-08-22

; PRIOR APPLICATION NUMBER: 60/336,049

; PRIOR FILING DATE: 2001-11-19

; PRIOR APPLICATION NUMBER: 60/338,692

; PRIOR FILING DATE: 2001-12-11

; PRIOR APPLICATION NUMBER: 10/171,468

; PRIOR FILING DATE: 2002-06-14

; PRIOR APPLICATION NUMBER: 10/225,066

; PRIOR FILING DATE: 2002-08-09

; PRIOR APPLICATION NUMBER: 10/225,067

; PRIOR FILING DATE: 2002-08-09

; PRIOR APPLICATION NUMBER: 10/225,068

; PRIOR FILING DATE: 2002-08-09

; NUMBER OF SEQ ID NOS: 2906

; SOFTWARE: Patent In version 3.2

; SEQ ID NO 2387

; LENGTH: 1661

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

; FEATURE:

; OTHER INFORMATION: G631

US-10-374-780A-2387

Query Match 73.3%; Score 17.6; DB 17; Length 1661;

Best Local Similarity 83.3%; Pred. No. 76;

Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCGTGAGGCTTAC 24

Db 610 TCCAAGTCGGTTCGTGAGGCTTAC 587

RESULT 30

US-10-412-699B-411/c

; Sequence 411, Application US/10412699B

; Publication No. US20040045049A1

; GENERAL INFORMATION:

; APPLICANT: Mendel Biotechnology, Inc.

; APPLICANT: Zhang, James

; APPLICANT: Fromm, Michael E.

; APPLICANT: Heard, Jacqueline E.

; APPLICANT: Riechmann, Jose Luis

; APPLICANT: Adam, Luc J.

; APPLICANT: Broun, Pierre E.

; APPLICANT: Pineda, Omaira

; APPLICANT: Reuber, T. Lynne

; APPLICANT: Keddle, James S.

; APPLICANT: Yu, Guo-Liang

; APPLICANT: Jiang, Cai-Zhong

; APPLICANT: Samaha, Raymond R.

; APPLICANT: Pilgrim, Marsha L.

; APPLICANT: Creelman, Robert A.

```

RESULT 31
US-10-425-114-12992/c
; Sequence 12992, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53)1313B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 12992
; LENGTH: 1727
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana columbia
; FEATURE:
; OTHER INFORMATION: Clone ID: JC-ATXLIB327418P1A06_FLI
US-10-425-114-12992

```

```

RESULT 33
US-10-815-480-4/c
; Sequence 4, Application US/10815480
; Publication No. US20040229261A1
; GENERAL INFORMATION:
; APPLICANT: Young, Karen K. Y.
; APPLICANT: Roche Molecular Systems, Inc.
; TITLE OF INVENTION: Compositions and Methods for Detecting Certain
; TITLE OF INVENTION: Flaviviruses, Including Members of the Japanese
; TITLE OF INVENTION: Encephalitis Virus Serogroup
; FILE REFERENCE: 022101-0002300S
; CURRENT APPLICATION NUMBER: US/10/815,480
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US 60/459,491
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/552,454
; PRIOR FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: US 60/555,530
; PRIOR FILING DATE: 2004-03-22
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:West Nile vir
; OTHER INFORMATION: Primer 1
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8)
; OTHER INFORMATION: n = t or absent

```

US-10-815-480-4

Query Match 70.0%; Score 16.8; DB 18; Length 26;
Best Local Similarity 78.9%; Pred. No. 2e+02;
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTGAGGC 19
|||||:|||||:|||||:|
Db 25 TCCGARRCGGTTCTGRNG 7

RESULT 34

US-09-918-995-5377/c
; Sequence 5377, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5377
; LENGTH: 487
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(487)
; OTHER INFORMATION: n = A,T,C or G

US-09-918-995-5377

Query Match 70.0%; Score 16.8; DB 10; Length 487;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTGAGGC 20
|||||:|||||:|||||:|
Db 47 TCCGGCGCGGTTCTGAGGC 28

RESULT 35

US-10-437-963-80309/c
; Sequence 80309, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 80309
; LENGTH: 704
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(704)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_79946C.1
US-10-437-963-80309

Query Match 70.0%; Score 16.8; DB 18; Length 704;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCGAGACGGTTCTGAGGGCT 21
|||||:|||||:|||||:|
Db 566 CCGAGACGGTTCTGAGGGCT 547

RESULT 36

US-10-437-963-21906
; Sequence 21906, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 21906
; LENGTH: 1416
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_27132C.1

US-10-437-963-21906

Query Match 70.0%; Score 16.8; DB 18; Length 1416;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTGAGGC 20
|||||:|||||:|||||:|
Db 1091 TCCGAGACGGATCTGAGGC 1110

RESULT 37

US-10-261-175A-3
; Sequence 3, Application US/10261175A
; Publication No. US20040038222A1
; GENERAL INFORMATION:
; APPLICANT: DIETRICH, WILLIAM
; APPLICANT: WATERS, JAMES W.
; TITLE OF INVENTION: ANTHRAX SUSCEPTIBILITY GENE
; FILE REFERENCE: 56491(71250)
; CURRENT APPLICATION NUMBER: US/10/261,175A
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: 60/325,864
; PRIOR FILING DATE: 2001-09-29
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2802
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: KifLC nucleic
; OTHER INFORMATION: acid sequence

US-10-261-175A-3

Query Match 70.0%; Score 16.8; DB 17; Length 2802;

```

Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCGAGACGGTCTCGAGGGCT 21
Db 444 CCGAGGAGGTTCTGAGGGCT 463

RESULT 38
US-10-085-117-235
; Sequence 235, Application US/10085117
; Publication No. US2003023233A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: 529452000121
; CURRENT APPLICATION NUMBER: US/10/085,117
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 235
; LENGTH: 33488
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: variation
; LOCATION: (1)...(33488)
; OTHER INFORMATION: n = any nucleotide
US-10-085-117-235

Query Match 70.0%; Score 16.8; DB 17; Length 33488;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 AGACGGTCTCGAGGGCTTAC 24
Db 31534 AGAGGGTCTCGAGGGCTTCC 31553

RESULT 39
US-10-322-281-232
; Sequence 232, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 232
; LENGTH: 135827
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(135827)
; OTHER INFORMATION: n = A,T,C or G
US-10-322-281-232

Query Match 70.0%; Score 16.8; DB 18; Length 135827;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCGAGGC 20
Db 21789 TCCGAGAGGTTCTGAGGC 21808

Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCGAGACGGTCTCGAGGGCT 21
Db 444 CCGAGGAGGTTCTGAGGGCT 463

RESULT 40
US-10-357-930-55914
; Sequence 55914, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BECN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55914
; LENGTH: 597
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: 28
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-55914

Query Match 69.2%; Score 16.6; DB 18; Length 597;
Best Local Similarity 82.6%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCGAGGGCTTA 23
Db 65 TCAGAAACGGTCTGATGGCTTA 87

RESULT 41
US-09-919-580-6
; Sequence 6, Application US/09919580
; Patent No. US2002010832A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 723
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 643, 670, 694, 721
; OTHER INFORMATION: n = A,T,C or G
US-09-919-580-6

```

US-09-919-580-6

Query Match 69.2%; Score 16.6; DB 9; Length 723;
Best Local Similarity 79.2%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTCAGGGCTTAC 24
DB 689 TCACANACTTCTCAGGGCTTAC 712

RESULT 42

US-10-369-493-24654
; Sequence 24654, Application US/10369493
; Publication No. US20030233675A1

GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 24654

; LENGTH: 1671

; TYPE: DNA

; ORGANISM: Archaeoglobus fulgidus

US-10-369-493-24654

Query Match 69.2%; Score 16.6; DB 17; Length 1671;
Best Local Similarity 82.6%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CCGAGACGGTTCTCAGGGCTTAC 24
DB 554 CGGNACGGTTGAGGGCTTAC 576

RESULT 43

US-10-815-480-5/c

; Sequence 5, Application US/10815480

; Publication No. US20040229261A1

GENERAL INFORMATION:

; APPLICANT: Young, Karen K. Y.

; APPLICANT: Roche Molecular Systems, Inc.

; TITLE OF INVENTION: Compositions and Methods for Detecting Certain

; TITLE OF INVENTION: Flaviviruses, Including Members of the Japanese

; TITLE OF INVENTION: Encephalitis Virus Serogroup

; FILE REFERENCE: 022101-000230US

; CURRENT APPLICATION NUMBER: US/10/815,480

; CURRENT FILING DATE: 2004-03-31

; PRIOR APPLICATION NUMBER: US 60/459,491

; PRIOR FILING DATE: 2003-03-31

; PRIOR APPLICATION NUMBER: US 60/552,454

; PRIOR FILING DATE: 2004-03-12

; PRIOR APPLICATION NUMBER: US 60/555,530

; PRIOR FILING DATE: 2004-03-22

; NUMBER OF SEQ ID NOS: 74

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 5

; LENGTH: 26

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Japanese

; OTHER INFORMATION: encephalitis virus Primer 1

; FEATURE:

; NAME/KEY: modified_base

; LOCATION: (8)

; OTHER INFORMATION: n = absent

US-10-815-480-5

Query Match 68.3%; Score 16.4; DB 18; Length 26;
Best Local Similarity 73.7%; Pred. No. 3.2e+02;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTCAGGG 19
DB 25 TCCGACRGGTTTGGAGNG 7

RESULT 44

US-09-938-842A-1241

; Sequence 1241, Application US/09938842A

; Patent No. US20020160378A1

GENERAL INFORMATION:

; APPLICANT: Harper, Jeff

; APPLICANT: Kreps, Joel

; APPLICANT: Wang, Xun

; APPLICANT: Zhu, Tong

; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

; TITLE OF INVENTION: SAME, AND METHODS OF USE

; FILE REFERENCE: SCRIPT300-3

; CURRENT APPLICATION NUMBER: US/09/938,842A

; CURRENT FILING DATE: 2001-08-24

; PRIOR APPLICATION NUMBER: US 60/227,866

; PRIOR FILING DATE: 2000-08-24

; PRIOR APPLICATION NUMBER: US 60/264,647

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/300,111

; PRIOR FILING DATE: 2001-06-22

; NUMBER OF SEQ ID NOS: 5379

; SEQ ID NO 1241

; LENGTH: 1929

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

US-09-938-842A-1241

Query Match 68.3%; Score 16.4; DB 9; Length 1929;
Best Local Similarity 94.4%; Pred. No. 3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGACGGTTCTCAGGGCTT 22
DB 1535 AGACGGTTCTCAGGGATT 1552

RESULT 45

US-09-938-842A-1241

; Sequence 1241, Application US/09938842A

; Publication No. US20040009476A9

GENERAL INFORMATION:

; APPLICANT: Harper, Jeff

; APPLICANT: Kreps, Joel

; APPLICANT: Wang, Xun

; APPLICANT: Zhu, Tong

; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

; TITLE OF INVENTION: SAME, AND METHODS OF USE

; FILE REFERENCE: SCRIPT300-3

; CURRENT APPLICATION NUMBER: US/09/938,842A

; CURRENT FILING DATE: 2001-08-24

; PRIOR APPLICATION NUMBER: US 60/227,866

; PRIOR FILING DATE: 2000-08-24

; PRIOR APPLICATION NUMBER: US 60/264,647

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/300,111

; PRIOR FILING DATE: 2001-06-22

; NUMBER OF SEQ ID NOS: 5379

; SEQ ID NO 1241

; LENGTH: 1929


```
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1241

Query Match      68.3%; Score 16.4; DB 11; Length 1929;
Best Local Similarity 94.4%; Pred. No. 3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGACGGTTCTGAGGGCTT 22
    |||||
Db 1535 AGACGGTTCTGAGGGATT 1552

RESULT 46
US-10-449-857A-67/c
; Sequence 67, Application US/10449857A
; Publication No. US20040043931A1
; GENERAL INFORMATION:
; APPLICANT: Hereshberg, Robert M.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Raodoh
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF INFLAMMATORY BOWEL DISEASE
; FILE REFERENCE: 584C1
; CURRENT APPLICATION NUMBER: US/10/449,857A
; CURRENT FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: Corixa Invention Disclosure Database
; SEQ ID NO 67
; LENGTH: 616
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Unknown Bacterium
US-10-449-857A-67

Query Match      67.5%; Score 16.2; DB 17; Length 616;
Best Local Similarity 85.7%; Pred. No. 3.8e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCCGACACGGTTCTGAGGGCT 21
    |||||
Db 444 TCCGACACGGTTCTGATAGCT 424

RESULT 47
US-10-425-114-6252
; Sequence 6252, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 6252
; LENGTH: 1055
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700558722_FLI
US-10-425-114-6252

Query Match      67.5%; Score 16.2; DB 17; Length 1055;
Best Local Similarity 85.7%; Pred. No. 3.8e+02;

US-10-688-489-75.rnpb

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GAGACGGTTCTGAGGGCTTAC 24
    |||||
Db 339 GAGACGGTTCTGAGGGCTAAC 359

RESULT 48
US-10-424-599-35449
; Sequence 35449, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 35449
; LENGTH: 1122
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1122)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_132013C.1
US-10-424-599-35449

Query Match      67.5%; Score 16.2; DB 17; Length 1122;
Best Local Similarity 85.7%; Pred. No. 3.8e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GAGACGGTTCTGAGGGCTTAC 24
    |||||
Db 406 GAGACGGTTCTGAGGGCTAAC 426

RESULT 49
US-10-424-599-73661/c
; Sequence 73661, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 73661
; LENGTH: 1275
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_37530C.1
US-10-424-599-73661

Query Match      67.5%; Score 16.2; DB 17; Length 1275;
Best Local Similarity 85.7%; Pred. No. 3.8e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CGAGACGGTTCTGAGGGCTTA 23
    |||||
Db 44 CGGACGAGTCTGAGGGCTTA 24
```

RESULT 50
US-10-437-963-83700
; Sequence 83700, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 83700
; LENGTH: 1685
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_83005C.1
US-10-437-963-83700

Query Match 67.5%; Score 16.2; DB 18; Length 1685;
Best Local Similarity 85.7%; Pred. No. 3.8e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CCGAGACGGTTCTGAGGGCTT 22
|||||
Db 361 CCGAGTCGGTTCAGAGGGTTT 361
|||||

Search completed: March 25, 2005, 14:03:20
Job time : 305.714 secs

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OM nucleic - nucleic search, using sw model

Run on: March 25, 2005, 09:34:25 ; Search time 663.429 Seconds
(without alignments)
1314.676 Million cell updates/sec

Title: US-10-688-489-64
Perfect score: 18
Sequence: 1 cgccaccggaagttagt 18
Scoring table: IDENTITY.NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pt.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	456	14	AF458351 Kunjin vi
2	18	100.0	458	14	AF458356 Kunjin vi
3	18	100.0	462	14	AF458350 West Nile
4	18	100.0	463	14	AF458343 West Nile
5	18	100.0	463	14	AF458344 West Nile
6	18	100.0	463	14	AF458347 West Nile
7	18	100.0	463	14	AF458348 West Nile
8	18	100.0	463	14	AF458355 West Nile
9	18	100.0	463	14	AF458360 West Nile
10	18	100.0	463	14	AF458361 West Nile
11	18	100.0	464	14	AF458361 West Nile
12	18	100.0	464	14	AF458361 West Nile
13	18	100.0	464	14	AF458361 West Nile
14	18	100.0	464	14	AF458361 West Nile
15	18	100.0	464	14	AF458361 West Nile
16	18	100.0	464	14	AF458361 West Nile
17	18	100.0	464	14	AF458361 West Nile
18	18	100.0	464	14	AF458361 West Nile
19	18	100.0	464	14	AF458361 West Nile

20	18	100.0	464	14	AY590199	West Nile
21	18	100.0	464	14	AY590200	West Nile
22	18	100.0	464	14	AY590201	West Nile
23	18	100.0	464	14	AY590202	West Nile
24	18	100.0	464	14	AY590203	West Nile
25	18	100.0	464	14	AY590204	West Nile
26	18	100.0	464	14	AY590205	West Nile
27	18	100.0	464	14	AY590206	West Nile
28	18	100.0	464	14	AY590207	West Nile
29	18	100.0	464	14	AY590208	West Nile
30	18	100.0	464	14	AY590209	West Nile
31	18	100.0	542	14	AF297854	Kunjin vi
32	18	100.0	545	14	AF297850	Kunjin vi
33	18	100.0	585	14	AF297840	Kunjin vi
34	18	100.0	587	14	KUNNS5GAA	L48978 Kunjin viru
35	18	100.0	587	14	KUNNS5GAB	L48979 Kunjin viru
36	18	100.0	593	14	AF297847	AF297847 Kunjin vi
37	18	100.0	593	14	AF297852	AF297852 Kunjin vi
38	18	100.0	594	14	AF297853	AF297853 Kunjin vi
39	18	100.0	600	14	AF297846	AF297846 Kunjin vi
40	18	100.0	601	14	AF297844	AF297844 Kunjin vi
41	18	100.0	607	14	AF297841	AF297841 Kunjin vi
42	18	100.0	609	14	AF297856	AF297856 Kunjin vi
43	18	100.0	616	14	AF297845	AF297845 Kunjin vi
44	18	100.0	620	14	AF297859	AF297859 Kunjin vi
45	18	100.0	622	14	AF297842	AF297842 Kunjin vi
46	18	100.0	623	14	AF297843	AF297843 Kunjin vi
47	18	100.0	627	14	KUNNONCOB	L24512 Kunjin viru
48	18	100.0	633	14	AF297858	AF297858 Kunjin vi
49	18	100.0	644	14	AF297848	AF297848 Kunjin vi
50	18	100.0	645	14	AY187012	AY187012 West Nile
51	18	100.0	645	14	AY187013	AY187013 West Nile
52	18	100.0	645	14	AY187014	AY187014 West Nile
53	18	100.0	645	14	AY187015	AY187015 West Nile
54	18	100.0	652	14	AF297855	AF297855 Kunjin vi
55	18	100.0	657	14	AF297849	AF297849 Kunjin vi
56	18	100.0	659	14	AF196536	AF196536 West Nile
57	18	100.0	669	14	AF196541	AF196541 West Nile
58	18	100.0	670	14	AF196542	AF196542 West Nile
59	18	100.0	1524	14	AF017254	AF017254 West Nile
60	18	100.0	10842	14	AF278442	AF278442 West Nile
61	18	100.0	10845	14	AY277252	AY277252 West Nile
62	18	100.0	10945	14	AF202541	AF202541 West Nile
63	18	100.0	10972	14	AF317203	AF317203 West Nile
64	18	100.0	10975	14	AF206518	AF206518 West Nile
65	18	100.0	10984	14	AF262283	AF262283 West Nile
66	18	100.0	10989	14	AY268132	AY268132 West Nile
67	18	100.0	10989	14	AY268133	AY268133 West Nile
68	18	100.0	10998	14	AY278441	AY278441 West Nile
69	18	100.0	11022	14	AY274504	AY274504 Kunjin vi
70	18	100.0	11022	14	AY274505	AY274505 Kunjin vi
71	18	100.0	11028	14	AY490240	AY490240 West Nile
72	18	100.0	11029	6	AX576542	AX576542 Sequence
73	18	100.0	11029	6	AX577796	AX577796 Sequence
74	18	100.0	11029	14	AB185914	AB185914 West Nile
75	18	100.0	11029	14	AB185915	AB185915 West Nile
76	18	100.0	11029	14	AB185916	AB185916 West Nile
77	18	100.0	11029	14	AB185917	AB185917 West Nile
78	18	100.0	11029	14	AF196835	AF196835 West Nile
79	18	100.0	11029	14	AF260967	AF260967 West Nile
80	18	100.0	11029	14	AF260968	AF260968 West Nile
81	18	100.0	11029	14	AF260969	AF260969 West Nile
82	18	100.0	11029	14	AF404753	AF404753 West Nile
83	18	100.0	11029	14	AF404754	AF404754 West Nile
84	18	100.0	11029	14	AF404755	AF404755 West Nile
85	18	100.0	11029	14	AF404756	AF404756 West Nile
86	18	100.0	11029	14	AF404757	AF404757 West Nile
87	18	100.0	11029	14	AF481864	AF481864 West Nile
88	18	100.0	11029	14	AF533540	AF533540 West Nile
89	18	100.0	11029	14	AF289214	AF289214 West Nile
90	17	94.4	395	14	AF458358	AF458358 West Nile
91	17	94.4	481	14	AF458349	AF458349 West Nile
92	17	94.4	481	14	AF458359	AF458359 West Nile

93	17	94.4	483	14	AF458345	West Nile	166	15.4	85.6	163970	3	AC010580
94	17	94.4	483	14	AF458357	West Nile	167	15.4	85.6	169902	3	AC008209
95	17	94.4	484	14	AF458354	West Nile	C 168	15.4	85.6	170750	2	AC103898
96	17	94.4	497	14	AF458346	West Nile	C 169	15.4	85.6	173603	10	AC132222
97	17	94.4	591	14	AF196543	West Nile	C 170	15.4	85.6	178602	9	AC078859
98	17	94.4	593	14	AF196543	West Nile	C 171	15.4	85.6	178357	9	AC013286
99	17	94.4	677	14	AF196535	West Nile	C 172	15.4	85.6	178965	9	AC012048
100	17	94.4	687	14	AF196535	West Nile	C 173	15.4	85.6	179305	9	AC144411
101	17	94.4	917	14	AF208017	West Nile	C 174	15.4	85.6	182408	9	AC144411
102	17	94.4	10962	14	WNFCG	West Nile	C 175	15.4	85.6	182408	9	AC144411
103	17	94.4	11057	14	AF688948	West Nile	C 176	15.4	85.6	186008	2	AC018776
104	17	94.4	11064	14	AF453412	West Nile	C 177	15.4	85.6	186458	2	AC074052
105	17	94.4	11066	14	AF453411	West Nile	C 178	15.4	85.6	190187	5	AC074052
106	16.4	91.1	451	14	AF458352	West Nile	C 179	15.4	85.6	191810	2	AC137503
107	16.4	91.1	593	14	AF297857	West Nile	C 180	15.4	85.6	193050	1	AC141419
108	16.4	91.1	604	14	KUNNS5	West Nile	C 181	15.4	85.6	202798	2	AC026553
109	16.4	91.1	644	14	AF196538	West Nile	C 182	15.4	85.6	204922	2	AC0760274
110	16.4	91.1	648	14	AF196540	West Nile	C 183	15.4	85.6	205602	10	AF325177
111	16.4	91.1	664	14	AF196537	West Nile	C 184	15.4	85.6	206082	2	AC128554
112	16.4	91.1	10741	14	AV277251	West Nile	C 185	15.4	85.6	207345	9	AC009062
113	16.4	91.1	110000	2	AC006497_5	Continuation (6 of	C 186	15.4	85.6	207441	2	AC140719
114	16.4	91.1	137296	2	AC006497_5	Continuation (6 of	C 187	15.4	85.6	209113	2	CR388368
115	16.4	91.1	150975	5	AC006497_5	Continuation (6 of	C 188	15.4	85.6	211278	10	AC093346
116	16.4	91.1	174539	9	AC033558	Continuation (6 of	C 189	15.4	85.6	212520	9	AC093731
117	16.4	91.1	177384	9	AC097639	Continuation (6 of	C 190	15.4	85.6	220515	2	AC113303
118	16.4	91.1	184541	2	AC073715	Continuation (6 of	C 191	15.4	85.6	220922	2	AC103466
119	16.4	91.1	241836	10	AC019302	Continuation (6 of	C 192	15.4	85.6	223728	2	AC097906
120	16	88.9	1323	6	AX663976	Sequence	C 193	15.4	85.6	226793	3	AE003753
121	16	88.9	3931	10	AB041543	Mus muscu	C 194	15.4	85.6	230200	2	AC129375
122	16	88.9	3986	10	BC066816	Mus muscu	C 195	15.4	85.6	231274	2	AC099393
123	16	88.9	4000	10	AK128931	Mus muscu	C 196	15.4	85.6	231910	2	AC099393
124	16	88.9	4753	10	AK173281	Mus muscu	C 197	15.4	85.6	232124	2	AC129365
125	16	88.9	31068	6	CO612365	Sequence	C 198	15.4	85.6	233428	2	AC0102984
126	16	88.9	61969	6	CO612365	Sequence	C 199	15.4	85.6	235612	2	AC011064
127	16	88.9	110000	1	AE000516_14	Continuation (15 o	C 200	15.4	85.6	241151	2	AC125675
128	16	88.9	124373	10	AC012104	Mus muscu	C 201	15.4	85.6	254644	2	AC136836
129	16	88.9	169273	3	AC009916	Mus muscu	C 202	15.4	85.6	255763	2	AC099281
130	16	88.9	215711	3	AC008205	Mus muscu	C 203	15.4	85.6	256032	2	AC114054
131	16	88.9	228433	3	AE003749	Mus muscu	C 204	15.4	85.6	256511	2	AC135040
132	16	88.9	299450	1	BK248338	Mycobacte	C 205	15.4	85.6	256807	2	AC105547
133	16	88.9	348264	1	BK842576	Mycobacte	C 206	15.4	85.6	262721	2	AC106265
134	15.6	86.7	21	6	CO815914	Sequence	C 207	15.4	85.6	290680	2	AC099478
135	15.4	85.6	391	8	AF203459	Arabidops	C 208	15	83.3	3436	6	AE017135
136	15.4	85.6	524	14	AF297851	Arabidops	C 209	15	83.3	436	6	AR305566
137	15.4	85.6	562	14	FVMSNGAH	Arabidops	C 210	15	83.3	600	8	AR305579
138	15.4	85.6	741	6	CO805118	Sequence	C 211	15	83.3	616	6	BT008964
139	15.4	85.6	741	8	AY039999	Arabidops	C 212	15	83.3	673	6	AR305576
140	15.4	85.6	882	8	AY085388	Arabidops	C 213	15	83.3	1863	6	AR305575
141	15.4	85.6	931	8	AF360183	Arabidops	C 214	15	83.3	1863	6	BD162638
142	15.4	85.6	2329	5	DRU57973	Arabidops	C 215	15	83.3	1969	6	AX120521
143	15.4	85.6	2878	8	SCU18116	Arabidops	C 216	15	83.3	35652	2	AX773825
144	15.4	85.6	6947	1	AB033988	Arabidops	C 217	15	83.3	52872	2	AC017428
145	15.4	85.6	9923	1	AB033780	Arabidops	C 218	15	83.3	110000	2	CO576911
146	15.4	85.6	10863	1	AB005678	Arabidops	C 219	15	83.3	134728	8	AC090683
147	15.4	85.6	37346	9	AC137777	Arabidops	C 220	15	83.3	139182	2	AC109917
148	15.4	85.6	37972	2	AC137601	Arabidops	C 221	15	83.3	147702	2	AC109917
149	15.4	85.6	45133	2	AC142207	Arabidops	C 222	15	83.3	152383	9	HSF18108
150	15.4	85.6	63314	2	AC017803	Arabidops	C 223	15	83.3	169283	10	AC131581
151	15.4	85.6	80770	8	AB005240	Arabidops	C 224	15	83.3	171105	3	AC007532
152	15.4	85.6	84761	9	AC093648	Arabidops	C 225	15	83.3	181009	3	AC007575
153	15.4	85.6	98348	9	ATF136103	Human DNA	C 226	15	83.3	195696	10	AC125058
154	15.4	85.6	99008	8	ATF136103	Human DNA	C 227	15	83.3	206167	2	AC113586
155	15.4	85.6	107074	8	AP003917	Arabidops	C 228	15	83.3	214508	2	AC103532
156	15.4	85.6	110000	1	AE016827_21	Continuation (22 o	C 229	15	83.3	215391	2	AC120168
157	15.4	85.6	110000	1	EX936398_28	Continuation (29 o	C 230	15	83.3	216912	2	AC114349
158	15.4	85.6	120725	9	AC023813_2	Continuation (3 of	C 231	15	83.3	227299	10	AC138722
159	15.4	85.6	127275	2	AC023813_2	Continuation (3 of	C 232	15	83.3	295289	3	BE003603
160	15.4	85.6	130665	10	AF289666	Mus muscu	C 233	15	83.3	307337	1	BE003603
161	15.4	85.6	132742	2	AC145412	Mus muscu	C 234	15	83.3	318862	2	AC109547
162	15.4	85.6	146185	8	AP005542	Mus muscu	C 235	15	83.3	328050	1	AP005275
163	15.4	85.6	151457	8	AP003410	Mus muscu	C 236	15	83.3	340000	9	HS21C046
164	15.4	85.6	156850	8	AP002901	Mus muscu	C 237	15	83.3	349887	1	BE003603
165	15.4	85.6	163240	2	AC069422	Mus muscu	C 238	15	83.3	349980	6	AX127144

AC010580 Drosophil
AC008209 Drosophil
AC103898 Bos tauru
AC132222 Mus muscu
AC078859 Homo sapi
AC013286 Homo sapi
AC012048 Homo sapi
AC144411 Homo sapi
AC078638 Human DNA
AC018776 Homo sapi
AC074052 Homo sapi
BX511138 Zebrafish
AC137503 Homo sapi
AJ414149 Veroinia
AC026553 Homo sapi
AL670274 Homo sapi
AF325177 Mus muscu
AC128554 Rattus no
AC009062 Homo sapi
AC140719 Homo sapi
CR388368 Danio rer
AC093346 Mus muscu
AC099731 Homo sapi
AC113303 Mus muscu
AC103466 Rattus no
AC097906 Rattus no
AE003753 Drosophil
AC029375 Rattus no
AC099393 Rattus no
AC128365 Rattus no
AC102984 Rattus no
AC011064 Drosophil
AC113621 Rattus no
AC125675 Rattus no
AC136836 Rattus no
AC099281 Rattus no
AC14054 Rattus no
AC135040 Rattus no
AC105547 Rattus no
AC106265 Rattus no
AC099478 Rattus no
AE017135 Veroinia
AR305566 Sequence
AR305579 Sequence
BT008964 Triticum
AR305576 Sequence
AR305575 Sequence
BD162638 Novel pol
AX120521 Sequence
AX773825 Sequence
AC017428 Drosophil
CO576911 Sequence
Continuation (3 of
AC090683 Oryza sat
AC109917 Bos tauru
AC109917 Bos tauru
AJ006995 Homo sapi
AC131581 Mus muscu
AC007532 Drosophil
AC007575 Drosophil
AC125058 Mus muscu
AC113586 Mus muscu
AC103532 Rattus no
AC120168 Mus muscu
AC14349 Rattus no
AC138722 Mus muscu
AE003603 Drosophil
BX842656 Bdelovib
AC109547 Rattus no
AP005275 Corynebac
AL63246 Homo sapi
BX927149 Corynebac
AX127144 Sequence

C 239	14.8	82.2	100	6	AX992189	Sequence	AX992189	Sequence	C 312	14.8	82.2	17576	1	AE004913
C 240	14.8	82.2	100	6	AX992190	Sequence	AX992190	Sequence	313	14.8	82.2	18071	1	D90830
C 241	14.8	82.2	389	6	AX070097	Sequence	AX070097	Sequence	C 314	14.8	82.2	28512	1	AC013069
C 242	14.8	82.2	406	6	AX070045	Sequence	AX070045	Sequence	315	14.8	82.2	32538	3	CEZK829
C 243	14.8	82.2	451	14	AF458353	Sequence	AF458353	West Nile	316	14.8	82.2	35842	3	CEZK228
C 244	14.8	82.2	520	6	AX388876	Sequence	AX388876	Sequence	317	14.8	82.2	39283	3	CET04A11
C 245	14.8	82.2	809	6	BD149535	Primer fo	BD149535	Primer fo	318	14.8	82.2	4532	2	AC121274
C 246	14.8	82.2	809	6	AX869473	Sequence	AX869473	Sequence	C 319	14.8	82.2	46165	2	AC136498
C 247	14.8	82.2	872	6	CQ491220	Sequence	CQ491220	Sequence	C 320	14.8	82.2	47198	2	AC090252
C 248	14.8	82.2	872	6	CQ497087	Sequence	CQ497087	Sequence	C 321	14.8	82.2	49175	6	C0869591
C 249	14.8	82.2	901	9	BC009627	Sequence	BC009627	Sequence	C 322	14.8	82.2	51428	2	AC011062
C 250	14.8	82.2	945	6	AX506831	Sequence	AX506831	Sequence	C 323	14.8	82.2	59967	6	CQ592721
C 251	14.8	82.2	967	8	AY630776	Arabisdops	AY630776	Arabisdops	324	14.8	82.2	67199	9	AC025162
C 252	14.8	82.2	1118	6	BD195240	Nucleotid	BD195240	Nucleotid	C 325	14.8	82.2	77137	3	AC004422
C 253	14.8	82.2	1125	6	BD165547	Novel pol	BD165547	Novel pol	C 326	14.8	82.2	77567	8	ATT19P6
C 254	14.8	82.2	1125	6	AX123430	Sequence	AX123430	Sequence	327	14.8	82.2	77793	8	ATT30C3
C 255	14.8	82.2	1346	3	PCTRNA	P. carnea ge	X68436	P. carnea ge	C 328	14.8	82.2	79125	8	AB024033
C 256	14.8	82.2	1368	6	AX015292	Sequence	AX015292	Sequence	C 329	14.8	82.2	80386	8	ATW70J2
C 257	14.8	82.2	1368	14	ZCHEUCPMA	Z22759	Zucchini ye	Z22759	330	14.8	82.2	80386	8	ATW70J2
C 258	14.8	82.2	1368	14	ZYMHCPRO	X77756	Zucchini ye	X77756	331	14.8	82.2	82020	9	AC090448
C 259	14.8	82.2	1452	8	AY070426	Arabisdops	AY070426	Arabisdops	C 332	14.8	82.2	83876	2	AC020009
C 260	14.8	82.2	1565	1	UBA420322	unculture	AY420322	unculture	C 333	14.8	82.2	89826	8	ATT32A16
C 261	14.8	82.2	1566	1	UBA306782	unculture	AJ306782	unculture	C 334	14.8	82.2	92724	8	AP006074
C 262	14.8	82.2	1719	8	AB095092	Labyrinth	AB095092	Labyrinth	C 335	14.8	82.2	99758	8	F3F19
C 263	14.8	82.2	1915	8	AY093149	Arabisdops	AY093149	Arabisdops	C 336	14.8	82.2	101010	9	HS445N2
C 264	14.8	82.2	2103	6	AF153911	Novel pol	BD164897	Novel pol	C 337	14.8	82.2	103061	2	AC151680
C 265	14.8	82.2	2103	6	AX122780	Sequence	AX122780	Sequence	C 338	14.8	82.2	109490	9	AC026342
C 266	14.8	82.2	2103	6	AB046081	Macaca fa	AB046081	Macaca fa	C 339	14.8	82.2	110000	8	CR380954.01
C 267	14.8	82.2	2111	6	CQ842277	Sequence	CQ842277	Sequence	340	14.8	82.2	110000	8	CR380954.01
C 268	14.8	82.2	2666	6	AX125260	Homo sapi	AX125260	Homo sapi	C 341	14.8	82.2	110000	9	AC026342
C 269	14.8	82.2	2880	6	AX506216	Sequence	AX506216	Sequence	342	14.8	82.2	114946	2	AC151691
C 270	14.8	82.2	2880	6	AX651838	Sequence	AX651838	Sequence	C 343	14.8	82.2	116156	8	ATAC002343
C 271	14.8	82.2	2880	6	CQ842048	Sequence	CQ842048	Sequence	C 344	14.8	82.2	117244	5	AL772219
C 272	14.8	82.2	2946	6	CQ842048	Sequence	CQ842048	Sequence	C 345	14.8	82.2	121922	9	HS7927M24
C 273	14.8	82.2	2946	9	AK123576	Homo sapi	AK123576	Homo sapi	C 346	14.8	82.2	127776	2	AC133780
C 274	14.8	82.2	3193	8	BT005776	Arabisdops	BT005776	Arabisdops	C 347	14.8	82.2	131184	10	AL844513
C 275	14.8	82.2	3270	8	AK102379	Oryza sat	AK102379	Oryza sat	C 348	14.8	82.2	134369	9	AC104825
C 276	14.8	82.2	3334	8	AB013815	Arabisdops	AB013815	Arabisdops	349	14.8	82.2	138051	1	BX927157
C 277	14.8	82.2	3470	5	BC071116	Xenopus l	BC071116	Xenopus l	C 350	14.8	82.2	140057	8	AC084817
C 278	14.8	82.2	3547	14	ZYMP13PROT	Zucchini ye	L35590	Zucchini ye	C 351	14.8	82.2	144689	8	AP004307
C 279	14.8	82.2	3597	6	CQ727087	Sequence	CQ727087	Sequence	C 352	14.8	82.2	148134	2	AC141787
C 280	14.8	82.2	3631	14	AB098081	Zucchini	AB098081	Zucchini	C 353	14.8	82.2	148650	1	AF416331
C 281	14.8	82.2	3829	6	CQ842970	Sequence	CQ842970	Sequence	C 354	14.8	82.2	150636	2	AC027529
C 282	14.8	82.2	3829	9	AK125916	Homo sapi	AK125916	Homo sapi	C 355	14.8	82.2	156772	8	AC087553
C 283	14.8	82.2	4092	1	ECU888319	Escherichia	U88319	Escherichia	C 356	14.8	82.2	157466	10	AL591440
C 284	14.8	82.2	4122	9	HS805530	Homo sapi	AL634436	Homo sapi	C 357	14.8	82.2	166000	9	AL390731
C 285	14.8	82.2	4619	10	AF484524	Sequence	AF484524	Sequence	C 358	14.8	82.2	168111	9	HS255L6
C 286	14.8	82.2	4666	5	AX386319	Danio rer	AX386319	Danio rer	C 359	14.8	82.2	168177	2	AC023914
C 287	14.8	82.2	4724	10	AK129241	Mus muscu	AK129241	Mus muscu	C 360	14.8	82.2	168637	5	AL844187
C 288	14.8	82.2	4858	9	BC047482	Homo sapi	BC047482	Homo sapi	C 361	14.8	82.2	169931	3	AC008321
C 289	14.8	82.2	5151	6	AR378431	Sequence	AB081470	Mus muscu	C 362	14.8	82.2	169931	9	AL353616
C 290	14.8	82.2	5902	10	AB081470	Sequence	AB081470	Mus muscu	C 363	14.8	82.2	172203	3	AC023742
C 291	14.8	82.2	6105	3	CIN55711	Ciona int	AJ515711	Ciona int	C 364	14.8	82.2	174452	2	AC137149
C 292	14.8	82.2	6176	10	AF430845	Mus muscu	AF430845	Mus muscu	C 365	14.8	82.2	173088	8	AC109365
C 293	14.8	82.2	6507	6	CQ592722	Sequence	CQ592722	Sequence	C 366	14.8	82.2	174623	5	EX005044
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C 295	14.8	82.2	7109	10	AK122470	Mus muscu	AK122470	Mus muscu	C 368	14.8	82.2	177697	10	AC124364
C 296	14.8	82.2	8152	3	DNTOC	Y14157	Drosophila	Y14157	C 369	14.8	82.2	179789	10	AC125172
C 297	14.8	82.2	8729	8	AF076155	Arabisdops	AF076155	Arabisdops	C 370	14.8	82.2	184142	10	AC132356
C 298	14.8	82.2	9466	14	AY600517	Feline im	AY600517	Feline im	C 371	14.8	82.2	184554	3	AC099022
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C 303	14.8	82.2	9593	14	ZYE307036	Zucchini	AJ307036	Zucchini	C 376	14.8	82.2	194849	2	AC147015
C 304	14.8	82.2	9593	14	ZYE316229	Zucchini	AJ316229	Zucchini	C 377	14.8	82.2	195644	10	AC102784
C 305	14.8	82.2	9593	14	ZYMPOLPOLR	Zucchini ye	L31350	Zucchini ye	C 378	14.8	82.2	195677	10	AL772152
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C 307	14.8	82.2	11541	8	AF233343	Candida g	AF233343	Candida g	C 380	14.8	82.2	198777	8	ATCHRIV63
C 308	14.8	82.2	11718	8	AF294788	Nectria h	AF294788	Nectria h	C 381	14.8	82.2	199345	2	AC084102
C 309	14.8	82.2	13703	1	AE005410	Escherich	AE005410	Escherich	C 382	14.8	82.2	199476	2	AC143053
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AE004913 Pseudomon
D90830 E.coli geno
AC013069 Drosophil
Z73899 Caenorhabdi
Z82086 Caenorhabdi
Z83123 Caenorhabdi
AC121274 Mus muscu
AC136498 Drosophil
AC090252 Homo sapi
CQ869591 Sequence
AC011062 Drosophil
CQ592721 Sequence
AC025162 Homo sapi
AC004422 Drosophil
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BX927157 Corynebact
AP004307 Oryza sat
AC141787 Apis mell
AF416331 Ruegeria
AC027529 Homo sapi
AC087553 Oryza sat
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AL023807 Human DNA
AC023914 Homo sapi
AL844187 Zebrafish
AC008321 Drosophil
AL353616 Human DNA
AC023742 Drosophil
AC137149 Mus muscu
AC109365 Oryza sat
BX005044 Zebrafish
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depending upon virus genotype
 Virology 296 (1), 17-23 (2002)
 JOURNAL MEDLINE
 22033887
 PUBMED
 12036314
 REFERENCE
 2 (bases 1 to 463)
 Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
 Direct Submission
 Submitted (14-DEC-2001) Department of Pathology and WHO
 Collaborating Center for Tropical Diseases, The University of Texas
 Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
 JOURNAL
 Location/Qualifiers

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 AF458344
 VERSION
 AF458344.1 GI:21636467
 KEYWORDS
 SOURCE
 ORGANISM
 West Nile virus (WNV)
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 Flavivirus; Japanese encephalitis virus group.

REFERENCE
 AUTHORS
 Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
 TITLE
 Mouse neuroinvasive phenotype of West Nile virus strains varies
 depending upon virus genotype
 Virology 296 (1), 17-23 (2002)
 JOURNAL MEDLINE
 22033887
 PUBMED
 12036314
 REFERENCE
 2 (bases 1 to 463)
 Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
 Direct Submission
 Submitted (14-DEC-2001) Department of Pathology and WHO
 Collaborating Center for Tropical Diseases, The University of Texas
 Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
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 Location/Qualifiers

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 AF458347
 ACCESSION
 AF458347.1 GI:21636473
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 West Nile virus (WNV)
 West Nile virus
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 Flavivirus; Japanese encephalitis virus group.

REFERENCE
 AUTHORS
 Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
 TITLE
 Mouse neuroinvasive phenotype of West Nile virus strains varies
 depending upon virus genotype
 Virology 296 (1), 17-23 (2002)
 JOURNAL MEDLINE
 22033887
 PUBMED
 12036314
 REFERENCE
 2 (bases 1 to 463)
 Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
 Direct Submission
 Submitted (14-DEC-2001) Department of Pathology and WHO
 Collaborating Center for Tropical Diseases, The University of Texas
 Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
 JOURNAL
 Location/Qualifiers

FEATURES
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 partial cds.
 AF458348
 VERSION
 AF458348.1 GI:21636475
 KEYWORDS
 SOURCE
 ORGANISM
 West Nile virus (WNV)
 West Nile virus
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 Flavivirus; Japanese encephalitis virus group.


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ACCESSION AF458348
VERSION AF458348.1 GI:21636475
SOURCE West Nile virus (WNV)
ORGANISM West Nile virus (WNV)
REFERENCE Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
AUTHORS Flavivirus; Japanese encephalitis virus group.
TITLE 1 (bases 1 to 463)
JOURNAL Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
MEDLINE Mouse neuroinvasive phenotype of West Nile virus strains varies
PUBMED depending upon virus genotype
22033887 Virology 296 (1), 17-23 (2002)
12036314
REFERENCE 2 (bases 1 to 463)
AUTHORS Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-2001) Department of Pathology and WHO
Collaborating Center for Tropical Diseases, The University of Texas
Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
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DEFINITION cds.
ACCESSION AF458360
VERSION AF458360.1 GI:21636499
KEYWORDS
SOURCE West Nile virus (WNV)
ORGANISM West Nile virus
REFERENCE Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
AUTHORS Flavivirus; Japanese encephalitis virus group.
1 (bases 1 to 463)
Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
TITLE Mouse neuroinvasive phenotype of West Nile virus strains varies
depending upon virus genotype
JOURNAL Virology 296 (1), 17-23 (2002)
MEDLINE 22033887
PUBMED 12036314
REFERENCE 2 (bases 1 to 463)
AUTHORS Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-2001) Department of Pathology and WHO
Collaborating Center for Tropical Diseases, The University of Texas
Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
Location/Qualifiers
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DEFINITION Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
partial cds.
ACCESSION AF458355
VERSION AF458355.1 GI:21636489
KEYWORDS
SOURCE West Nile virus (WNV)
ORGANISM West Nile virus
REFERENCE Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
AUTHORS Flavivirus; Japanese encephalitis virus group.
1 (bases 1 to 463)
Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
TITLE Mouse neuroinvasive phenotype of West Nile virus strains varies
depending upon virus genotype
JOURNAL Virology 296 (1), 17-23 (2002)
MEDLINE 22033887
PUBMED 12036314
REFERENCE 2 (bases 1 to 463)
AUTHORS Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-2001) Department of Pathology and WHO
Collaborating Center for Tropical Diseases, The University of Texas
Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
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Db 300 CGCCACCGGAAGTTGAGT 317
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DEFINITION Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
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ACCESSION AF458355
VERSION AF458355.1 GI:21636489
KEYWORDS
SOURCE West Nile virus (WNV)
ORGANISM West Nile virus
REFERENCE Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
AUTHORS Flavivirus; Japanese encephalitis virus group.
1 (bases 1 to 463)
Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
TITLE Mouse neuroinvasive phenotype of West Nile virus strains varies
depending upon virus genotype
JOURNAL Virology 296 (1), 17-23 (2002)
MEDLINE 22033887
PUBMED 12036314
REFERENCE 2 (bases 1 to 463)
AUTHORS Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-2001) Department of Pathology and WHO
Collaborating Center for Tropical Diseases, The University of Texas
Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
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Db 300 CGCCACCGGAAGTTGAGT 317

RESULT 10
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DEFINITION AF458361 463 bp RNA linear VRL 18-JUN-2003
ACCESSION AF458361 GI:21636501
VERSION AF458361.1
KEYWORDS West Nile virus (WNV)
SOURCE West Nile virus
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 463)
AUTHORS Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
TITLE Mouse neuroinvasive phenotype of West Nile virus strains varies
depending upon virus genotype
JOURNAL Virology 296 (1), 17-23 (2002)
MEDLINE 22033887
PUBMED 12036314
REFERENCE 2 (bases 1 to 463)
AUTHORS Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-2001) Department of Pathology and WHO
Collaborating Center for Tropical Diseases, The University of Texas
Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
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ACCESSION AY590190 GI:47121677
VERSION AY590190.1
KEYWORDS West Nile virus (WNV)
SOURCE West Nile virus
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 464)
AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
TITLE Genetic and phenotypic variation of West Nile virus in New York,
2000-2003
JOURNAL Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE 2 (bases 1 to 464)
AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
TITLE Direct Submission
JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
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ACCESSION AY590191 GI:47121678
VERSION AY590191.1
KEYWORDS West Nile virus (WNV)
SOURCE West Nile virus
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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REFERENCE 1 (bases 1 to 464)
AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
TITLE Genetic and phenotypic variation of West Nile virus in New York,
2000-2003
JOURNAL Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE 2 (bases 1 to 464)
AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
TITLE Direct Submission
JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
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VERSION AY590192.1 GI:47121679
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SOURCE West Nile virus (WNV)
ORGANISM West Nile virus
REFERENCE 1 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
AUTHORS Ebelt,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
TITLE Genetic and phenotypic variation of West Nile virus in New York,
2000-2003
JOURNAL Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE 2 (bases 1 to 464)
AUTHORS Ebelt,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
TITLE Direct Submission
JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
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DEFINITION West Nile virus strain 03001426 3' UTR, partial sequence.
ACCESSION AY590193
VERSION AY590193.1 GI:47121680
KEYWORDS
SOURCE West Nile virus (WNV)
ORGANISM West Nile virus
REFERENCE 1 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
AUTHORS Ebelt,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
TITLE Genetic and phenotypic variation of West Nile virus in New York,
2000-2003
JOURNAL Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE 2 (bases 1 to 464)
AUTHORS Ebelt,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
TITLE Direct Submission
JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
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DEFINITION West Nile virus strain 03001543 3' UTR, partial sequence.
ACCESSION AY590195
VERSION AY590195.1 GI:47121682
KEYWORDS
SOURCE West Nile virus (WNV)
ORGANISM West Nile virus
REFERENCE 1 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
AUTHORS Ebelt,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
TITLE Genetic and phenotypic variation of West Nile virus in New York,
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Db 1 CGCCACCGGAAGTTGAGT 18

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DEFINITION West Nile virus strain 03001516 3' UTR, partial sequence.
ACCESSION AY590194
VERSION AY590194.1 GI:47121681
KEYWORDS
SOURCE West Nile virus (WNV)
ORGANISM West Nile virus
REFERENCE 1 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
AUTHORS Ebelt,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
TITLE Genetic and phenotypic variation of West Nile virus in New York,
2000-2003
JOURNAL Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE 2 (bases 1 to 464)
AUTHORS Ebelt,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
TITLE Direct Submission
JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
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DEFINITION West Nile virus strain 03001543 3' UTR, partial sequence.
ACCESSION AY590195
VERSION AY590195.1 GI:47121682
KEYWORDS
SOURCE West Nile virus (WNV)
ORGANISM West Nile virus
REFERENCE 1 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
AUTHORS Ebelt,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
TITLE Genetic and phenotypic variation of West Nile virus in New York,
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2000-2003
 JOURNAL Am. J. Trop. Med. Hyg. (2004) In press
 REFERENCE 2 (bases 1 to 464)
 AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and Kramer,L.D.
 TITLE Direct Submission
 JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
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 Db 1 CGCCACCGGAAGTTGAGT 18

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 VERSION AY590196.1 GI:47121683
 KEYWORDS
 SOURCE
 ORGANISM
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 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 Flavivirus; Japanese encephalitis virus group.
 REFERENCE 1 (bases 1 to 464)
 AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and Kramer,L.D.
 TITLE Genetic and phenotypic variation of West Nile virus in New York, 2000-2003
 JOURNAL Am. J. Trop. Med. Hyg. (2004) In press
 REFERENCE 2 (bases 1 to 464)
 AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and Kramer,L.D.
 TITLE Direct Submission
 JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
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 SOURCE
 ORGANISM
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 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 Flavivirus; Japanese encephalitis virus group.
 REFERENCE 1 (bases 1 to 464)
 AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and Kramer,L.D.
 TITLE Genetic and phenotypic variation of West Nile virus in New York, 2000-2003
 JOURNAL Am. J. Trop. Med. Hyg. (2004) In press
 REFERENCE 2 (bases 1 to 464)
 AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and Kramer,L.D.
 TITLE Direct Submission
 JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
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 LOCUS
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 ACCESSION
 VERSION AY590198.1 GI:47121685
 KEYWORDS
 SOURCE
 ORGANISM
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 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 Flavivirus; Japanese encephalitis virus group.
 REFERENCE 1 (bases 1 to 464)
 AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and Kramer,L.D.
 TITLE Genetic and phenotypic variation of West Nile virus in New York, 2000-2003
 JOURNAL Am. J. Trop. Med. Hyg. (2004) In press
 REFERENCE 2 (bases 1 to 464)
 AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and Kramer,L.D.
 TITLE Direct Submission
 JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
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Db 1 CGCCACCGGAAGTTGAGT 18

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ACCESSION  AY590199
VERSION     AY590199.1 GI:47121686
KEYWORDS
SOURCE      West Nile virus (WNV)
ORGANISM    West Nile virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Flavivirus; Japanese encephalitis virus group.
REFERENCE   1 (bases 1 to 464)
AUTHORS     Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
            Kramer,L.D.
TITLE       Genetic and phenotypic variation of West Nile virus in New York,
            2000-2003
JOURNAL     Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE   2 (bases 1 to 464)
AUTHORS     Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
            Kramer,L.D.
TITLE       Direct Submission
JOURNAL     Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
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DEFINITION West Nile virus strain 03001816 3' UTR, partial sequence.
ACCESSION  AY590200
VERSION     AY590200.1 GI:47121687
KEYWORDS
SOURCE      West Nile virus (WNV)
ORGANISM    West Nile virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Flavivirus; Japanese encephalitis virus group.
REFERENCE   1 (bases 1 to 464)
AUTHORS     Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
            Kramer,L.D.
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Genetic and phenotypic variation of West Nile virus in New York,
2000-2003
JOURNAL     Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE   2 (bases 1 to 464)
AUTHORS     Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
            Kramer,L.D.
TITLE       Direct Submission
JOURNAL     Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
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LOCUS      464 bp RNA linear VRL 30-MAY-2004
DEFINITION West Nile virus strain 03001869 3' UTR, partial sequence.
ACCESSION  AY590201
VERSION     AY590201.1 GI:47121688
KEYWORDS
SOURCE      West Nile virus (WNV)
ORGANISM    West Nile virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Flavivirus; Japanese encephalitis virus group.
REFERENCE   1 (bases 1 to 464)
AUTHORS     Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
            Kramer,L.D.
TITLE       Genetic and phenotypic variation of West Nile virus in New York,
            2000-2003
JOURNAL     Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE   2 (bases 1 to 464)
AUTHORS     Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
            Kramer,L.D.
TITLE       Direct Submission
JOURNAL     Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
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LOCUS      464 bp RNA linear VRL 30-MAY-2004
DEFINITION West Nile virus strain 03001816 3' UTR, partial sequence.
ACCESSION  AY590202
VERSION     AY590202.1 GI:47121687
KEYWORDS
SOURCE      West Nile virus (WNV)
ORGANISM    West Nile virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Flavivirus; Japanese encephalitis virus group.
REFERENCE   1 (bases 1 to 464)
AUTHORS     Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
            Kramer,L.D.
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RESULT 23
AY590202
LOCUS      AY590202                464 bp    RNA        linear    VRL 30-MAY-2004
DEFINITION West Nile virus strain 03001895 3' UTR, partial sequence.
ACCESSION  AY590202
VERSION     AY590202.1 GI:47121689
KEYWORDS
SOURCE      West Nile virus (WNV)
ORGANISM    West Nile virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Flavivirus; Japanese encephalitis virus group.
REFERENCE   1 (bases 1 to 464)
AUTHORS     Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
            Kramer,L.D.
TITLE       Genetic and phenotypic variation of West Nile virus in New York,
            2000-2003
JOURNAL     Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE   2 (bases 1 to 464)
AUTHORS     Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
            Kramer,L.D.
TITLE       Direct Submission
JOURNAL     Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
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LOCUS      AY590203                464 bp    RNA        linear    VRL 30-MAY-2004
DEFINITION West Nile virus strain 03001956 3' UTR, partial sequence.
ACCESSION  AY590203
VERSION     AY590203.1 GI:47121690
KEYWORDS
SOURCE      West Nile virus (WNV)
ORGANISM    West Nile virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Flavivirus; Japanese encephalitis virus group.
REFERENCE   1 (bases 1 to 464)
AUTHORS     Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
            Kramer,L.D.
TITLE       Genetic and phenotypic variation of West Nile virus in New York,
            2000-2003
JOURNAL     Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE   2 (bases 1 to 464)
AUTHORS     Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
            Kramer,L.D.
TITLE       Direct Submission
JOURNAL     Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
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Db 1 CGCCACCGGAGTTGAGT 18

RESULT 25
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LOCUS      AY590204                464 bp    RNA        linear    VRL 30-MAY-2004
DEFINITION West Nile virus strain 03001986 3' UTR, partial sequence.
ACCESSION  AY590204
VERSION     AY590204.1 GI:47121691
KEYWORDS
SOURCE      West Nile virus (WNV)
ORGANISM    West Nile virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Flavivirus; Japanese encephalitis virus group.
REFERENCE   1 (bases 1 to 464)
AUTHORS     Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
            Kramer,L.D.
TITLE       Genetic and phenotypic variation of West Nile virus in New York,
            2000-2003
JOURNAL     Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE   2 (bases 1 to 464)
AUTHORS     Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
            Kramer,L.D.
TITLE       Direct Submission
JOURNAL     Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
            Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
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Db 1 CGCCACCGGAGTTGAGT 18

RESULT 26
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LOCUS      AY590205                464 bp    RNA        linear    VRL 30-MAY-2004
DEFINITION West Nile virus strain 03002018 3' UTR, partial sequence.
ACCESSION  AY590205
VERSION     AY590205.1 GI:47121692
KEYWORDS
SOURCE      West Nile virus (WNV)
ORGANISM    West Nile virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Flavivirus; Japanese encephalitis virus group.
REFERENCE   1 (bases 1 to 464)
AUTHORS     Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
            Kramer,L.D.
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QY 1 CGCCACCGGAGTTGAGT 18
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Db 1 CGCCACCGGAGTTGAGT 18

RESULT 25
AY590204
LOCUS      AY590204                464 bp    RNA        linear    VRL 30-MAY-2004
DEFINITION West Nile virus strain 03001986 3' UTR, partial sequence.
ACCESSION  AY590204
VERSION     AY590204.1 GI:47121691
KEYWORDS
SOURCE      West Nile virus (WNV)
ORGANISM    West Nile virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Flavivirus; Japanese encephalitis virus group.
REFERENCE   1 (bases 1 to 464)
AUTHORS     Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
            Kramer,L.D.
TITLE       Genetic and phenotypic variation of West Nile virus in New York,
            2000-2003
JOURNAL     Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE   2 (bases 1 to 464)
AUTHORS     Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
            Kramer,L.D.
TITLE       Direct Submission
JOURNAL     Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
            Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
FEATURES    source
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            /db_xref="taxon:11082"
            /country="USA"
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Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGTTGAGT 18
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Db 1 CGCCACCGGAGTTGAGT 18

RESULT 26
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LOCUS      AY590205                464 bp    RNA        linear    VRL 30-MAY-2004
DEFINITION West Nile virus strain 03002018 3' UTR, partial sequence.
ACCESSION  AY590205
VERSION     AY590205.1 GI:47121692
KEYWORDS
SOURCE      West Nile virus (WNV)
ORGANISM    West Nile virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Flavivirus; Japanese encephalitis virus group.
REFERENCE   1 (bases 1 to 464)
AUTHORS     Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
            Kramer,L.D.
            /organism="West Nile virus"
            /viroion
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Kramer,L.D.
Genetic and phenotypic variation of West Nile virus in New York,
2000-2003.
TITLE
JOURNAL
REFERENCE
AUTHORS
Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
Direct Submission
Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
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Db 1 CGCCACCGGAAGTTGAGT 18

RESULT 27
AY590206
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
West Nile virus (WNV)
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
1 (bases 1 to 464)
Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
Direct Submission
Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
FEATURES
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/organism="West Nile virus"
/virion
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/specific_host="American crow"
/db_xref="taxon:11082"
/country="USA"
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCCACCGGAAGTTGAGT 18
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Db 1 CGCCACCGGAAGTTGAGT 18

RESULT 28
AY590207
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
West Nile virus (WNV)
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
1 (bases 1 to 464)
Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
Direct Submission
Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
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Db 1 CGCCACCGGAAGTTGAGT 18

RESULT 29
AY590208
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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
West Nile virus (WNV)
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
1 (bases 1 to 464)
Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
Direct Submission
Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
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Db 1 CGCCACCGGAAGTTGAGT 18

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RESULT 28
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
West Nile virus (WNV)
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
1 (bases 1 to 464)
Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
Direct Submission
Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
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Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CGCCACCGGAAGTTGAGT 18

RESULT 29
AY590208
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
West Nile virus (WNV)
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
1 (bases 1 to 464)
Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
Direct Submission
Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
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Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCCACCGGAAGTTGAGT 18
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Db 1 CGCCACCGGAAGTTGAGT 18

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/country="USA"
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Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCCACCGGAAGTTGAGT 18
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Db 1 CGCCACCGGAAGTTGAGT 18

RESULT 30
AY590209 464 bp RNA linear VRL 30-MAY-2004
LOCUS West Nile virus strain 03002086 3' UTR, partial sequence.
DEFINITION AY590209
ACCESSION AY590209
VERSION AY590209.1 GI:47121696
KEYWORDS
SOURCE West Nile virus (WNV)
ORGANISM West Nile virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 464)
AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
TITLE Genetic and phenotypic variation of West Nile virus in New York,
2000-2003
JOURNAL Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE 2 (bases 1 to 464)
AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
TITLE Direct Submission
JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
FEATURES
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCCACCGGAAGTTGAGT 18
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Db 1 CGCCACCGGAAGTTGAGT 18

RESULT 31
AF297854 542 bp RNA linear VRL 05-MAR-2002
LOCUS Kunjin virus isolate WK436 nonstructural protein 5 gene, partial
DEFINITION AF297854
ACCESSION AF297854
VERSION AF297854.1 GI:11991998
KEYWORDS
SOURCE Kunjin virus
ORGANISM Kunjin virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 545)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE The relationships between West Nile and Kunjin viruses
JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE 21469816
PUBMED 11585535
REFERENCE 2 (bases 1 to 545)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
and Hall,R.A.
TITLE Definitive studies of the relationships between West Nile and
Kunjin viruses
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 545)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
and Hall,R.A.
TITLE Direct Submission

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REFERENCE 1 (bases 1 to 542)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE The relationships between West Nile and Kunjin viruses
JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE 21469816
PUBMED 11585535
REFERENCE 2 (bases 1 to 542)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
and Hall,R.A.
TITLE Definitive studies of the relationships between West Nile and
Kunjin viruses
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 542)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
and Hall,R.A.
TITLE Direct Submission
JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University
of Queensland, St Lucia, QLD 4072, Australia
FEATURES
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/mol_type="genomic RNA"
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/product="nonstructural protein 5"
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/db_xref="GI:11991999"
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Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCCACCGGAAGTTGAGT 18
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Db 364 CGCCACCGGAAGTTGAGT 381

RESULT 32
AF297850 545 bp RNA linear VRL 05-MAR-2002
LOCUS Kunjin virus isolate K6590 nonstructural protein 5 gene, partial
DEFINITION AF297850
ACCESSION AF297850
VERSION AF297850.1 GI:11991990
KEYWORDS
SOURCE Kunjin virus
ORGANISM Kunjin virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 545)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE The relationships between West Nile and Kunjin viruses
JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE 21469816
PUBMED 11585535
REFERENCE 2 (bases 1 to 545)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
and Hall,R.A.
TITLE Definitive studies of the relationships between West Nile and
Kunjin viruses
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 545)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
and Hall,R.A.
TITLE Direct Submission

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JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University
FEATURES of Queensland, St Lucia, QLD 4072, Australia
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1..545
/organism="Kunjin virus"
/mol_type="genomic RNA"
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/codon_start=2
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/protein_id="AAG42388.1"
/db_xref="GI:11991991"
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KYVDYMSLSKRYEDTTLVEDTAL"

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Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18
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Db 326 CGCCACCGGAAGTTGAGT 343

RESULT 33
LOCUS AF297840 585 bp RNA linear VRL 05-WAR-2002
DEFINITION Kunjin virus isolate Boort nonstructural protein 5 gene, partial
ACCESSION AF297840
VERSION AF297840.1 GI:11991970
KEYWORDS
SOURCE Kunjin virus
ORGANISM Kunjin virus
REFERENCE
1 (bases 1 to 585)
AUTHORS Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
Lipkin,W.I., Briese,F., Gould,E.A. and Hall,R.A.
TITLE The relationships between West Nile and Kunjin viruses
JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE 21469816
PUBMED 11595535
REFERENCE
2 (bases 1 to 585)
AUTHORS Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE Definitive studies of the relationships between West Nile and
Kunjin viruses
JOURNAL Unpublished
REFERENCE
3 (bases 1 to 585)
AUTHORS Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE Direct Submission
JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18
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Db 348 CGCCACCGGAAGTTGAGT 365

RESULT 34
LOCUS KUNNSGAA 587 bp ss-RNA linear VRL 07-JUN-1996
DEFINITION Kunjin virus nonstructural protein (NS5) gene, 3' end of cds.
ACCESSION L48978
VERSION L48978.1 GI:1066802
KEYWORDS NS5 gene; nonstructural protein.
SOURCE Kunjin virus
ORGANISM Kunjin virus
REFERENCE
1 (bases 1 to 587)
AUTHORS Poldinger,M., Hall,R.A. and Mackenzie,J.S.
TITLE Molecular characterization of the Japanese encephalitis serocomplex
of the flavivirus genus
JOURNAL Virology 218 (2), 417-421 (1996)
MEDLINE 96193756
PUBMED 8610471
COMMENT Original source text: Kunjin virus (strain MRM61C) cDNA to genomic
RNA.
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/mol_type="genomic RNA"
/strain="MRM61C"
/db_xref="taxon:11077"
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/codon_start=1
/product="nonstructural protein"
/protein_id="AAB02077.1"
/db_xref="GI:1066803"
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Query Match 100.0%; Score 18; DB 14; Length 587;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18
|||||
Db 356 CGCCACCGGAAGTTGAGT 373

RESULT 35
LOCUS KUNNSGAB 587 bp ss-RNA linear VRL 07-JUN-1996
DEFINITION Kunjin virus nonstructural protein (NS5) gene, 3' end of cds.
ACCESSION L48979
VERSION L48979.1 GI:1066804
KEYWORDS NS5 gene; nonstructural protein.
SOURCE Kunjin virus
ORGANISM Kunjin virus
REFERENCE
1 (bases 1 to 587)
AUTHORS Poldinger,M., Hall,R.A. and Mackenzie,J.S.
TITLE Molecular characterization of the Japanese encephalitis serocomplex
of the flavivirus genus
JOURNAL Virology 218 (2), 417-421 (1996)

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MEDLINE	96193756
PUBMED	8610471
COMMENT	Original source text: Kunjin virus (strain MRML6) cDNA to genomic RNA.
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	/product="nonstructural protein"
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Best Local Similarity	100.0%; Pred. No. 15;
Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 CGCCACCGGAAGTTGACT 18
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RESULT 36	
AF297847	
LOCUS	Kunjin virus isolate Hu6774 nonstructural protein 5 gene, partial cds.
DEFINITION	AF297847 593 bp RNA linear VRL 05-MAR-2002
ACCESSION	AF297847 GI:11991984
VERSION	
KEYWORDS	Kunjin virus
SOURCE	Kunjin virus
ORGANISM	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group.
REFERENCE	1 (bases 1 to 593)
AUTHORS	Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V., Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE	The relationships between West Nile and Kunjin viruses
JOURNAL	Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE	21469815
PUBMED	11585535
REFERENCE	2 (bases 1 to 593)
AUTHORS	Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.
TITLE	Definitive studies of the relationships between West Nile and Kunjin viruses
JOURNAL	Unpublished
REFERENCE	3 (bases 1 to 593)
AUTHORS	Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.
TITLE	Direct Submission
JOURNAL	Submitted (22-AUG-2000) Microbiology and Parasitology, University of Queensland, St Lucia, QLD 4072, Australia
FEATURES	Location/Qualifiers
source	1..593
	/organism="Kunjin virus"
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	/isolate="Hu6774"
	/db_xref="taxon:11077"
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	/note="NS5"
CDS	/codon_start=2
	/product="nonstructural protein 5"
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AUTHORS	Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.
TITLE	Definitive studies of the relationships between West Nile and Kunjin viruses
JOURNAL	Unpublished
REFERENCE	3 (bases 1 to 600)
AUTHORS	Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.
TITLE	Direct Submission
JOURNAL	Submitted (22-AUG-2000) Microbiology and Parasitology, University of Queensland, St Lucia, QLD 4072, Australia
FEATURES	Location/Qualifiers
source	1. .600
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	/note="NS5"
	/codon_start=3
	/product="nonstructural protein 5"
	/protein_id="AAG42384.1"
	/db_xref="GI:11991983"
	/translation="MEDTTPVSKSDVPVSGKREDIWCGLIGTRARATWAEDIQVAI NQRVSIIGDEKVDYMSLLKRYEDTTLVEDTVL"
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Query Match	100.0%; Score 18; DB 14; Length 600;
Best Local Similarity	100.0%; Pred. No. 15;
Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CGCCACCGGAAGTTGAGT 18
Db	357 CGCCACCGGAAGTTGAGT 374
RESULT 40	
AF297844	
LOCUS	Kunjin virus isolate CH16549E nonstructural protein 5 gene, partial cds.
DEFINITION	AF297844 601 bp RNA linear VRL 05-MAR-2002
ACCESSION	AF297844
VERSION	AF297844.1 GI:11991978
KEYWORDS	.
SOURCE	Kunjin virus
ORGANISM	Kunjin virus
REFERENCE	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group.
AUTHORS	Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V., Liptin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE	The relationships between West Nile and Kunjin viruses
JOURNAL	Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE	21469816
PUBMED	11585535
REFERENCE	2 (bases 1 to 601)
AUTHORS	Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.
TITLE	Definitive studies of the relationships between West Nile and Kunjin viruses
JOURNAL	Unpublished
REFERENCE	3 (bases 1 to 601)
AUTHORS	Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.
TITLE	Direct Submission
JOURNAL	Submitted (22-AUG-2000) Microbiology and Parasitology, University of Queensland, St Lucia, QLD 4072, Australia
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Kunjin virus
Kunjin virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
1 (bases 1 to 607)
AUTHORS
Schretter,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE
The relationships between West Nile and Kunjin viruses
JOURNAL
MEDLINE
21469816
PUBMED
REFERENCE
2 (bases 1 to 607)
AUTHORS
Schretter,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE
Definitive studies of the relationships between West Nile and
Kunjin viruses
JOURNAL
REFERENCE
3 (bases 1 to 607)
AUTHORS
Schretter,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE
Direct Submission
JOURNAL
REFERENCE
3 (bases 1 to 607)
AUTHORS
Schretter,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE
Submitted (22-AUG-2000) Microbiology and Parasitology, University
of Queensland, St Lucia, QLD 4072, Australia
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Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCCACCGGAAGTTGAGT 18
Db 385 CGCCACCGGAAGTTGAGT 402

RESULT 43
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DEFINITION
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cde.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Kunjin virus
Kunjin virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
1 (bases 1 to 616)
AUTHORS
Schretter,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.

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<p>TITLE The relationships between West Nile and Kunjin viruses</p> <p>JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)</p> <p>MEDLINE 21469816</p> <p>PUBMED 11585535</p> <p>REFERENCE 2 (bases 1 to 616)</p> <p>AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.</p> <p>TITLE Definitive studies of the relationships between West Nile and Kunjin viruses</p> <p>JOURNAL Unpublished</p> <p>REFERENCE 3 (bases 1 to 616)</p> <p>AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.</p> <p>TITLE Direct Submission</p> <p>JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University of Queensland, St Lucia, QLD 4072, Australia</p> <p>FEATURES</p> <p>source</p> <p>1. .616</p> <p>/organism="Kunjin virus"</p> <p>/mol_type="genomic RNA"</p> <p>/isolate="CX255"</p> <p>/db_xref="taxon:11077"</p> <p><1. .226</p> <p>/note="NS5"</p> <p>/codon_start=2</p> <p>/product="nonstructural protein 5"</p> <p>/protein_id="AAG42383.1"</p> <p>/db_xref="GI:11991981"</p> <p>/translation="TTPVEKQSDVPYSGKREDIWCGSLIGTRATWAENIQVAITQVRSIIIGDEKYVDYMSLSKRYEDTTLVEDTVL"</p> <p>ORIGIN</p> <p>Query Match 100.0%; Score 18; DB 14; Length 616;</p> <p>Best Local Similarity 100.0%; Pred. 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Dis. 7 (4), 697-705 (2001)</p> <p>MEDLINE 21469816</p> <p>PUBMED 11585535</p> <p>REFERENCE 2 (bases 1 to 620)</p> <p>AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.</p> <p>TITLE Definitive studies of the relationships between West Nile and Kunjin viruses</p> <p>JOURNAL Unpublished</p> <p>REFERENCE 3 (bases 1 to 620)</p> <p>AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.</p> <p>TITLE Direct Submission</p> <p>JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University of Queensland, St Lucia, QLD 4072, Australia</p> <p>FEATURES</p> <p>source</p> <p>1. .620</p> <p>/organism="Kunjin virus"</p> <p>/mol_type="genomic RNA"</p> <p>/isolate="MRM5373"</p> <p>/db_xref="taxon:11077"</p> <p><1. .251</p> <p>/note="NS5"</p> <p>/codon_start=3</p> <p>/product="nonstructural protein 5"</p> <p>/protein_id="AAG42397.1"</p> <p>/db_xref="GI:11992009"</p> <p>/translation="EENEEMEDKTPVEKQSDVPYSGKREDIWCGSLIGTRATWAENIQVAINQVRSIIIGDEKYVDYMSLSKRYEDTTLVEDTVL"</p> <p>ORIGIN</p> <p>Query Match 100.0%; Score 18; DB 14; Length 620;</p> <p>Best Local Similarity 100.0%; Pred. No. 15;</p> <p>Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p> <p>Qy 1 CGCCACCGGAGTTGAGT 18</p> <p> </p> <p>Db 372 CGCCACCGGAGTTGAGT 389</p> <p>RESULT 45</p> <p>AF297842</p> <p>LOCUS AF297842.1 GI:11991974</p> <p>DEFINITION Kunjin virus isolate CH16514C nonstructural protein 5 gene, partial cds</p> <p>ACCESSION AF297842</p> <p>VERSION AF297842.1</p> <p>KEYWORDS</p> <p>SOURCE Kunjin virus</p> <p>ORGANISM Kunjin virus</p> <p>Viruses: ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group.</p> <p>REFERENCE 1 (bases 1 to 622)</p> <p>AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V., Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.</p> <p>TITLE The relationships between West Nile and Kunjin viruses</p> <p>JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)</p> <p>MEDLINE 21469816</p> <p>PUBMED 11585535</p> <p>REFERENCE 2 (bases 1 to 622)</p> <p>AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.</p> <p>TITLE Definitive studies of the relationships between West Nile and Kunjin viruses</p> <p>JOURNAL Unpublished</p> <p>REFERENCE 3 (bases 1 to 622)</p> <p>AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.</p> <p>TITLE Direct Submission</p> <p>JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University of Queensland, St Lucia, QLD 4072, Australia</p> <p>FEATURES</p> <p>source</p> <p>1. .622</p> <p>/organism="Kunjin virus"</p> <p>/mol_type="genomic RNA"</p> <p>/isolate="CH16514C"</p> <p>/db_xref="taxon:11077"</p> <p><1. .245</p> <p>/note="NS5"</p> <p>/codon_start=3</p> <p>/product="nonstructural protein 5"</p> <p>/protein_id="AAG42380.1"</p> <p>/db_xref="GI:11991975"</p> <p>/translation="NEWEMDKTPVEKQSDVPYSGKREDIWCGSLIGTRATWAENIQVAINQVRSIIIGDEKYVDYMSLSKRYEDTTLVEDTVL"</p> <p>ORIGIN</p> <p>Query Match 100.0%; Score 18; DB 14; Length 622;</p> <p>Best Local Similarity 100.0%; Pred. 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Db 366 CGCCACCGGAGTTGAGT 383

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DEFINITION Kunjin virus isolate CH16532C nonstructural protein 5 gene, partial cds.
ACCESSION AF297843
VERSION AF297843.1 GI:11991976
KEYWORDS Kunjin virus
SOURCE Kunjin virus
ORGANISM Kunjin virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
REFERENCE 1 (bases 1 to 623)
AUTHORS Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V., Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE The relationships between West Nile and Kunjin viruses
JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE 21469816
PUBMED 11585535
REFERENCE 2 (bases 1 to 623)
AUTHORS Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.
TITLE Definitive studies of the relationships between West Nile and Kunjin viruses
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 623)
AUTHORS Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.
TITLE Direct Submission
JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University of Queensland, St Lucia, QLD 4072, Australia
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Best Local Similarity 100.0%; Pred. No. 15;
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Db 367 CGCCACCGGAGTTGAGT 384

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LOCUS Kunjin virus 3' UTR.
DEFINITION L24512
ACCESSION L24512
VERSION L24512.1 GI:403464
KEYWORDS Kunjin virus
SOURCE Kunjin virus
ORGANISM Kunjin virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

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REFERENCE 1 (bases 1 to 627)
AUTHORS Coia,G., Parker,M.D., Speight,G., Byrne,M.E. and Westaway,E.G.
TITLE Nucleotide and complete amino acid sequences of Kunjin virus; definitive gene order and characteristics of the virus-specified proteins
JOURNAL J. Gen. Virol. 69 (Pt 1), 1-21 (1988)
MEDLINE 8809524
PUBMED 2826659
REFERENCE 2 (bases 1 to 627)
AUTHORS Khromykh,A.A. and Westaway,E.G.
TITLE Completion of Kunjin virus RNA sequence and recovery of an infectious RNA transcribed from stably cloned full-length cDNA
JOURNAL J. Virol. 68 (7), 4580-4588 (1994)
MEDLINE 94267921
PUBMED 8207832
COMMENT Original source text: Kunjin virus (strain MRM 61C) mature RNA.
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Db 122 CGCCACCGGAGTTGAGT 139

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DEFINITION AF297858.1 GI:11992006
ACCESSION AF297858
VERSION AF297858.1
KEYWORDS Kunjin virus
SOURCE Kunjin virus
ORGANISM Kunjin virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
REFERENCE 1 (bases 1 to 633)
AUTHORS Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V., Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE The relationships between West Nile and Kunjin viruses
JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE 21469816
PUBMED 11585535
REFERENCE 2 (bases 1 to 633)
AUTHORS Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.
TITLE Definitive studies of the relationships between West Nile and Kunjin viruses
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 633)
AUTHORS Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.
TITLE Direct Submission
JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University of Queensland, St Lucia, QLD 4072, Australia
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ACCESSION
AF297848
VERSION
AF297848.1 GI:11991986
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Kunjin virus
SOURCE
Kunjin virus
ORGANISM
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
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Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
The relationships between West Nile and Kunjin viruses
Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE
21469816
PUBMED
11585535
REFERENCE
2 (bases 1 to 644)
Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
Definitive studies of the relationships between West Nile and
Kunjin viruses
Unpublished
JOURNAL
3 (bases 1 to 644)
Scherret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
Direct Submission
TITLE
Submitted (22-AUG-2000) Microbiology and Parasitology, University
of Queensland, St Lucia, QLD 4072, Australia
JOURNAL
Location/Qualifiers
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Job time : 722.429 secs

Db 380 CGCCACCGGAAGTTGAGT 397

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DEFINITION
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ACCESSION
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VERSION
AF187012.1 GI:30983578
KEYWORDS
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SOURCE
West Nile virus
ORGANISM
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
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Beasley,D.W., Davis,C.T., Guzman,H., Vanlandingham,D.L., Travassos
da Rosa,A.P., Parsons,R.E., Higgs,S., Tesh,R.B. and Barrett,A.D.
Limited evolution of West Nile virus has occurred during its
southwesterly spread in the United States
Virology 309 (2), 190-195 (2003)
MEDLINE
22644768
PUBMED
12758166
REFERENCE
2 (bases 1 to 645)
Beasley,D.W.C., Davis,C.T., Guzman,H., Vanlandingham,D.L.,
Travassos da Rosa,A.P.A., Parsons,R.E., Higgs,S., Tesh,R.B. and
Barrett,A.D.T.
Direct Submission
TITLE
Submitted (26-NOV-2002) Pathology, University of Texas Medical
Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
JOURNAL
Location/Qualifiers
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Job time : 722.429 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 25, 2005, 09:32:36 ; Search time 171.857 Seconds
(without alignments)
620.023 Million cell updates/sec

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	18	100.0	21	12	ADN36741 West Nile
5	18	100.0	31	12	ADN36737 West Nile
6	18	100.0	10945	13	ADR32078 Genomic D
7	18	100.0	10945	13	ADR67768 West Nile
8	18	100.0	10975	12	ADN98022 West Nile
9	18	100.0	11029	8	ABZ68481 Nucleotid
10	18	100.0	11029	10	ABV74821 West Nile
11	18	100.0	11029	12	ADN98023 West Nile
12	17	94.4	17	6	ACN07291 WNV Amber
13	17	94.4	17	6	ACN07465 WNV minus
14	17	94.4	17	6	ACN07464 WNV minus
15	17	94.4	18	12	ADN36743 West Nile
16	17	94.4	19	12	ADN36739 West Nile
17	17	94.4	19	12	ADN36738 West Nile
18	17	94.4	10962	12	ADK13681 West Nile
19	16	88.9	17	6	ACN09628 WNV minus
20	16	88.9	17	6	ACN07290 WNV Amber

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ADN73634 Thale cre		15.4	85.6	741	12	ADN73634
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AAC35195 Arabidops		15.4	85.6	882	3	AAC35195
ADQ39648 Yeast Bdf		15.4	85.6	2878	12	ADQ39648
ADQ97983 Mouse can		15.4	85.6	35998	12	ADQ97983
ACN14228 WNV minus		15.4	85.6	64721	13	ABD33203
ACN03350 WNV Inozy		15	83.3	17	6	ACN14228
ACN04649 WNV Zinz		15	83.3	17	6	ACN03350
AC127596 Human mic		15	83.3	25	9	ACI27596
ACH03748 Wheat ste		15	83.3	436	9	ACH03748
ACH03761 Wheat ste		15	83.3	600	9	ACH03761
ACH03758 Corn ster		15	83.3	616	9	ACH03758
ACH03757 Corn ster		15	83.3	673	9	ACH03757
Ah65402 C glutami		15	83.3	1863	5	AAH65402
ADL65984 C. glutam		15	83.3	1969	11	ADL65984
AB104952 Drosophil		15	83.3	52872	4	ABL04952
Ah68525 C glutami		15	83.3	34980	5	AAH68525
ACD72382 E. coli K		14.8	82.2	100	8	ACD72382
ADQ16356 Nucleotid		14.8	82.2	363	12	ADQ16356
ADQ16357 Nucleotid		14.8	82.2	363	12	ADQ16357
Aat64813 Novel hum		14.8	82.2	389	5	AAF64813
Aat64761 Novel hum		14.8	82.2	406	5	AAF64761
ABn63337 Human can		14.8	82.2	520	6	ABN63337
Ah07543 Human CDN		14.8	82.2	809	4	AAH07543
Aa878026 DNA encod		14.8	82.2	831	5	AA878026
ABV28936 Human pro		14.8	82.2	872	5	ABV28936
ABV23098 Human pro		14.8	82.2	872	5	ABV23098
AB13721 Arabidops		14.8	82.2	945	6	ABZ13721
AAC42336 Arabidops		14.8	82.2	1083	3	AAC42336
Aa873496 DNA encod		14.8	82.2	1104	5	AA873496
Aav31213 E. coli J		14.8	82.2	1118	2	AAV31213
Aa68311 C. glutami		14.8	82.2	1125	5	AAH68311
ACA19044 Prokaryot		14.8	82.2	1149	8	ACA19044
ABD16121 Pseudomon		14.8	82.2	1203	11	ABD16121
ABD15999 Pseudomon		14.8	82.2	1233	11	ABD15999
ABD16422 Pseudomon		14.8	82.2	1329	11	ABD16422
AAC46753 Arabidops		14.8	82.2	1411	3	AAC46753
ACA19657 Prokaryot		14.8	82.2	1479	8	ACA19657
ABD17374 Pseudomon		14.8	82.2	1806	11	ABD17374
Aa67661 C. glutam		14.8	82.2	2103	5	AAH67661
ACA01132 C. glutam		14.8	82.2	2151	8	ACA01132
ABD17697 Pseudomon		14.8	82.2	2289	11	ABD17697
ADQ63763 Novel hum		14.8	82.2	2666	12	ADQ63763
ABZ13106 Arabidops		14.8	82.2	2880	6	ABZ13106
ADA68417 Arabidops		14.8	82.2	2880	6	ADA68417
ADQ63534 Novel hum		14.8	82.2	2946	12	ADQ63534
AD30772 Plant yie		14.8	82.2	3004	10	ADD30772
Adi41958 Plant tra		14.8	82.2	3004	12	ADI41958
ADQ64456 Novel hum		14.8	82.2	3829	12	ADQ64456
ACD06281 Human CDN		14.8	82.2	4096	9	ACD06281
Adf03152 Bacteri		14.8	82.2	5151	10	ADF03152
AB115493 Drosophil		14.8	82.2	6507	4	ABL15493
AAG35297 ZYMV geno		14.8	82.2	9593	2	AAQ35297
ABD32540 Human can		14.8	82.2	49175	13	ABD32540
AB115492 Drosophil		14.8	82.2	5967	4	ABL15492
Aa68534 C glutami		14.8	82.2	309400	5	AAH68534
Aa68532 C glutami		14.8	82.2	34980	5	AAH68532
ABQ07561 Oligonucl		14.4	80.0	24	6	ABQ07561
ABQ07520 Oligonucl		14.4	80.0	24	6	ABQ07520
ABQ01790 Oligonucl		14.4	80.0	24	6	ABQ01790
ABK63304 Rat seque		14.4	80.0	475	6	ABK63304
AB52117 Primary r		14.4	80.0	475	10	AB52117
ABT41596 Toxicity		14.4	80.0	475	10	ABT41596
ADP72384 Renal tox		14.4	80.0	475	12	ADP72384

C 94	14.4	80.0	550	3	AAc94950	Aac94950 Cat flea	C 167	13.8	76.7	684	13	ADT44836	Adt44836 Bacterial
C 95	14.4	80.0	550	9	ACc73171	Acc73171 Cat flea	C 168	13.8	76.7	711	4	AA556132	Aa556132 Salmonell
C 96	14.4	80.0	550	12	ADL09816	Adl09816 Cat flea	C 169	13.8	76.7	711	8	ACA52014	AcA52014 Prokaryot
C 97	14.4	80.0	550	12	ADc2202	Adc2202 Transcrip	C 170	13.8	76.7	720	10	ADH82147	Adh82147 Enterococ
C 98	14.4	80.0	550	12	AAx98956	Aax98956 Human val	C 171	13.8	76.7	744	2	AAQ43288	AaQ43288 Multivale
C 99	14.4	80.0	550	10	ADc23800	Adc23800 DNA seque	C 172	13.8	76.7	744	2	AAQ43288	AaQ43288 DNA encod
C 100	14.4	80.0	550	12	ADH35901	Adh35901 Chemical	C 173	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 101	14.4	80.0	550	12	ADG93602	Adg93602 Nitrilase	C 174	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 102	14.4	80.0	550	12	ADi62199	Adi62199 DNA encod	C 175	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 103	14.4	80.0	550	12	ADi62199	Adi62199 DNA encod	C 176	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 104	14.4	80.0	550	12	ADi62199	Adi62199 DNA encod	C 177	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 105	14.4	80.0	550	12	ADi62199	Adi62199 DNA encod	C 178	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 106	14.4	80.0	550	12	ADi62199	Adi62199 DNA encod	C 179	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 107	14.4	80.0	550	12	ADi62199	Adi62199 DNA encod	C 180	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 108	14.4	80.0	550	12	ADi62199	Adi62199 DNA encod	C 181	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 109	14.4	80.0	550	12	ADi62199	Adi62199 DNA encod	C 182	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 110	14.4	80.0	550	12	ADi62199	Adi62199 DNA encod	C 183	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 111	14.4	80.0	550	12	ADi62199	Adi62199 DNA encod	C 184	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 112	14.4	80.0	550	12	ADi62199	Adi62199 DNA encod	C 185	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 113	14.4	80.0	550	12	ADi62199	Adi62199 DNA encod	C 186	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 114	14.4	80.0	550	12	ADi62199	Adi62199 DNA encod	C 187	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 115	14.4	80.0	550	12	ADi62199	Adi62199 DNA encod	C 188	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 116	14.4	80.0	550	12	ADi62199	Adi62199 DNA encod	C 189	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 117	14.4	80.0	550	12	ADi62199	Adi62199 DNA encod	C 190	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 118	14.4	80.0	550	12	ADi62199	Adi62199 DNA encod	C 191	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 119	14.4	80.0	550	12	ADi62199	Adi62199 DNA encod	C 192	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 120	14.4	80.0	550	12	ADi62199	Adi62199 DNA encod	C 193	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 121	14.4	80.0	550	12	ADi62199	Adi62199 DNA encod	C 194	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 122	14.4	80.0	550	12	ADi62199	Adi62199 DNA encod	C 195	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 123	14.4	80.0	550	12	ADi62199	Adi62199 DNA encod	C 196	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 124	14.4	80.0	550	12	ADi62199	Adi62199 DNA encod	C 197	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 125	14.4	80.0	550	12	ADi62199	Adi62199 DNA encod	C 198	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 126	14.4	80.0	550	12	ADi62199	Adi62199 DNA encod	C 199	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 127	14.4	80.0	550	12	ADi62199	Adi62199 DNA encod	C 200	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 128	14.4	80.0	550	12	ADi62199	Adi62199 DNA encod	C 201	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 129	14.4	80.0	550	12	ADi62199	Adi62199 DNA encod	C 202	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 130	14.4	80.0	550	12	ADi62199	Adi62199 DNA encod	C 203	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 131	14.4	80.0	550	12	ADi62199	Adi62199 DNA encod	C 204	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 132	14.4	80.0	550	12	ADi62199	Adi62199 DNA encod	C 205	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 133	14.4	80.0	550	12	ADi62199	Adi62199 DNA encod	C 206	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 134	14.4	80.0	550	12	ADi62199	Adi62199 DNA encod	C 207	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 135	14.4	80.0	550	12	ADi62199	Adi62199 DNA encod	C 208	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 136	14.4	80.0	550	12	ADi62199	Adi62199 DNA encod	C 209	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 137	14.4	80.0	550	12	ADi62199	Adi62199 DNA encod	C 210	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 138	14.4	80.0	550	12	ADi62199	Adi62199 DNA encod	C 211	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 139	14.4	80.0	550	12	ADi62199	Adi62199 DNA encod	C 212	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 140	14.4	80.0	550	12	ADi62199	Adi62199 DNA encod	C 213	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 141	14.4	80.0	550	12	ADi62199	Adi62199 DNA encod	C 214	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 142	14.4	80.0	550	12	ADi62199	Adi62199 DNA encod	C 215	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 143	14.4	80.0	550	12	ADi62199	Adi62199 DNA encod	C 216	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 144	14.4	80.0	550	12	ADi62199	Adi62199 DNA encod	C 217	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 145	14.4	80.0	550	12	ADi62199	Adi62199 DNA encod	C 218	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 146	14.4	80.0	550	12	ADi62199	Adi62199 DNA encod	C 219	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 147	14.4	80.0	550	12	ADi62199	Adi62199 DNA encod	C 220	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 148	13.8	76.7	19	6	ABA01459	AbA01459 Streptoco	C 221	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 149	13.8	76.7	25	9	ACI35252	ACi35252 Human mic	C 222	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 150	13.8	76.7	69	10	ADD55911	AdD55911 Chicken m	C 223	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 151	13.8	76.7	100	8	ACD80582	ACd80582 E. coli K	C 224	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 152	13.8	76.7	100	8	ACD80582	ACd80582 E. coli K	C 225	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 153	13.8	76.7	195	8	ABX54248	ABx54248 Bovine ES	C 226	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 154	13.8	76.7	271	7	ADS70977	ADs70977 Corn seed	C 227	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 155	13.8	76.7	359	3	AAZ58767	Aaz58767 Human hun	C 228	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 156	13.8	76.7	365	6	ABT10291	ABt10291 Human bre	C 229	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 157	13.8	76.7	380	2	AAx41129	Aax41129 Human sec	C 230	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 158	13.8	76.7	406	12	ADP57134	ADp57134 Maize car	C 231	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 159	13.8	76.7	420	3	AAI16112	AAi16112 Human sec	C 232	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 160	13.8	76.7	466	9	ACH34526	ACH34526 Human end	C 233	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 161	13.8	76.7	475	3	AAc43552	AAc43552 Zea mays	C 234	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 162	13.8	76.7	503	12	ADN13034	ADn13034 Human pro	C 235	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 163	13.8	76.7	541	3	AAa44532	AAa44532 Human sec	C 236	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 164	13.8	76.7	628	6	ABQ66147	ABq66147 Arabidops	C 237	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 165	13.8	76.7	632	2	ADr01359	ADr01359 A. gossyp	C 238	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 166	13.8	76.7	660	4	ABL24327	ABl24327 Drosophil	C 239	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 167	13.8	76.7	684	13	ADT44836	Adt44836 Bacterial	C 240	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 168	13.8	76.7	711	4	AA556132	Aa556132 Salmonell	C 241	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 169	13.8	76.7	711	8	ACA52014	AcA52014 Prokaryot	C 242	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 170	13.8	76.7	720	10	ADH82147	Adh82147 Enterococ	C 243	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 171	13.8	76.7	744	2	AAQ43288	AaQ43288 Multivale	C 244	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 172	13.8	76.7	744	2	AAQ43288	AaQ43288 DNA encod	C 245	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 173	13.8	76.7	744	3	AA59617	Aa59617 DNA encod	C 246	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 174	13.8	76.7	744	3	AA59617	Aa59617 DNA encod	C 247	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 175	13.8	76.7	744	3	AA59617	Aa59617 DNA encod	C 248	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 176	13.8	76.7	744	3	AA59617	Aa59617 DNA encod	C 249	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 177	13.8	76.7	744	3	AA59617	Aa59617 DNA encod	C 250	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 178	13.8	76.7	744	3	AA59617	Aa59617 DNA encod	C 251	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 179	13.8	76.7	744	3	AA59617	Aa59617 DNA encod	C 252	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 180	13.8	76.7	744	3	AA59617	Aa59617 DNA encod	C 253	13.8	76.7	744	3	AA59617	Aa59617 DNA encod
C 181	13.8	76.7	744	3	AA59617	Aa59617 DNA encod	C 254	13.8	76.7	744	3	AA5961	

C 240	13.8	76.7	978	12	ADD78348	Novel hum	C 313	13.8	76.7	2298	13	ADS60815	Ades60815 Bacterial
C 241	13.8	76.7	978	12	ADDE21171	Novel hum	C 314	13.8	76.7	2304	13	ADS48003	Ades48003 Bacterial
C 242	13.8	76.7	978	12	ADD77286	Novel hum	C 315	13.8	76.7	2330	4	ABL25027	Abi25027 Drosophil
C 243	13.8	76.7	978	12	ADDE20433	Novel hum	C 316	13.8	76.7	2374	4	ABL22972	Abi22972 Drosophil
C 244	13.8	76.7	978	12	ADDE20433	Novel hum	C 317	13.8	76.7	2374	4	ABL22972	Abi22972 Drosophil
C 245	13.8	76.7	978	12	ADDE20433	Novel hum	C 318	13.8	76.7	2390	4	ABL202769	Abi202769 Drosophil
C 246	13.8	76.7	978	12	ADD74014	Human PRO	C 319	13.8	76.7	2396	3	AAA75081	Aaa75081 CDNA enco
C 247	13.8	76.7	978	12	ADD74260	Human PRO	C 320	13.8	76.7	2396	4	AAA91113	Aaa91113 Mouse hep
C 248	13.8	76.7	978	12	ADD75990	Novel hum	C 321	13.8	76.7	2396	10	ADG88833	Adg88833 Mouse hpa
C 249	13.8	76.7	978	12	ADDE85482	Novel hum	C 322	13.8	76.7	2396	10	ADG88833	Adg88833 Mouse hpa
C 250	13.8	76.7	978	12	ADDE05031	Human PRO	C 323	13.8	76.7	2396	12	ADL16412	Adl16412 Mouse cDN
C 251	13.8	76.7	978	12	ADDE75244	Human PRO	C 324	13.8	76.7	2396	12	ADL16414	Adl16414 Mouse cDN
C 252	13.8	76.7	978	12	ADDE76788	Novel hum	C 325	13.8	76.7	2396	12	ADM48749	Adm48749 Mouse hpa
C 253	13.8	76.7	978	12	ADDE86556	Novel hum	C 326	13.8	76.7	2402	5	AA669796	Aa669796 DNA enco
C 254	13.8	76.7	978	12	ADD778024	Novel hum	C 327	13.8	76.7	2508	4	ABL15911	Abi15911 Drosophil
C 255	13.8	76.7	978	12	ADD77532	Novel hum	C 328	13.8	76.7	2540	4	ABL24550	Abi24550 Drosophil
C 256	13.8	76.7	978	12	ADD77778	Novel hum	C 329	13.8	76.7	2554	6	AA999908	Aa999908 Polynucle
C 257	13.8	76.7	978	12	ADDE85236	Novel hum	C 330	13.8	76.7	2659	4	AA160389	Aa160389 Human pol
C 258	13.8	76.7	978	12	ADD74506	Human PRO	C 331	13.8	76.7	2659	4	AA160390	Aa160390 Human pol
C 259	13.8	76.7	978	12	ADD77034	Novel hum	C 332	13.8	76.7	2715	2	AAV80665	Aav80665 Human DNA
C 260	13.8	76.7	978	12	ADDE85728	Novel hum	C 333	13.8	76.7	2715	2	AAV80665	Aav80665 Human DNA
C 261	13.8	76.7	978	12	ADDE05277	Human PRO	C 334	13.8	76.7	2715	6	AA26282	Aa26282 Human mac
C 262	13.8	76.7	978	12	ADDE74752	Novel hum	C 335	13.8	76.7	2740	6	ABQ76022	Abq76022 Human mac
C 263	13.8	76.7	978	12	ADG05564	Novel hum	C 336	13.8	76.7	2796	5	AA941111	Aa941111 DNA enco
C 264	13.8	76.7	978	12	ADG27118	Human PRO	C 337	13.8	76.7	2859	11	ABD17008	Abd17008 Pseudomon
C 265	13.8	76.7	978	12	ADG11181	Novel hum	C 338	13.8	76.7	2863	4	ABL24326	Abi24326 Drosophil
C 266	13.8	76.7	978	12	ADG11960	Novel hum	C 339	13.8	76.7	2896	5	AA80134	Aa80134 DNA enco
C 267	13.8	76.7	978	12	ADDF94517	Novel hum	C 340	13.8	76.7	2969	4	ABL10148	Abi10148 Drosophil
C 268	13.8	76.7	978	12	ADG06613	Human PRO	C 341	13.8	76.7	2973	10	ADA53314	Ada53314 Human cod
C 269	13.8	76.7	978	12	ADH38957	Novel hum	C 342	13.8	76.7	2975	2	AAAT38325	Aaat38325 Signal tr
C 270	13.8	76.7	978	12	ADG34047	Novel hum	C 343	13.8	76.7	3027	8	ABT18986	Abt18986 Aspergill
C 271	13.8	76.7	978	12	ADI33517	Human PRO	C 344	13.8	76.7	3029	10	ACF36710	Acf36710 Human Tol
C 272	13.8	76.7	978	12	ADH69611	Human PRO	C 345	13.8	76.7	3029	10	ADK61029	Adk61029 Ovarian c
C 273	13.8	76.7	978	12	ADI29772	Novel hum	C 346	13.8	76.7	3057	10	ADE85942	Ade85942 Human Tol
C 274	13.8	76.7	978	12	ADM27169	Novel hum	C 347	13.8	76.7	3057	10	ACC72737	Acc72737 Human can
C 275	13.8	76.7	978	12	ADK66527	Human PRO	C 348	13.8	76.7	3057	12	ADP56653	Adp56653 Human Tol
C 276	13.8	76.7	986	5	AA669791	DNA enco	C 349	13.8	76.7	3057	12	ADP48594	Adp48594 Human Tol
C 277	13.8	76.7	1056	6	ABK43187	DNA enco	C 350	13.8	76.7	3081	8	ABT18392	Abt18392 Aspergill
C 278	13.8	76.7	1068	9	ADA31143	DNA enco	C 351	13.8	76.7	3180	2	AAQ94645	Aaq94645 Recombina
C 279	13.8	76.7	1101	4	AAK63517	Human imm	C 352	13.8	76.7	3180	2	AAAT12676	Aat12676 F. browni
C 280	13.8	76.7	1107	3	AAK54915	Arabidops	C 353	13.8	76.7	3198	8	ABT20806	Abt20806 Aspergill
C 281	13.8	76.7	1110	3	AAK54027	Arabidops	C 354	13.8	76.7	3210	6	ABQ70990	Abq70990 Listeria
C 282	13.8	76.7	1133	4	ABU13097	Drosophil	C 355	13.8	76.7	3309	13	ADS48485	Ades48485 Bacterial
C 283	13.8	76.7	1149	2	AAK02109	Yeast FEN	C 356	13.8	76.7	3311	8	ABT20208	Abt20208 Aspergill
C 284	13.8	76.7	1178	8	ABZ57353	Human zin	C 357	13.8	76.7	3319	4	ABL13634	Abi13634 Drosophil
C 285	13.8	76.7	1179	8	ADA69875	Rice gene	C 358	13.8	76.7	3584	8	ABX63341	Abx63341 Human cDN
C 286	13.8	76.7	1260	13	ACN37649	Tumour-as	C 359	13.8	76.7	3815	4	ABL15910	Abi15910 Drosophil
C 287	13.8	76.7	1281	13	ADH45289	Bacterial	C 360	13.8	76.7	3855	4	ABL27710	Abi27710 Drosophil
C 288	13.8	76.7	1317	11	ABD13141	Pseudomon	C 361	13.8	76.7	4054	4	ABL13096	Abi13096 Drosophil
C 289	13.8	76.7	1380	2	AAK37261	Murine he	C 362	13.8	76.7	4232	2	AAK13008	Aak13008 Enterococ
C 290	13.8	76.7	1383	5	AAK70995	DNA enco	C 363	13.8	76.7	4232	6	ABS98803	Abs98803 Enterococ
C 291	13.8	76.7	1411	6	ABK43189	DNA enco	C 364	13.8	76.7	4233	3	AAZ90198	Aaz90198 Rat mdrib
C 292	13.8	76.7	1455	11	ABD00580	Klebsiell	C 365	13.8	76.7	4233	4	AAF27498	Aaf27498 Rat mdrib
C 293	13.8	76.7	1460	2	AAQ43291	Sequence	C 366	13.8	76.7	4251	5	ABA21002	Abat21002 Human ner
C 294	13.8	76.7	1460	2	AAQ04745	DNA enco	C 367	13.8	76.7	4251	5	AA669796	Aa669796 DNA enco
C 295	13.8	76.7	1460	3	AAA59620	DNA enco	C 368	13.8	76.7	4701	5	AA669796	Aa669796 DNA enco
C 296	13.8	76.7	1460	3	AAZ57093	Divalent	C 369	13.8	76.7	4701	13	ADL14476	Adl14476 Human NF-
C 297	13.8	76.7	1460	3	AAZ59088	DNA enco	C 370	13.8	76.7	4851	8	ACA37619	Aca37619 Protarot
C 298	13.8	76.7	1460	3	AAZ90342	DNA enco	C 371	13.8	76.7	4892	4	AAI58604	Aai58604 Human pol
C 299	13.8	76.7	1460	3	ACA62246	Divalent	C 372	13.8	76.7	4892	4	ADQ98822	Adq98822 DNA enco
C 300	13.8	76.7	1563	5	AAE93097	DNA enco	C 373	13.8	76.7	4892	9	ADB48582	Adb48582 Human hum
C 301	13.8	76.7	1617	12	ADJ40236	Plant cDN	C 374	13.8	76.7	4964	4	AAI58603	Aai58603 Human pol
C 302	13.8	76.7	1692	11	ABD13283	Pseudomon	C 375	13.8	76.7	4964	5	ADQ98821	Adq98821 DNA enco
C 303	13.8	76.7	1702	6	ABK43190	DNA enco	C 376	13.8	76.7	4964	9	ADB48581	Adb48581 Human hum
C 304	13.8	76.7	1737	13	ABR07621	Full leng	C 377	13.8	76.7	5081	8	ABT17798	Abt17798 Aspergill
C 305	13.8	76.7	1845	10	ADD47716	Human gen	C 378	13.8	76.7	5226	6	ADI39469	Adi39469 Arabidops
C 306	13.8	76.7	2000	10	ACC60755	Gene sequ	C 379	13.8	76.7	5311	8	ABT19612	Abt19612 Aspergill
C 307	13.8	76.7	2000	10	ADK61933	Disease t	C 380	13.8	76.7	5513	3	AA63529	Aa63529 Slit prot
C 308	13.8	76.7	2005	3	AAZ90422	Maize ace	C 381	13.8	76.7	5650	8	ACD13203	Acd13203 cDNA enco
C 309	13.8	76.7	2061	13	ADS47086	Bacterial	C 382	13.8	76.7	5874	6	ADI39470	Adi39470 A thalian
C 310	13.8	76.7	2148	11	ABD04060	Pseudomon	C 383	13.8	76.7	6106	4	ABL22974	Abi22974 Drosophil
C 311	13.8	76.7	2163	11	ABD04406	Pseudomon	C 384	13.8	76.7	6120	10	ADE63138	Ad663138 Human gen
C 312	13.8	76.7	2291	10	ADA52811	Human cod	C 385	13.8	76.7	6120	10	ADD46316	Add46316 Human gen

C 386	13.8	76.7	6270	4	ABL25026	Ab125026 Drosophil
C 387	13.8	76.7	6291	4	ABL16851	Ab116851 Drosophil
C 388	13.8	76.7	6291	13	ADQ89605	Adq89605 Antagonis
C 389	13.8	76.7	6291	10	ADQ89605	Adq89605 Antagonis
C 390	13.8	76.7	7106	4	ABL14908	Ab114908 Drosophil
C 391	13.8	76.7	8265	4	ABL42165	Ab42165 Genomic s
C 392	13.8	76.7	8527	4	ABL16850	Ab116850 Drosophil
C 393	13.8	76.7	9434	4	ABL17110	Ab117110 Drosophil
C 394	13.8	76.7	9636	4	AAK90449	AAK90449 Human dig
C 395	13.8	76.7	10401	4	AAK42164	AAK42164 Genomic s
C 396	13.8	76.7	14460	6	ABA01440	AbA01440 Streptoco
C 397	13.8	76.7	15441	4	ABL06029	Ab106029 Drosophil
C 398	13.8	76.7	20706	4	ABL06028	Ab106028 Drosophil
C 399	13.8	76.7	21646	11	ACN44454	ACN44454 Human gen
C 400	13.8	76.7	2157	6	ABA01448	AbA01448 Streptoco
C 401	13.8	76.7	27499	13	ABD32620	Abd32620 Human can
C 402	13.8	76.7	33012	8	ABSS5899	Abss5899 Bovine ad
C 403	13.8	76.7	33113	8	ABSS5900	Abss5900 Bovine ad
C 404	13.8	76.7	33306	8	ABSS5901	Abss5901 Bovine ad
C 405	13.8	76.7	33310	8	ABSS5902	Abss5902 Bovine ad
C 406	13.8	76.7	34079	8	ABSS5902	Abss5902 Bovine ad
C 407	13.8	76.7	34185	3	AAK622130	AAK622130 Nucleotid
C 408	13.8	76.7	34185	3	ABSS5888	Abss5888 Bovine ad
C 409	13.8	76.7	34185	10	ADQ17118	Adq17118 Bovine ad
C 410	13.8	76.7	35133	4	ABL50991	Ab150991 Thermus c
C 411	13.8	76.7	35134	4	ABL50990	Ab150990 Thermus c
C 412	13.8	76.7	38734	2	AAK90077	AAK90077 Human MFT
C 413	13.8	76.7	38734	5	AAK90077	AAK90077 Human MFT
C 414	13.8	76.7	47066	2	ABU11514	Abu11514 Drosophil
C 415	13.8	76.7	51259	2	AAK833007	AAK833007 Partial m
C 416	13.8	76.7	58665	11	ACN45164	ACN45164 Mouse gen
C 417	13.8	76.7	65454	12	ADN01773	Adn01773 Human hun
C 418	13.8	76.7	81098	11	ACN45202	ACN45202 Human gen
C 419	13.8	76.7	88953	11	ACN43904	ACN43904 Mouse gen
C 420	13.8	76.7	110000	4	AAI199682_30	AAI199682_30 Continuation (31 o
C 421	13.8	76.7	110000	4	AAI199682_31	AAI199682_31 Continuation (32 o
C 422	13.8	76.7	110000	4	AAI199683_30	AAI199683_30 Continuation (31 o
C 423	13.8	76.7	110000	4	AAI199683_31	AAI199683_31 Continuation (32 o
C 424	13.8	76.7	151826	3	AAI22291	AAI22291 BAC conta
C 425	13.8	76.7	175561	8	ADQ55694	Adq55694 Human THB
C 426	13.8	76.7	175561	12	ADL08129	Adl08129 Human gen
C 427	13.8	76.7	226475	9	AAU58279	AAU58279 Human tum
C 428	13.8	76.7	304905	11	ADP75180	Adp75180 Human End
C 429	13.8	76.7	348101	12	ADQ97146	Adq97146 Human can
C 430	13.8	76.7	349980	5	AAH411225	AAH411225 Pyrococcu
C 431	13.4	74.4	20	4	ADL11810	Adl11810 Salmonell
C 432	13.4	74.4	25	9	ACI27597	ACI27597 Human mic
C 433	13.4	74.4	100	8	ACD80252	ACD80252 E. coli K
C 434	13.4	74.4	134	4	AAI20894	AAI20894 Probe #10
C 435	13.4	74.4	134	4	ABA65966	AbA65966 Human foe
C 436	13.4	74.4	134	4	AAI46133	AAI46133 Probe #14
C 437	13.4	74.4	134	4	ABA48081	AbA48081 Human bre
C 438	13.4	74.4	134	4	ABA33058	AbA33058 Probe #11
C 439	13.4	74.4	134	4	AAK40118	AAK40118 Human bon
C 440	13.4	74.4	134	4	AAK14389	AAK14389 Human bra
C 441	13.4	74.4	134	4	AAK39703	AAK39703 Human liv
C 442	13.4	74.4	134	5	AAI06602	AAI06602 Probe #65
C 443	13.4	74.4	134	6	ABS14185	AbS14185 Human gen
C 444	13.4	74.4	151	7	ADQ68645	ADQ68645 Corn seed
C 445	13.4	74.4	189	8	ACC48810	ACC48810 Human EVI
C 446	13.4	74.4	275	7	ABS70372	ABs70372 Corn seed
C 447	13.4	74.4	275	10	ABX86179	ABx86179 Corn ear-
C 448	13.4	74.4	322	13	ADS4782	AdS4782 Bacterial
C 449	13.4	74.4	324	10	ADF02123	Adf02123 Bacterial
C 450	13.4	74.4	334	3	AAA31143	AAa31143 Plant mic
C 451	13.4	74.4	366	2	AAQ61221	AAq61221 Human bra
C 452	13.4	74.4	377	6	ABE178745	ABE178745 Human ova
C 453	13.4	74.4	381	11	ACH98703	ACH98703 Klebsiell
C 454	13.4	74.4	390	6	ABN27012	ABn27012 Human ORF
C 455	13.4	74.4	414	4	AAK91317	AAK91317 Human pol
C 456	13.4	74.4	435	8	ABX35016	ABx35016 Bovine ES
C 457	13.4	74.4	454	3	AAA31071	AAa31071 Plant mic
C 458	13.4	74.4	456	11	ABD02030	ABd02030 Pseudomon

ALIGNMENTS

RESULT 1
ADN36742
ID ADN36742 standard; DNA; 18 BP.
XX AC ADN36742;
XX AC ADN36742;
DT 15-JUL-2004 (first entry)
XX West Nile virus detection-related PCR primer SeqID64.
DE DE hybridisation assay probe; nucleic acid detection;
XX target-complementary sequence; flavivirus; West Nile virus; WNV;
KW RNA virus; infection; meningitis; encephalitis;
KW high throughput screening; PCR; primer; ss.
XX West Nile virus.
OS WO2004036190-A2.
XX PD 29-APR-2004.
XX 10-OCT-2003; 2003WO-US033639.
XX 16-OCT-2002; 2002US-0418891P.
PR 25-NOV-2002; 2002US-0429006P.
PR 24-FEB-2003; 2003US-0449810P.

XX PA (GENP-) GEN-PROBE INC.
 XX PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
 XX XX WPI; 2004-389590/36.
 XX DR
 XX PT New hybridization assay probe comprising target-complementary sequence of
 XX PT bases, useful in detecting flavivirus, e.g. West Nile virus.
 XX XX
 XX PS Claim 26; SEQ ID NO 64; 135pp; English.
 XX CC This invention relates to a novel hybridisation assay probe, for
 XX CC detecting a nucleic acid, which is a probe sequence that comprises a
 XX CC target-complementary sequence of bases, and optionally one or more base
 XX CC sequences that are not complementary to the nucleic acid that is to be
 XX CC detected. The hybridisation assay probes and the kits are useful in
 XX CC detecting and amplifying a target nucleic acid sequence, for example
 XX CC flavivirus like West Nile virus, that may be present in a biological
 XX CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
 XX CC birds and culex mosquitoes, with humans and horses serving as incidental
 XX CC hosts. Infection of humans can lead to meningitis or encephalitis. The
 XX CC invention may allow for accurate and efficient high throughput screening.
 XX CC The present sequence is that of a PCR primer which is related to the
 XX CC invention.
 XX SQ Sequence 18 BP; 4 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
 Query Match 100.0%; Score 18; DB 12; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.5;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGCCACCGGAGTTGAGT 18
 DB 1 CGCCACCGGAGTTGAGT 18
 RESULT 2
 ADN36744
 ID ADN36744 standard; DNA; 19 BP.
 AC ADN36744;
 XX 15-JUL-2004 (first entry)
 XX West Nile virus detection-related oligonucleotide probe SeqID66.
 XX hybridisation assay probe; nucleic acid detection;
 KW target-complementary sequence; flavivirus; West Nile virus; WNV;
 KW RNA virus; infection; meningitis; encephalitis;
 KW high throughput screening; probe; ss.
 XX West Nile virus.
 XX WO2004036190-A2.
 XX 29-APR-2004.
 XX 10-OCT-2003; 2003WO-US033639.
 XX 16-OCT-2002; 2002US-0418891P.
 XX 25-NOV-2002; 2002US-0429006P.
 XX 24-FEB-2003; 2003US-0449810P.
 XX (GENP-) GEN-PROBE INC.
 XX Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
 XX WPI; 2004-389590/36.
 XX New hybridization assay probe comprising target-complementary sequence of
 XX PT bases, useful in detecting flavivirus, e.g. West Nile virus.
 XX PT

PS Claim 26; SEQ ID NO 66; 135pp; English.
 XX CC This invention relates to a novel hybridisation assay probe, for
 XX CC detecting a nucleic acid, which is a probe sequence that comprises a
 XX CC target-complementary sequence of bases, and optionally one or more base
 XX CC sequences that are not complementary to the nucleic acid that is to be
 XX CC detected. The hybridisation assay probes and the kits are useful in
 XX CC detecting and amplifying a target nucleic acid sequence, for example
 XX CC flavivirus like West Nile virus, that may be present in a biological
 XX CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
 XX CC birds and culex mosquitoes, with humans and horses serving as incidental
 XX CC hosts. Infection of humans can lead to meningitis or encephalitis. The
 XX CC invention may allow for accurate and efficient high throughput screening.
 XX CC The present sequence is that of an oligonucleotide probe which is related
 XX CC to the invention.
 XX SQ Sequence 19 BP; 5 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
 Query Match 100.0%; Score 18; DB 12; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.6;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGCCACCGGAGTTGAGT 18
 DB 1 CGCCACCGGAGTTGAGT 18
 RESULT 3
 ADN36740
 ID ADN36740 standard; DNA; 20 BP.
 XX AC ADN36740;
 XX 15-JUL-2004 (first entry)
 XX West Nile virus detection-related oligonucleotide probe SeqID62.
 XX hybridisation assay probe; nucleic acid detection;
 KW target-complementary sequence; flavivirus; West Nile virus; WNV;
 KW RNA virus; infection; meningitis; encephalitis;
 KW high throughput screening; probe; ss.
 XX West Nile virus.
 XX WO2004036190-A2.
 XX 29-APR-2004.
 XX 10-OCT-2003; 2003WO-US033639.
 XX 16-OCT-2002; 2002US-0418891P.
 XX 25-NOV-2002; 2002US-0429006P.
 XX 24-FEB-2003; 2003US-0449810P.
 XX (GENP-) GEN-PROBE INC.
 XX Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
 XX WPI; 2004-389590/36.
 XX New hybridization assay probe comprising target-complementary sequence of
 XX PT bases, useful in detecting flavivirus, e.g. West Nile virus.
 XX PT
 XX PS Claim 26; SEQ ID NO 62; 135pp; English.
 XX CC This invention relates to a novel hybridisation assay probe, for
 XX CC detecting a nucleic acid, which is a probe sequence that comprises a
 XX CC target-complementary sequence of bases, and optionally one or more base
 XX CC sequences that are not complementary to the nucleic acid that is to be
 XX CC detected. The hybridisation assay probes and the kits are useful in
 XX CC detecting and amplifying a target nucleic acid sequence, for example
 XX CC flavivirus like West Nile virus, that may be present in a biological
 XX CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
 XX CC

CC birds and culex mosquitoes, with humans and horses serving as incidental
 CC hosts. Infection of humans can lead to meningitis or encephalitis. The
 CC invention may allow for accurate and efficient high throughput screening.
 CC The present sequence is that of an oligonucleotide probe which is related
 CC to the invention.
 XX

SQ Sequence 20 BP; 4 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 12; Length 20;

Best Local Similarity 100.0%; Pred. No. 4.6;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18

DB 3 CGCCACCGGAAGTTGAGT 20

RESULT 4

ADN36741

ID ADN36741 standard; DNA; 21 BP.

XX

AC ADN36741;

XX

DT 15-JUL-2004 (first entry)

XX

DE West Nile virus detection-related oligonucleotide probe SeqID63.

XX

KW hybridisation assay probe; nucleic acid detection;

KW target-complementary sequence; flavivirus; West Nile virus; WNV;

KW RNA virus; infection; meningitis; encephalitis;

KW high throughput screening; probe; ss.

XX

OS West Nile virus.

XX

PN WO2004036190-A2.

XX

PD 29-APR-2004.

XX

PF 10-OCT-2003; 2003WO-US033639.

XX

PR 16-OCT-2002; 2002US-0418891P.

XX

PR 25-NOV-2002; 2002US-0429006P.

XX

PR 24-FEB-2003; 2003US-0449810P.

XX

PA (GENP-) GEN-PROBE INC.

XX

PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;

XX

DR WPI; 2004-389590/36.

XX

PT New hybridization assay probe comprising target-complementary sequence of

PT bases, useful in detecting flavivirus, e.g. West Nile virus.

XX

PS Claim 26; SEQ ID NO 63; 135pp; English.

XX

CC This invention relates to a novel hybridisation assay probe, for
 CC detecting a nucleic acid, which is a probe sequence that comprises a
 CC target-complementary sequence of bases, and optionally one or more base
 CC sequences that are not complementary to the nucleic acid that is to be
 CC detected. The hybridisation assay probes and the kits are useful in
 CC detecting and amplifying a target nucleic acid sequence, for example
 CC flavivirus like West Nile virus, that may be present in a biological
 CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
 CC birds and culex mosquitoes, with humans and horses serving as incidental
 CC hosts. Infection of humans can lead to meningitis or encephalitis. The
 CC invention may allow for accurate and efficient high throughput screening.
 CC The present sequence is that of an oligonucleotide probe which is related
 CC to the invention.

SQ Sequence 21 BP; 5 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

Query Match

Best Local Similarity 100.0%; Score 18; DB 12; Length 21;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18

DB 3 CGCCACCGGAAGTTGAGT 20

RESULT 5

ADN36737

ID ADN36737 standard; DNA; 31 BP.

XX

AC ADN36737;

XX

DT 15-JUL-2004 (first entry)

XX

DE West Nile virus detection-related oligonucleotide probe SeqID59.

XX

KW hybridisation assay probe; nucleic acid detection;

KW target-complementary sequence; flavivirus; West Nile virus; WNV;

KW RNA virus; infection; meningitis; encephalitis;

KW high throughput screening; probe; ss.

XX

OS West Nile virus.

XX

PN WO2004036190-A2.

XX

PD 29-APR-2004.

XX

PF 10-OCT-2003; 2003WO-US033639.

XX

PR 16-OCT-2002; 2002US-0418891P.

XX

PR 25-NOV-2002; 2002US-0429006P.

XX

PR 24-FEB-2003; 2003US-0449810P.

XX

PA (GENP-) GEN-PROBE INC.

XX

PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;

XX

DR WPI; 2004-389590/36.

XX

PT New hybridization assay probe comprising target-complementary sequence of

PT bases, useful in detecting flavivirus, e.g. West Nile virus.

XX

PS Claim 18; SEQ ID NO 59; 135pp; English.

XX

CC This invention relates to a novel hybridisation assay probe, for
 CC detecting a nucleic acid, which is a probe sequence that comprises a
 CC target-complementary sequence of bases, and optionally one or more base
 CC sequences that are not complementary to the nucleic acid that is to be
 CC detected. The hybridisation assay probes and the kits are useful in
 CC detecting and amplifying a target nucleic acid sequence, for example
 CC flavivirus like West Nile virus, that may be present in a biological
 CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
 CC birds and culex mosquitoes, with humans and horses serving as incidental
 CC hosts. Infection of humans can lead to meningitis or encephalitis. The
 CC invention may allow for accurate and efficient high throughput screening.
 CC The present sequence is that of an oligonucleotide probe which is related
 CC to the invention.

SQ Sequence 31 BP; 6 A; 8 C; 11 G; 6 T; 0 U; 0 Other;

Query Match

Best Local Similarity 100.0%; Score 18; DB 12; Length 31;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18

DB 3 CGCCACCGGAAGTTGAGT 20

RESULT 6

ADR32078

ID ADR32078 standard; DNA; 10945 BP.

```

XX AC ADR32078;
XX DT 18-NOV-2004 (first entry)
XX DE Genomic DNA of a West Nile virus.
XX KW analysis; target; real time PCR; ds; genomic.
XX OS West Nile virus.
XX PN WO2004072230-A2.
XX PD 26-AUG-2004.
XX PF 10-FEB-2004; 2004WO-US002012.
XX PR 10-FEB-2003; 2003US-00361004.
XX PA (CLEA-) CLEARANT INC.
XX PI Mckenney K, Gillmeister L, Marlowe K, Armistead D;
XX DR WPI; 2004-625843/60.
XX PT Analyzing a target nucleic acid sequence in a biological material by real
XX PT time PCR using nucleic acid primers that are separated by at least 750
XX PT nucleic acid residues in the target sequence.
XX PS Disclosure; SEQ ID NO 5; 96pp; English.
XX CC The invention relates to a novel method for analysing a target nucleic
XX CC acid sequence in a biological material. The method comprises adding at
XX CC least two nucleic acid primers that hybridise under stringent conditions
XX CC to predetermined nucleic acid sequences of the target nucleic acid
XX CC sequence that are separated by at least 750 nucleic acid residues,
XX CC amplifying the target nucleic acid sequence by PCR, and detecting and
XX CC quantifying the target nucleic acid sequence. The methods and
XX CC compositions of the present invention are useful for analysing a target
XX CC nucleic acid sequence in a biological material by real time PCR using
XX CC nucleic acid primers that are separated by at least 750 nucleic acid
XX CC residues in the target sequence. This polynucleotide sequence represents
XX CC the genomic DNA of a West Nile virus used in the target analysis method
XX CC of the invention.
XX SQ Sequence 10945 BP; 2999 A; 2457 C; 3143 G; 2346 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 13; Length 10945;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGTTGAGT 18
Db 10482 CGCCACCGGAGTTGAGT 10499

RESULT 7
ADR67768
ID ADR67768 standard; DNA; 10945 BP.
XX AC ADR67768;
XX DT 18-NOV-2004 (first entry)
XX DE West Nile virus DNA detected by novel detection method.
XX KW ds; detection; pathogen.
XX OS West Nile virus.
XX PN WO2004072231-A2.
XX PD 26-AUG-2004.

XX 10-FEB-2004; 2004WO-US002013.
XX 10-FEB-2003; 2003US-00361002.
XX (CLEA-) CLEARANT INC.
XX PI Mckenney K, Gillmeister L, Marlowe K, Armistead D;
XX DR WPI; 2004-625844/60.
XX PT Determining level of potentially active biological pathogens in
XX PT biological material, by adding nucleic acid primer pairs to biological
XX PT material, amplifying target nucleic acid by PCR, detecting and
XX PT quantifying target nucleic acid.
XX PS Disclosure; SEQ ID NO 5; 11pp; English.
XX CC The invention relates to a method of determining (M1) level of
XX CC potentially active biological pathogens in biological material, involves
XX CC adding at least two nucleic acid primer pairs to biological material,
XX CC amplifying target nucleic acid sequences by PCR, and detecting and
XX CC quantifying target nucleic acid sequences, where quantity of the nucleic
XX CC acid sequences is proportional to number of biological pathogens in
XX CC biological material. (M1) is useful for determining level of potentially
XX CC active biological pathogens in a biological material such as cells,
XX CC tissues, blood or blood components, proteins, enzymes, immunoglobulins,
XX CC botanicals, food, ligaments, tendons, nerves, bone, teeth, skin grafts,
XX CC bone marrow, heart valves, cartilage, corneas, arteries, veins, organs,
XX CC lipids, carbohydrates, collagen, chitin and its derivatives, forensic
XX CC samples, mummified material, human or animal remains, stem cells, islet
XX CC of Langerhans cells, cells for transplantation, red blood cells, white
XX CC blood cells or platelets. The biological pathogen is chosen from
XX CC bacteria, viruses, fungi and single cell parasites. The biological
XX CC pathogen is chosen from Aspergillus, Candida, Histoplasma,
XX CC Saccharomyces, Clostridioides, Cryptococcus, Escherichia, Bacillus,
XX CC Campylobacter, Helicobacter, Listeria, Clostridium, Streptococcus,
XX CC Enterococcus, Staphylococcus, Brucella, Haemophilus, Salmonella,
XX CC Yersinia, Pseudomonas, Serratia, Enterobacter, Klebsiella, Proteus,
XX CC Citrobacter, Corynebacterium, Propionibacterium and Coxiella. The
XX CC biological pathogen is chosen from Adeno-associated virus (AAV),
XX CC California encephalitis virus, Coronavirus, Coxsackievirus-A,
XX CC Coxsackievirus-B, Eastern equine encephalitis virus (EDEV), Hepatitis
XX CC Hantavirus, Hepatitis A virus (HAV), Hepatitis C virus (HCV), Hepatitis
XX CC delta virus (HDV), Hepatitis E virus (HEV), Hepatitis G virus (HGV), HIV,
XX CC Human T-lymphotropic virus (HTLV), Influenza virus (Flu virus), Measles
XX CC virus (Rubella), Mumps virus, Norwalk virus, Parainfluenza virus, Polio
XX CC virus, Rabies virus, Respiratory Syncytial virus, Rhinovirus, Rubella
XX CC virus, Saint Louis encephalitis virus, Western equine encephalitis virus
XX CC (WEEV), Yellow fever virus, Adenovirus, Cytomegalovirus (CMV), Epstein-
XX CC Barr virus (EBV), Hepatitis B virus (HBV), Herpes simplex virus 1, Herpes
XX CC simplex virus 2, Molluscum contagiosum, Papilloma virus (HPV), Smallpox
XX CC virus (Variola), Vaccinia virus, Venezuelan equine encephalitis virus
XX CC (VEEV), Ebola virus, West Nile virus, Human Parvovirus B19 and Rotavirus.
XX CC (M1) is useful for determining the effectiveness of a sterilization
XX CC process applied to a biological material. (M1) is useful in determining
XX CC whether the biological pathogen is inactive or active. (M1) enables
XX CC determination of whether the particular biological pathogen is present in
XX CC a biological material as shown by amplification of first target sequence
XX CC and whether the biological pathogen is inactive or active. (M1) enables
XX CC evaluation of the effectiveness of sterilization processes, and
XX CC determination of both the original level and the residual level of
XX CC potentially active biological pathogens. This sequence corresponds to a
XX CC West Nile virus DNA detected by the method of the invention.
XX SQ Sequence 10945 BP; 2999 A; 2457 C; 3143 G; 2346 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 13; Length 10945;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY -1 CGCCACCGGAGTTGAGT 18
|||||

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XX PN WO200281741-A2.
XX PD 17-OCT-2002.
XX PF
XX PR 04-APR-2002; 2002WO-FR001169.
XX PX 04-APR-2001; 2001FR-00004598.
XX PY (INSP ) INST PASTEUR.
XX PA (CNRS ) CNRS CENT NAT RECH SCI.
XX PI Guenet J, Mashimo T, Simon-Chazottes D, Montagutelli X;
PI Frenkiel M, Despres P, Deubel V, Bonhomme F, Lucas M;
XX WPI; 2003-058566/05.
XX DR P-PSDB; ABB98821.
XX
XX Identifying stimulators of oligoadenylate synthase family genes, useful
PT as antiviral agents against Flavivirus, also mutated genes responsible
PT for sensitivity to virus.
XX
XX Example 1; Page 52-67; 93pp; -French.
XX
XX The present invention relates to a method for identifying compounds (I)
CC that can stimulate a gene of the OAS (2'-5'-oligoadenylate synthase)
CC family. The method comprises: (a) inducing expression of the OAS gene in
CC a culture of cells from a non-human mammal (Flvr/Flvr or Flvr/Flvs;
CC indicating resistance or sensitivity to Flavivirus infection); (b)
CC treating cells with test compound; and (c) measuring activity of OAS gene
CC relative to a control. (I) are potentially useful as antiviral agents for
CC treating infections by Flaviviruses (e.g. hepatitis C; dengue; yellow
CC fever and various forms of encephalitis). Genomic OAS DNA and derived
CC cDNA, also the encoded proteins, are useful: (a) for treating Flavivirus
CC infection; (b) in screening for anti-Flavivirus agents, and (c) for
CC evaluating sensitivity of subjects to Flavivirus infection and their
CC likely response to interferon treatment, e.g. to identify patients at
CC risk of developing severe forms of such infections. The present sequence
CC is West Nile Virus strain NY99-flamingo 382-99 (IS-98-STI) complete
CC genome, which was used in an example from the invention. West Nile Virus
CC is one such Flavivirus
XX
SQ Sequence 11029 BP; 3019 A; 2471 C; 3167 G; 2372 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 10; Length 11029;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGTTGAGT 18
Db 10524 CGCCACCGGAGTTGAGT 10541

RESULT 11
ADN98023
ID ADN98023 standard; DNA; 11029 BP.
AC ADN98023;
XX
XX 29-JUL-2004 (first entry)
XX
XX West Nile Virus isolate 3356 complete genome sequence.
XX
XX ds; West Nile Virus; envelope protein; glycoprotein E; flavivirus;
XX Japanese encephalitis virus; Dengue virus; St Louis encephalitis virus.
XX
XX West Nile virus.
XX
XX WO2004040263-A2.
XX
XX 13-MAY-2004.
XX
XX 31-OCT-2003; 2003WO-US034823.

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XX 31-OCT-2002; 2002US-0422755P.
XX 06-JUN-2003; 2003US-0476513P.
XX
XX (HEAL-) HEALTH RES INC.
XX
XX Wong SJ, Pei-Yong S;
XX
XX WPI; 2004-400223/37.
XX GENBANK; AF404756.
XX
XX New diagnostic kit comprising West Nile Virus (WNV) envelope protein
PT reactive with antibody against WNV and cross-reactive with antibody
PT against a flavivirus, useful in diagnosing flavivirus infection caused by
PT DENV, WNV, JEV or SLEV.
XX
XX Disclosure; Fig 38; 212pp; English.
XX
XX The invention relates to a diagnostic kit comprising at least one
CC isolated and purified polypeptide comprising a West Nile Virus (WNV)
CC envelope (E) protein or its immunogenic fragment having a native
CC conformation or non-denatured structure and that is reactive with
CC antibodies against WNV and cross-reactive with antibodies against a
CC flavivirus. The diagnostic kit is useful in diagnosing flavivirus
CC infection caused by DENV, WNV, JEV or SLEV. This sequence corresponds to
CC the complete nucleotide sequence of the WNV isolate 3356.
XX
XX Sequence 11029 BP; 3017 A; 2466 C; 3172 G; 2374 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 18; DB 12; Length 11029;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGTTGAGT 18
Db 10524 CGCCACCGGAGTTGAGT 10541

RESULT 12
ACN07291
ID ACN07291 standard; RNA; 17 BP.
XX
XX ACN07291;
XX
XX 22-APR-2004 (first entry)
XX
XX WNV Amberzyme substrate SEQ ID NO 7294.
XX
XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
XX virucide; neuroprotective; antibacterial; replication; pancreatitis;
XX encephalitis; myocarditis; meningitis; infection; hepatitis;
XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
XX Amberzyme; Zinzyme; ss.
XX
XX West Nile Virus.
XX
XX WO200268637-A2.
XX
XX 06-SEP-2002.
XX
XX 19-OCT-2001; 2001WO-US048350.
XX
XX 20-OCT-2000; 2000US-0242411P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGGEN J A.
XX
XX Blatt L, Mcswiggen JA;
XX
XX WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus

```

PT (WNV), useful for treating a condition related to WNV infection e.g. pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 XX
 PS Claim 23; SEQ ID NO 7294; 495pp; English.
 XX
 CC The invention relates to nucleic acid molecules that modulate replication of the West Nile Virus (WNV). The nucleic acid molecules are useful for treating a condition related to WNV infection e.g. pancreatitis, encephalitis, myocarditis, meningitis, neurologic infection, hepatitis, liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid molecule is selected from the group of ribozymes consisting of Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The nucleic acid molecules further comprise at least five ribose residues, at least ten 2'-O-methyl modifications, phosphorothioate linkages on at least three of the 5' terminal nucleotides and a 3' end modification of a 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080 are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given in the specification. The present sequence is that of a nucleic acid molecule of the invention
 XX
 SQ Sequence 17 BP; 4 A; 5 C; 6 G; 0 T; 2 U; 0 Other;

Query Match 94.4%; Score 17; DB 6; Length 17;
 Best Local Similarity 88.2%; Pred. No. 16;
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGTTGAG 17
 |||||
 Db 1 CGCCACCGGAGTTGAG 17

RESULT 13
 ACN07465/c
 ID ACN07465 standard; RNA; 17 BP.

AC ACN07465;

22-APR-2004 (first entry)

WNV minus strand Hammerhead Ribozyme substrate SEQ ID NO 7468.

WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic; virucide; neuroprotective; antibacterial; replication; pancreatitis; encephalitis; myocarditis; meningitis; infection; hepatitis; liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme; Amberzyme; Zinzyme; ss.

West Nile Virus.

WO200268637-A2.

06-SEP-2002.

19-OCT-2001; 2001WO-US048350.

20-OCT-2000; 2000US-0242411P.

(RIBO-) RIBOZYME PHARM INC.

(BLAT/) BLATT L.

(MCSW/) MCSWIGGEN J A.

Blatt L, Mcswiggen JA;

WPI; 2002-706994/76.

New nucleic acid molecule that modulates replication of West Nile Virus (WNV), useful for treating a condition related to WNV infection e.g. pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

Claim 23; SEQ ID NO 7468; 495pp; English.

The invention relates to nucleic acid molecules that modulate replication of the West Nile Virus (WNV). The nucleic acid molecules are useful for

CC treating a condition related to WNV infection e.g. pancreatitis, encephalitis, myocarditis, meningitis, neurologic infection, hepatitis, liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid molecule is selected from the group of ribozymes consisting of Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The nucleic acid molecules further comprise at least five ribose residues, at least ten 2'-O-methyl modifications, phosphorothioate linkages on at least three of the 5' terminal nucleotides and a 3' end modification of a 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080 are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given in the specification. The present sequence is that of a nucleic acid molecule of the invention
 XX
 SQ Sequence 17 BP; 2 A; 6 C; 5 G; 0 T; 4 U; 0 Other;

Query Match 94.4%; Score 17; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGTTGAG 17
 |||||
 Db 17 CGCCACCGGAGTTGAG 1

RESULT 14
 ACN07464/c
 ID ACN07464 standard; RNA; 17 BP.

AC ACN07464;

22-APR-2004 (first entry)

WNV minus strand Hammerhead Ribozyme substrate SEQ ID NO 7467.

WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic; virucide; neuroprotective; antibacterial; replication; pancreatitis; encephalitis; myocarditis; meningitis; infection; hepatitis; liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme; Amberzyme; Zinzyme; ss.

West Nile Virus.

WO200268637-A2.

06-SEP-2002.

19-OCT-2001; 2001WO-US048350.

20-OCT-2000; 2000US-0242411P.

(RIBO-) RIBOZYME PHARM INC.

(BLAT/) BLATT L.

(MCSW/) MCSWIGGEN J A.

Blatt L, Mcswiggen JA;

WPI; 2002-706994/76.

New nucleic acid molecule that modulates replication of West Nile Virus (WNV), useful for treating a condition related to WNV infection e.g. pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

Claim 23; SEQ ID NO 7467; 495pp; English.

The invention relates to nucleic acid molecules that modulate replication of the West Nile Virus (WNV). The nucleic acid molecules are useful for treating a condition related to WNV infection e.g. pancreatitis, encephalitis, myocarditis, meningitis, neurologic infection, hepatitis, liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid molecule is selected from the group of ribozymes consisting of Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The nucleic acid molecules further comprise at least five ribose residues, at least ten 2'-O-methyl modifications, phosphorothioate linkages on at

CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention

XX SQ Sequence 17 BP; 3 A; 6 C; 4 G; 0 T; 4 U; 0 Other;
Query Match 94.4%; Score 17; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCACCGGAAGTTGAGT 18
|||||
Db 17 GCCACCGGAAGTTGAGT 1

RESULT 15

ADN36743

ID ADN36743 standard; DNA; 18 BP.

XX AC

ADN36743;

XX DT

15-JUL-2004 (first entry)

XX DE

West Nile virus detection-related oligonucleotide probe SeqID65.

XX KW

hybridisation assay probe; nucleic acid detection;

XX KW

target-complementary sequence; flavivirus; West Nile virus; WNV;

XX KW

RNA virus; infection; meningitis; encephalitis;

XX KW

high throughput screening; probe; ss.

XX OS

West Nile virus.

XX FH

Key

modified_base 1

/*tag= a

/mod_base= i

FT FT

WO2004036190-A2.

XX PN

29-APR-2004.

XX PD

10-OCT-2003; 2003WO-US033639.

XX PF

16-OCT-2002; 2002US-0418891P.

XX PR

25-NOV-2002; 2002US-0429006P.

XX PR

24-FEB-2003; 2003US-0449810P.

XX XX

(GENP-) GEN-PROBE INC.

XX PI

Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;

XX PS

WPI; 2004-389590/36.

XX DR

New hybridization assay probe comprising target-complementary sequence of

XX PT

bases, useful in detecting flavivirus, e.g. West Nile virus.

XX PS

Claim 26; SEQ ID NO 65; 135pp; English.

XX CC

This invention relates to a novel hybridisation assay probe, for

XX CC

detecting a nucleic acid, which is a probe sequence that comprises a

XX CC

target-complementary sequence of bases, and optionally one or more base

XX CC

sequences that are not complementary to the nucleic acid that is to be

XX CC

detected. The hybridisation assay probes and the kits are useful in

XX CC

detecting and amplifying a target nucleic acid sequence, for example

XX CC

flavivirus like West Nile virus, that may be present in a biological

XX CC

sample. West Nile virus (WNV) is an RNA virus that primarily infects

XX CC

birds and culex mosquitoes, with humans and horses serving as incidental

XX CC

hosts. Infection of humans can lead to meningitis or encephalitis. The

XX CC

invention may allow for accurate and efficient high throughput screening.

XX CC

The present sequence is that of an oligonucleotide probe which is related

XX CC

to the invention.

XX

SQ

Sequence 18 BP; 4 A; 4 C; 6 G; 3 T; 0 U; 1 Other;

Query Match

94.4%; Score 17; DB 12; Length 18;

Best Local Similarity

100.0%; Pred. No. 17;

Matches 17; Conservative

0; Mismatches 0; Indels 0; Gaps 0;

QY

2 GCCACCGGAAGTTGAGT 18

|||||

Db

2 GCCACCGGAAGTTGAGT 18

RESULT 16

ADN36739

ID ADN36739 standard; DNA; 19 BP.

XX AC

ADN36739;

XX DT

15-JUL-2004 (first entry)

XX DE

West Nile virus detection-related oligonucleotide probe SeqID61.

XX KW

hybridisation assay probe; nucleic acid detection;

XX KW

target-complementary sequence; flavivirus; West Nile virus; WNV;

XX KW

RNA virus; infection; meningitis; encephalitis;

XX KW

high throughput screening; probe; ss.

XX OS

West Nile virus.

XX FH

Key

modified_base 1

/*tag= a

/mod_base= i

FT FT

WO2004036190-A2.

XX PN

29-APR-2004.

XX PD

10-OCT-2003; 2003WO-US033639.

XX PF

16-OCT-2002; 2002US-0418891P.

XX PR

25-NOV-2002; 2002US-0429006P.

XX PR

24-FEB-2003; 2003US-0449810P.

XX XX

(GENP-) GEN-PROBE INC.

XX PI

Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;

XX PS

WPI; 2004-389590/36.

XX DR

New hybridization assay probe comprising target-complementary sequence of

XX PT

bases, useful in detecting flavivirus, e.g. West Nile virus.

XX PS

Disclosure; SEQ ID NO 61; 135pp; English.

XX CC

This invention relates to a novel hybridisation assay probe, for

XX CC

detecting a nucleic acid, which is a probe sequence that comprises a

XX CC

target-complementary sequence of bases, and optionally one or more base

XX CC

sequences that are not complementary to the nucleic acid that is to be

XX CC

detected. The hybridisation assay probes and the kits are useful in

XX CC

detecting and amplifying a target nucleic acid sequence, for example

XX CC

flavivirus like West Nile virus, that may be present in a biological

XX CC

sample. West Nile virus (WNV) is an RNA virus that primarily infects

XX CC

birds and culex mosquitoes, with humans and horses serving as incidental

XX CC

hosts. Infection of humans can lead to meningitis or encephalitis. The

XX CC

invention may allow for accurate and efficient high throughput screening.

XX CC

The present sequence is that of an oligonucleotide probe which is related

XX CC

to the invention.

SQ

Sequence 19 BP; 4 A; 6 C; 6 G; 2 T; 0 U; 1 Other;

Query Match

94.4%; Score 17; DB 12; Length 19;

Best Local Similarity

100.0%; Pred. No. 17;

KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
 KW Amberzyme; Zinzyne; ss.

OS West Nile Virus.

XX WO200268637-A2.

XX 06-SEP-2002.

XX 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA;

PI WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus
 (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX Claim 23; SEQ ID NO 9631; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication
 of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyne. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention

XX Sequence 17 BP; 2 A; 5 C; 6 G; 0 T; 4 U; 0 Other;

Query Match 88.9%; Score 16; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGA 16

Db 16 CGCCACCGGAAGTTGA 1

RESULT 20

ACN07290

ID ACN07290 standard; RNA; 17 BP.

AC ACN07290;

XX 22-APR-2004 (first entry)

XX WNV Amberzyme substrate SEQ ID NO 7293.

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
 KW Amberzyme; Zinzyne; ss.

OS West Nile Virus.

XX WO200268637-A2.

XX 06-SEP-2002.

XX 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus
 (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX Claim 23; SEQ ID NO 7293; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication
 of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyne. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention

XX Sequence 17 BP; 4 A; 6 C; 5 G; 0 T; 2 U; 0 Other;

Query Match 88.9%; Score 16; DB 6; Length 17;
 Best Local Similarity 87.5%; Pred. No. 61;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGA 16

Db 2 CGCCACCGGAAGTTGA 17

RESULT 21

ACN09627/c

ID ACN09627 standard; RNA; 17 BP.

XX ACN09627;

XX 22-APR-2004 (first entry)

XX WNV minus strand Inozyme substrate SEQ ID NO 9630.

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
 KW Amberzyme; Zinzyne; ss.

OS West Nile Virus.

XX WO200268637-A2.

XX '06-SEP-2002.

XX 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-0242411P.

PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L
PA (MCSW/) MCSWIGGEN J A.
XX
XX Blatt L, Mcswiggen JA;
XX
XX WPI; 2002-706994/76.
XX
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
XX (WNV), useful for treating a condition related to WNV infection e.g.
XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
XX Claim 23; SEQ ID NO 9630; 495pp; English.
XX
XX The invention relates to nucleic acid molecules that modulate replication
XX of the West Nile Virus (WNV). The nucleic acid molecules are useful for
XX treating a condition related to WNV infection e.g. pancreatitis,
XX encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
XX molecule is selected from the group of ribozymes consisting of
XX Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
XX nucleic acid molecules further comprise at least five ribose residues, at
XX least ten 2'-O-methyl modifications, phosphorothioate linkages on at
XX least three of the 5' terminal nucleotides and a 3' end modification of a
XX 3'-3', inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
XX are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
XX in the specification. The present sequence is that of a nucleic acid
XX molecule of the invention

Sequence 17 BP; 3 A; 5 C; 4 G; 0 T; 5 U; 0 Other;
Query Match 88.9%; Score 16; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCACCGGAAGTTGAGT 18
Db 17 CCACCGGAAGTTGAGT 2

RESULT 22
ABZ71129/c
ID ABZ71129 standard; DNA; 1323 BP.
XX
XX ABZ71129;
XX
XX 28-APR-2003 (first entry)
XX
XX Mycobacterium tuberculosis protein encoding DNA SEQ ID NO:136.
XX
XX Mycobacterium tuberculosis; infection; antibacterial; tuberculostatic;
XX immunostimulant; vaccine; gene therapy; mycobacterial infection; gene;
XX ds.
XX Mycobacterium tuberculosis.
XX
XX WO2003000721-A2.
XX
XX 03-JAN-2003.
XX
XX 21-JUN-2002; 2002WO-GB002845.
XX
XX 22-JUN-2001; 2001GB-00015365.
XX
XX 07-SEP-2001; 2001GB-00021780.
XX
XX (MICR-) MICROBIOLOGICAL RES AUTHORITY.
XX
XX James BW, Bacon J, Marsh P;
XX
XX WPI; 2003-201403/19.
XX
XX P-PSDB; ABP57503.
XX
XX New mycobacterial peptide, its fragment, variant or derivative, useful as

PT vaccine for treating or preventing mycobacterial infections, and as
PT diagnostic reagents for identifying such infections.
XX
XX Claim 15; Page 243-244; 245pp; English.
XX
XX ABP57436 to ABP57504 represent mycobacterial amino acid sequences (I)
XX encoded by ABZ71062 to ABZ71130 (II), which are isolated from
XX Mycobacterium tuberculosis. (I) are encoded by genes (II) whose
XX expression is induced or up-regulated during culture of a mycobacterium
XX under conditions defined by a dissolved oxygen tension of at least 10%
XX air saturation measured at 37 plus degrees Celsius, when compared with a
XX dissolved oxygen tension of at least 40% air saturation measured at 37
XX plus degrees Celsius. (I) and (II) have antibacterial, tuberculostatic
XX and immunostimulant activities, and can be used in vaccines and gene
XX therapy. (I) and (II) can be used for the manufacture of a medicament for
XX treating or preventing a mycobacterial infection. They can also be used
XX for the manufacture of a diagnostic reagent for identifying a
XX mycobacterial infection

Sequence 1323 BP; 228 A; 416 C; 450 G; 229 T; 0 U; 0 Other;
Query Match 88.9%; Score 16; DB 10; Length 1323;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCACCGGAAGTTGAG 17
Db 1037 GCCACCGGAAGTTGAG 1022

RESULT 23
AAH51995/c
ID AAH51995 standard; DNA; 1326 BP.
XX
XX AAH51995;
XX
XX 04-SEP-2001 (first entry)
XX
XX Mycobacterium tuberculosis potential drug target gene SEQ ID 49.
XX
XX Drug target; growth; organism viability; characterisation; ds.
XX
XX Mycobacterium tuberculosis.
XX
XX WO200135317-A1.
XX
XX 17-MAY-2001.
XX
XX 13-NOV-2000; 2000WO-US031152.
XX
XX 12-NOV-1999; 99US-0165086P.
XX
XX 12-NOV-1999; 99US-0165124P.
XX
XX 01-FEB-2000; 2000US-0179531P.
XX
XX (REGC) UNIV CALIFORNIA.
XX
XX Eisenberg D, Rotstein SH, Marcotte EM;
XX
XX WPI; 2001-329193/34.
XX
XX P-PSDB; AAG81144.
XX
XX Identifying nucleotide or polypeptide sequence for use as drug target,
XX involves providing algorithm that analyzes a functional relationship
XX between nucleotide or polypeptide sequences, and comparing the sequences.
XX
XX Disclosure; Page 82; 207pp; English.
XX
XX This invention relates to a method for identifying a nucleotide or
XX polypeptide sequence that may be a drug target, or essential for growth
XX or viability of an organism. Polynucleotide sequences AAH51947 - AAH52092
XX represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium
XX tuberculosis proteins which are potential drug targets. The DNA and
XX protein sequences are used to illustrate the method of the invention. The

CC method involves providing an unknown nucleotide or polypeptide sequences,
CC and comparing it to a number of sequences along with at least one
CC algorithm capable of analysing a functional relationship between
CC nucleotide and polypeptide sequences. The method is useful for
CC characterising the function of nucleic acids and polypeptides that may be
CC useful as a target for a drug or essential for the growth or viability of
CC an organism

XX SQ Sequence 1326 BP; 229 A; 416 C; 451 G; 230 T; 0 U; 0 Other;

Query Match 88.9%; Score 16; DB 4; Length 1326;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCACCGGAAGTTGAG 17

|||||

Db 1037 GCCACCGGAAGTTGAG 1022

RESULT 24

ABL28588/c

ID ABL28588 standard; DNA; 31068 BP.

XX AC ABL28588;

XX DT 26-MAR-2002 (first entry)

XX DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 37237.

XX KW Drosophila; developmental biology; cell signalling; insecticide;
pharmaceutical; gene; ds.

XX OS Drosophila melanogaster.

XX PN WO200171042-A2.

XX PD 27-SEP-2001.

XX PF 23-MAR-2001; 2001WO-US009231.

XX PR 23-MAR-2000; 2000US-0191637P.

XX PR 11-JUL-2000; 2000US-00614150.

XX XX (PEKE) PE CORP NY.

XX PA Venter JC, Adams M, Li PWD, Myers EW;

XX PI WPI; 2001-656860/75.

XX DR New isolated nucleic acid detection reagent for detecting 1000 or more
genes from Drosophila and for elucidating cell signalling and cell-cell
interactions.

XX PS Claim 1; SEQ ID NO 37237; 21pp + Sequence Listing; English.

XX CC The invention relates to an isolated nucleic acid detection reagent
capable of detecting 1000 or more genes from Drosophila. The invention is
useful in developmental biology and in elucidating cell signalling and
cell-cell interactions in higher eukaryotes for the development of
insecticides, therapeutics and pharmaceutical drugs. The invention
discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
ABB72072). The sequence data for this patent did not form part of the
printed specification, but was obtained in electronic format directly
from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 31068 BP; 8424 A; 6977 C; 7023 G; 8644 T; 0 U; 0 Other;

Query Match 88.9%; Score 16; DB 4; Length 31068;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGA 16

Db 2641 CGCCACCGGAAGTTGA 2626

RESULT 25

AAI99682_14/c

Continuation (15 of 45) of AAI99682 from base 1400001 (Mycobacterium tuberculosis strain
WP Sequence split into 45 fragments LOCUS AAI99682 Accession Aai99682

WP Fragment Name Begin End

WP AAI99682_00 1 110000

WP AAI99682_01 100001 210000

WP AAI99682_02 200001 310000

WP AAI99682_03 300001 410000

WP AAI99682_04 400001 510000

WP AAI99682_05 500001 610000

WP AAI99682_06 600001 710000

WP AAI99682_07 700001 810000

WP AAI99682_08 800001 910000

WP AAI99682_09 900001 1010000

WP AAI99682_10 1000001 1110000

WP AAI99682_11 1100001 1210000

WP AAI99682_12 1200001 1310000

WP AAI99682_13 1300001 1410000

WP AAI99682_14 1400001 1510000

WP AAI99682_15 1500001 1610000

WP AAI99682_16 1600001 1710000

WP AAI99682_17 1700001 1810000

WP AAI99682_18 1800001 1910000

WP AAI99682_19 1900001 2010000

WP AAI99682_20 2000001 2110000

WP AAI99682_21 2100001 2210000

WP AAI99682_22 2200001 2310000

WP AAI99682_23 2300001 2410000

WP AAI99682_24 2400001 2510000

WP AAI99682_25 2500001 2610000

WP AAI99682_26 2600001 2710000

WP AAI99682_27 2700001 2810000

WP AAI99682_28 2800001 2910000

WP AAI99682_29 2900001 3010000

WP AAI99682_30 3000001 3110000

WP AAI99682_31 3100001 3210000

WP AAI99682_32 3200001 3310000

WP AAI99682_33 3300001 3410000

WP AAI99682_34 3400001 3510000

WP AAI99682_35 3500001 3610000

WP AAI99682_36 3600001 3710000

WP AAI99682_37 3700001 3810000

WP AAI99682_38 3800001 3910000

WP AAI99682_39 3900001 4010000

WP AAI99682_40 4000001 4110000

WP AAI99682_41 4100001 4210000

WP AAI99682_42 4200001 4310000

WP AAI99682_43 4300001 4410000

WP AAI99682_44 4400001 4411529

Query Match 88.9%; Score 16; DB 4; Length 110000;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCACCGGAAGTTGAG 17

|||||

Db 50409 GCCACCGGAAGTTGAG 50394

RESULT 26

AAI99683_14/c

Continuation (15 of 44) of AAI99683 from base 1400001 (Mycobacterium tuberculosis strain
WP Sequence split into 44 fragments LOCUS AAI99683 Accession Aai99683

WP Fragment Name Begin End

WP AAI99683_00 1 110000

WP AAI99683_01 100001 210000

WP AAI99683_02 200001 310000

WP AAI99683_03 300001 410000

```

WP AAI99683_04 400001 510000
WP AAI99683_05 500001 610000
WP AAI99683_06 600001 710000
WP AAI99683_07 700001 810000
WP AAI99683_08 800001 910000
WP AAI99683_09 900001 1010000
WP AAI99683_10 1000001 1110000
WP AAI99683_11 1100001 1210000
WP AAI99683_12 1200001 1310000
WP AAI99683_13 1300001 1410000
WP AAI99683_14 1400001 1510000
WP AAI99683_15 1500001 1610000
WP AAI99683_16 1600001 1710000
WP AAI99683_17 1700001 1810000
WP AAI99683_18 1800001 1910000
WP AAI99683_19 1900001 2010000
WP AAI99683_20 2000001 2110000
WP AAI99683_21 2100001 2210000
WP AAI99683_22 2200001 2310000
WP AAI99683_23 2300001 2410000
WP AAI99683_24 2400001 2510000
WP AAI99683_25 2500001 2610000
WP AAI99683_26 2600001 2710000
WP AAI99683_27 2700001 2810000
WP AAI99683_28 2800001 2910000
WP AAI99683_29 2900001 3010000
WP AAI99683_30 3000001 3110000
WP AAI99683_31 3100001 3210000
WP AAI99683_32 3200001 3310000
WP AAI99683_33 3300001 3410000
WP AAI99683_34 3400001 3510000
WP AAI99683_35 3500001 3610000
WP AAI99683_36 3600001 3710000
WP AAI99683_37 3700001 3810000
WP AAI99683_38 3800001 3910000
WP AAI99683_39 3900001 4010000
WP AAI99683_40 4000001 4110000
WP AAI99683_41 4100001 4210000
WP AAI99683_42 4200001 4310000
WP AAI99683_43 4300001 4403765

Query Match 88.9%; Score 16; DB 4; Length 110000;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCACCGGAAGTTGAG 17
    |||||
Db 49933 GCCACCGGAAGTTGAG 49918

RESULT 27
ID ADO21519
AC ADO21519 standard; DNA; 21 BP.
XX
XX ADO21519;
XX
DT 12-AUG-2004 (first entry)
XX
DE West Nile virus forward RT-PCR primer WNV 1, SEQ ID NO:1.
XX
KW West Nile virus; WNV; recombinant host cell; adenovirus E1A protein;
KW whole-inactivated; large-scale production; antiviral; vaccine;
KW West Nile disease; reverse transcription-PCR; RT-PCR; primer; ss.
XX
OS West Nile virus.
XX
PN WO2004042042-A1.
XX
XX 21-MAY-2004.
XX
XX 07-NOV-2003; 2003WO-EF050806.
XX
XX 08-NOV-2002; 2002WO-NL000718.
XX
PR

PR 28-APR-2003; 2003WO-EF050129.
XX
XX (CRUC-) CRUCELL HOLLAND BV.
XX
XX
XX Uytdehaag AGCM, Schouten GJ, Goudsmit J;
XX
XX WPI; 2004-419706/39.
XX
XX Producing West Nile virus useful as vaccine against West Nile virus
XX infection, involves infecting cell, or culture of cell with West Nile
XX virus and culturing cells.
XX
XX Example 2; SEQ ID NO 1; 81pp; English.
XX
XX The invention relates to a method of producing West Nile viruses (WNVs)
XX by infecting a cell (preferably a human cell) which expresses an
XX adenovirus E1A protein with West Nile virus, or by transforming the cell
XX with the West Nile virus genome. The invention also relates to a West
XX Nile virus produced by the method of the invention; vaccine compositions
XX containing such viruses, or containing a whole-inactivated lineage II
XX West Nile virus; and human cells, named PER.C6 cells and deposited under
XX ECACC number 96022940, having at least an adenovirus E1A gene integrated
XX into its genome and which comprises a nucleic acid coding for a West Nile
XX virus. The method and cells of the invention produce high titres of West
XX Nile virus, enabling the large scale production of whole-inactivated West
XX Nile virus. Such viruses can be used in vaccines for the prophylaxis,
XX therapy and/or diagnosis of West Nile disease. These vaccines are also
XX useful for cross-vaccination against viruses that are highly similar to
XX West Nile virus. Sequences ADO21519-ADO21520 represent reverse
XX transcription-PCR (RT-PCR) primers used to detect West Nile virus RNA in
XX samples from infected human cells.
XX
XX Sequence 21 BP; 5 A; 5 C; 7 G; 3 T; 0 U; 1 Other;

Query Match 86.7%; Score 15.6; DB 12; Length 21;
Best Local Similarity 93.8%; Pred. No. 1e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCACCGGAAGTTGAGT 18
    |||||
Db 1 CCACCGGAAGTTGAGT 16

RESULT 28
ADN73634/c
ID ADN73634 standard; cDNA; 741 BP.
XX
XX AC
XX ADN73634;
XX
XX
DT 15-JUL-2004 (first entry)
XX
DE Thale cress cDNA repressed in E2Fa/Dpa expressing plants SeqID 1529.
XX
XX
KW gene; ss; plant; transgenic; E2Fa/Dpa transcription factor;
KW growth regulator; animal feed product; thale cress;
KW cell wall biosynthesis; nitrogen metabolism; carbon metabolism.
XX
XX Arabidopsis thaliana.
XX
XX WO2004035798-A2.
XX
XX 29-APR-2004.
XX
XX 20-OCT-2003; 2003WO-EF011658.
XX
XX 18-OCT-2002; 2002EP-00079408.
XX
XX (CROP-) CROPDESIGN NV.
XX
XX Inze D, De Veylder L, Vlieghe K;
XX
XX WPI; 2004-348466/32.
XX
XX P-PSDB; ADN73635.
XX
XX

```


XX Altering plant characteristics, useful for producing plants for enzyme or
PT pharmaceutical production comprising modifying in a plant, expression of
PT one or more nucleic acids and/or modifying level or activity of one or
PT more proteins.
XX
PS Claim 1; SEQ ID NO 1529; 134pp; English.
XX
CC This invention relates to a novel method for altering one or more plant
CC characteristics. Specifically, it refers to identifying genes that are up
CC - or down-regulated in transgenic plants overexpressing the heterodimeric
CC E2Fa/DPA transcription factor of Arabidopsis and using these sequences to
CC alter plant characteristics accordingly. The present invention describes
CC generating transgenic plants for the production of growth regulators,
CC enzymes, therapeutics, pharmaceuticals and animal feed products, where
CC the altered plant characteristics are selected from increased yield or
CC biomass, enhanced survival capacity, stress tolerance, plant architecture
CC or physiology, altered endoreduplication, biochemistry, signal
CC transduction, storage lipid mobilization and/or altered photosynthesis,
CC each relative to the corresponding wild type plants. Accordingly, these
CC sequences can also be useful as positive or negative selectable markers
CC during transformation of cells or tissues. The identified genes play a
CC role in a variety of biological processes such as DNA replication, cell
CC wall biosynthesis, nitrogen and/or carbon metabolism or they function as
CC transcription factors. This polynucleotide sequence is thale cress cDNA
CC repressed 1.3 fold or more in plants overexpressing the E2Fa/DPA
CC transcription factor, given in an exemplification of the invention.
XX
SQ Sequence 741 BP; 190 A; 203 C; 144 G; 204 T; 0 U; 0 Other;

Query Match 85.6%; Score 15.4; DB 12; Length 741;
Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGCTGAG 17
Db 628 CGCCACCGGAGCTGAG 612

RESULT 29
AAC48174/c
ID AAC48174 standard; DNA; 879 BP.
XX
AC AAC48174;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 56529.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 08-APR-1999; 99US-0128234P.
PR 06-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0128845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.

PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135333P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.

PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-01334256P.
PR 14-MAY-1999; 99US-01344218P.
PR 14-MAY-1999; 99US-01344219P.
PR 14-MAY-1999; 99US-01344221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143342P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144684P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.

PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 18-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.

21-OCT-1999; 99US-0160814P.
21-OCT-1999; 99US-0160815P.
22-OCT-1999; 99US-0160980P.
22-OCT-1999; 99US-0160981P.
22-OCT-1999; 99US-0160989P.
25-OCT-1999; 99US-0161404P.
25-OCT-1999; 99US-0161405P.
25-OCT-1999; 99US-0161406P.
26-OCT-1999; 99US-0161359P.
26-OCT-1999; 99US-0161360P.
26-OCT-1999; 99US-0161361P.
28-OCT-1999; 99US-0161920P.
28-OCT-1999; 99US-0161922P.
28-OCT-1999; 99US-0161933P.
29-OCT-1999; 99US-0162142P.
Query Match 85.6%; Score 15.4; DB 3; Length 882;
Best Local Similarity 94.1%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CGCCACCGGAAGTTGAG 17
Db 647 CGCCACCGGAAGTTGAG 631
RESULT 31
ADO39648
ID ADO39648 standard; DNA; 2878 BP.
AC ADO39648;
XX
DT 29-JUL-2004 (first entry)
DE Yeast Bdf1p (BDF1) gene.
XX
KW Heterologous gene; expression cassette; gene expression; yeast; BDF1;
KW gene; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN US2004092020-A1.
XX
PD 13-MAY-2004.
XX
PF 20-JUN-2003; 2003US-00600230.
XX
PR 20-JUN-2002; 2002US-0390529P.
XX
PA (WILK/) WILKINSON J Q.
PA (MCBR/) MCBRIDE K.
PA (BERT/) BERTAIN S.
XX
PI Wilkinson JQ, McBride K, Bertain S;
XX
DR WPI; 2004-374960/35.
DR GENBANK; U18116.
XX
PT New recombinant expression cassette comprising a promoter that is
PT functional in plants, operably linked with a coding sequence and a non-
PT plant 3' termination sequence, useful for gene expression in plant cells.
XX
PS Disclosure; SEQ ID NO 69; 74pp; English.
XX
CC The present invention relates to heterologous genes comprising non-plant
CC 3'-termination sequences and plant expression cassettes incorporating the
CC heterologous genes. The invention is useful for gene expression in plant
CC cells. The present sequence is yeast Bdf1p (BDF1) gene. This sequence is
CC used in the invention.
XX
SQ Sequence 2878 BP; 974 A; 582 C; 611 G; 711 T; 0 U; 0 Other;
Query Match 85.6%; Score 15.4; DB 12; Length 2878;
Best Local Similarity 94.1%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CGCCACCGGAAGTTGAG 17
Db 727 CGCCACCGGAAGTTGAG 743
RESULT 32
ADO97983
ID ADO97983 standard; DNA; 35998 BP.
XX
AC ADO97983;
XX
DT 07-OCT-2004 (first entry)
XX
DE Mouse cancer associated sequence MD11-036, SEQ ID 960.
XX
KW Cytostatic; Gene Therapy; cancer; leukemia; lymphoma; Mouse; ds.
XX
OS Mus musculus.
XX
PN WO2004060304-A2.
XX
PD 22-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US041389.
XX
PR 27-DEC-2002; 2002US-00330773.
XX
PA (SAGR-) SAGRES DISCOVERY INC.
XX
PI Morris DW, Malandro MS;
XX
DR WPI; 2004-543781/52.
XX
PT New isolated cancer associated nucleic acids comprising at least 10
PT contiguous nucleotides, useful for diagnosing, preventing and/or treating
PT cancers such as leukemia and lymphoma.
XX
PS Claim 1; SEQ ID NO 960; 199pp; English.
XX
CC The present invention relates to cancer associated sequences (ADO97025-
CC ADO98004). The sequences are useful for the diagnosis, prevention and/or
CC treatment of cancer, such as leukemia and lymphoma. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 35998 BP; 10248 A; 7246 C; 7916 G; 10588 T; 0 U; 0 Other;
Query Match 85.6%; Score 15.4; DB 12; Length 35998;
Best Local Similarity 94.1%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 GCCACCGGAAGTTGAGT 18
Db 26085 GTCACCGGAAGTTGAGT 26101
RESULT 33
ABD33203
ID ABD33203 standard; CDNA; 64721 BP.
XX
AC ABD33203;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human cancer-associated (CA) cDNA HR07-031 #1.
XX
KW Human; cancer-associated protein; CAP; cancer-associated gene; CA; gene;
KW ss; cancer; cytostatic.
XX
OS Homo sapiens.

```
XX PN WO2004058146-A2.
XX PD 15-JUL-2004.
XX PF 15-DEC-2003; 2003WO-US040081.
XX PR 17-DEC-2002; 2002US-00322281.
XX PS (SAGR-) SAGRES DISCOVERY INC.
XX PA Morris DW, Malandro MS;
XX PI WPI; 2004-499109/47.
XX PS P-PSDB; ABO84820.
XX PT Novel human cancer associated protein encoded within open reading frame
XX PT of cancer associated gene, useful as targets for diagnosing cancer.
XX PS Claim 1; SEQ ID NO 208; 182pp; English.
XX CC The invention relates to cancer-associated proteins (CAP) and the cancer-
XX CC associated (CA) nucleic acids encoding them. The invention also relates
XX CC to a method for treating cancers involving administering to a patient an
XX CC inhibitor of CAP, and a method of screening for anticancer activity in a
XX CC potential drug involving providing a cell that expresses a CA gene,
XX CC contacting a tissue sample derived from a cancer cell with an anticancer
XX CC drug candidate and monitoring the effect of the anticancer drug candidate
XX CC on expression of the CA gene. The CAP proteins are useful for detecting
XX CC cancer associated with expression of a CAP protein in a test cell sample
XX CC and for screening for a bioactive agent capable of modulating the
XX CC activity of a CAP protein. The CA nucleic acids are useful for diagnosing
XX CC cancer, involving determining the expression of a CA nucleic acid in a
XX CC tissue. This sequence represents human CA cDNA of the invention. Note:
XX CC The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 64721 BP; 12849 A; 15676 C; 15599 G; 15316 T; 0 U; 5281 Other;

Query Match 85.6%; Score 15.4; DB 13; Length 64721;
Best Local Similarity 94.1%; Pred. No. 3.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCCACCGGAAGTTGAGT 18
Db 68 GCCACCGGAAGTTGAGT 84

RESULT 34
ACN14228/c
ID ACN14228 standard; RNA; 17 BP.
XX AC ACN14228;
XX DT 22-APR-2004 (first entry)
XX DE WNV minus strand Amberzyme substrate SEQ ID NO 14231.
XX KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
XX KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
XX KW encephalitis; myocarditis; meningitis; infection; hepatitis;
XX KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
XX KW Amberzyme; Zinzyme; ss.
XX OS West Nile Virus.
XX PN WO200268637-A2.
XX PD 06-SEP-2002.
XX PF 19-OCT-2001; 2001WO-US048350.
XX PI
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PR 20-OCT-2000; 2000US-0242411P.
XX (RIBO-) RIBOZYME PHARM INC.
XX PA (BLAT/) BLATT L.
XX PS (MCSW/) MCSWIGGEN J A.
XX PI Blatt L, Mcswiggen JA;
XX XX WPI; 2002-706994/76.
XX PT New nucleic acid molecule that modulates replication of West Nile Virus
XX PT (WNV), useful for treating a condition related to WNV infection e.g.
XX PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX PS Claim 23; SEQ ID NO 14231; 495pp; English.
XX CC The invention relates to nucleic acid molecules that modulate replication
XX CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
XX CC treating a condition related to WNV infection e.g. pancreatitis,
XX CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
XX CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
XX CC molecule is selected from the group of ribozymes consisting of
XX CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
XX CC nucleic acid molecules further comprise at least five ribose residues, at
XX CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
XX CC least three of the 5' terminal nucleotides and a 3' end modification of a
XX CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
XX CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
XX CC in the specification. The present sequence is that of a nucleic acid
XX CC molecule of the invention
XX SQ Sequence 17 BP; 2 A; 5 C; 7 G; 0 T; 3 U; 0 Other;

Query Match 83.3%; Score 15; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTG 15
Db 15 CGCCACCGGAAGTTG 1

RESULT 35
ACN03350
ID ACN03350 standard; RNA; 17 BP.
XX AC ACN03350;
XX DT 22-APR-2004 (first entry)
XX DE WNV Inozyme substrate SEQ ID NO 3353.
XX KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
XX KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
XX KW encephalitis; myocarditis; meningitis; infection; hepatitis;
XX KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
XX KW Amberzyme; Zinzyme; ss.
XX OS West Nile Virus.
XX PN WO200268637-A2.
XX PD 06-SEP-2002.
XX PF 19-OCT-2001; 2001WO-US048350.
XX PR 20-OCT-2000; 2000US-0242411P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PS (BLAT/) BLATT L.
XX PI (MCSW/) MCSWIGGEN J A.
XX PI Blatt L, Mcswiggen JA;
```

XX DR WPI; 2002-706994/76.

XX CC New nucleic acid molecule that modulates replication of West Nile Virus

XX PT (WNV), useful for treating a condition related to WNV infection e.g.

XX PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX PS Claim 23; SEQ ID NO 3353; 495pp; English.

XX CC The invention relates to nucleic acid molecules that modulate replication

XX CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for

XX CC treating a condition related to WNV infection e.g. pancreatitis,

XX CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,

XX CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid

XX CC molecule is selected from the group of ribozymes consisting of

XX CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The

XX CC nucleic acid molecules further comprise at least five ribose residues, at

XX CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at

XX CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080

XX CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given

XX CC in the specification. The present sequence is that of a nucleic acid

XX CC molecule of the invention

XX SQ Sequence 17 BP; 3 A; 7 C; 5 G; 0 T; 2 U; 0 Other;

Query Match 83.3%; Score 15; DB 6; Length 17;

Best Local Similarity 86.7%; Pred. No. 2.2e+02;

Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCCACCGGAAGTTG 15

Db 3 CGCCACCGGAAGTUG 17

RESULT 36

ACN04649

ID ACN04649 standard; RNA; 17 BP.

XX AC ACN04649;

XX 22-APR-2004 (first entry)

XX MNV Zinzyme substrate SEQ ID NO 4652.

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;

XX virucide; neuroprotective; antibacterial; replication; pancreatitis;

XX encephalitis; myocarditis; meningitis; infection; hepatitis;

XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;

XX Amberzyme; Zinzyme; ss.

XX West Nile Virus.

OS WO200268637-A2.

PN 06-SEP-2002.

XX 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-024241P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus

XX PT (WNV), useful for treating a condition related to WNV infection e.g.

XX PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

PS Claim 23; SEQ ID NO 4652; 495pp; English.

XX CC The invention relates to nucleic acid molecules that modulate replication

XX CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for

XX CC treating a condition related to WNV infection e.g. pancreatitis,

XX CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,

XX CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid

XX CC molecule is selected from the group of ribozymes consisting of

XX CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The

XX CC nucleic acid molecules further comprise at least five ribose residues, at

XX CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at

XX CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080

XX CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given

XX CC in the specification. The present sequence is that of a nucleic acid

XX CC molecule of the invention

XX SQ Sequence 17 BP; 5 A; 3 C; 6 G; 0 T; 3 U; 0 Other;

Query Match 83.3%; Score 15; DB 6; Length 17;

Best Local Similarity 80.0%; Pred. No. 2.2e+02;

Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CACCGGAAGTTGAGT 18

Db 1 CACCGGAAGUUGAGU 15

RESULT 37

ACI27596

ID ACI27596 standard; DNA; 25 BP.

XX AC ACI27596;

XX 13-OCT-2003 (first entry)

XX Human microarray DNA oligonucleotide SEQ ID NO 27587.

XX EST; ss; probe; expressed sequence tag; microarray; gene expression;

XX Genetic variation; diallelic marker; polymorphism; human;

XX cross-species comparison.

XX Homo sapiens.

XX US2003104410-A1.

XX 05-JUN-2003.

XX 15-MAR-2002; 2002US-00098263.

XX 16-MAR-2001; 2001US-0276759P.

XX (AFFY-) AFFYMETRIX INC.

XX Mittmann MP;

XX WPI; 2003-567953/53.

XX New array of nucleic acid probes, useful for in situ hybridization, in

XX Southern, Northern or dot-blot hybridization to identify or detect the

XX sequence or specific mutations of any gene.

XX Claim 1; SEQ ID NO 27587; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic

XX acid probes including one of 2,018,500 fully defined sequences, or its

XX perfect match, perfect mismatch, antisense match or antisense mismatch.

XX Also disclosed is a method of gene expression analysis. The array is used

XX in monitoring gene expression levels by hybridisation to a DNA library,

XX in analysis of genetic variation or in hybridisation of tag-labelled

XX compounds. The nucleic acid probes are specifically designed for analysis

XX of at least one target sequence. The method of analysis comprises

XX hybridising at least one or more nucleic acids to at least two or more

CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying biallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html
 XX
 SQ Sequence 25 BP; 7 A; 6 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 83.3%; Score 15; DB 9; Length 25;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CACCGGAAGTTGAGT 18
 |||||
 DB 2 CACCGGAAGTTGAGT 16

RESULT 38
 ACH03748/c
 ID ACH03748 standard; cDNA; 436 BP.
 XX
 AC ACH03748;
 XX
 DT 26-SEP-2003 (first entry)
 XX
 DE Wheat steroid 22-alpha hydroxylase #1 cDNA.

XX Steroid 22-alpha hydroxylase; transgenic; plant; sterol biosynthesis;
 KW plant breeding; ss; Gene.

XX Triticum aestivum.
 XX US6545200-B1.
 XX 08-APR-2003.
 XX 15-DEC-1999; 99US-00464535.
 XX 16-DEC-1998; 98US-0112555P.
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 XX Cahoon RE, Famodu OO, Mcgonigle B, Rafalski JA, Sakai H;
 XX WPI; 2003-553970/52.
 DR P-PSDB; ABO44365.
 XX Novel isolated polynucleotide encoding a polypeptide comprising C-8,7
 PT sterol isomerase activity, useful in the production of a transformed host
 PT cell and in the production of a transgenic plant.

XX Disclosure; Col 41-42; 42pp; English.
 XX The invention relates to an isolated polynucleotide comprising a sequence
 CC encoding a polypeptide having C-8,7 sterol isomerase activity. The
 CC polynucleotide is useful for transforming a cell and producing a
 CC transgenic plant. The polynucleotide is useful in the production of
 CC altered levels of sterol biosynthetic enzyme in a transformed host cell.
 CC Nucleic acid fragments of the polynucleotide are useful to create
 CC transgenic plants in which sterol biosynthetic enzymes are present at
 CC higher or lower levels than normal or in cell types or developmental
 CC stages in which they are not normally found. The nucleic acid fragments
 CC are also useful as probes for genetically and physically mapping the
 CC genes that they are a portion of and as markers for traits linked to

CC those genes. Such information is useful in plant breeding to develop
 CC lines with desired phenotypes. The nucleic acid fragments are also useful
 CC as restriction fragment length polymorphism (RFLP) markers, for physical
 CC mapping and in direct fluorescence in situ hybridisation (FISH) mapping.
 CC The present sequence represents cDNA encoding a plant steroid 22-alpha
 CC hydroxylase

XX Sequence 436 BP; 102 A; 109 C; 127 G; 98 T; 0 U; 0 Other;
 SQ
 Query Match 83.3%; Score 15; DB 9; Length 436;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCACCGGAAGTTGAG 17
 |||||
 DB 157 CCACCGGAAGTTGAG 143

RESULT 39
 ACH03761/c
 ID ACH03761 standard; cDNA; 600 BP.

XX ACH03761;

XX 26-SEP-2003 (first entry)

XX Wheat steroid 22-alpha hydroxylase #2 cDNA.

XX Steroid 22-alpha hydroxylase; transgenic; plant; sterol biosynthesis;
 KW plant breeding; ss; Gene.

XX Triticum aestivum.

XX US6545200-B1.

XX 08-APR-2003.

XX 15-DEC-1999; 99US-00464535.

XX 16-DEC-1998; 98US-0112555P.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX Cahoon RE, Famodu OO, Mcgonigle B, Rafalski JA, Sakai H;

XX WPI; 2003-553970/52.

DR P-PSDB; ABO44378.

XX Novel isolated polynucleotide encoding a polypeptide comprising C-8,7
 PT sterol isomerase activity, useful in the production of a transformed host
 PT cell and in the production of a transgenic plant.

XX Disclosure; Col 71-74; 42pp; English.

XX The invention relates to an isolated polynucleotide comprising a sequence
 CC encoding a polypeptide having C-8,7 sterol isomerase activity. The
 CC polynucleotide is useful for transforming a cell and producing a
 CC transgenic plant. The polynucleotide is useful in the production of
 CC altered levels of sterol biosynthetic enzyme in a transformed host cell.
 CC Nucleic acid fragments of the polynucleotide are useful to create
 CC transgenic plants in which sterol biosynthetic enzymes are present at
 CC higher or lower levels than normal or in cell types or developmental
 CC stages in which they are not normally found. The nucleic acid fragments
 CC are also useful as probes for genetically and physically mapping the
 CC genes that they are a portion of and as markers for traits linked to
 CC those genes. Such information is useful in plant breeding to develop
 CC lines with desired phenotypes. The nucleic acid fragments are also useful
 CC as restriction fragment length polymorphism (RFLP) markers, for physical
 CC mapping and in direct fluorescence in situ hybridisation (FISH) mapping.
 CC The present sequence represents cDNA encoding a plant steroid 22-alpha
 CC hydroxylase

XX Sequence 600 BP; 147 A; 148 C; 163 G; 142 T; 0 U; 0 Other;

```
Query Match      83.3%; Score 15; DB 9; Length 600;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCACCGGAAGTTGAG 17
   |||||
Db 164 CCACCGGAAGTTGAG 150

RESULT 40
ACHO3758/c
ID ACH03758 standard; cDNA; 616 BP.
AC ACH03758;
XX
XX 26-SEP-2003 (first entry)
XX
XX Corn steroid 22-alpha hydroxylase #4 cDNA.
DE
XX Steroid 22-alpha hydroxylase; transgenic; plant; sterol biosynthesis;
KW plant breeding; ss; gene.
XX
XX Zea mays.
OS
XX US6545200-B1.
XX
XX 08-APR-2003.
PD
XX 15-DEC-1999; 99US-00464535.
PF
XX 16-DEC-1998; 98US-0112555P.
PR
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
PA
XX Cahoon RE, Famodu OO, Mcgonigle B, Rafalski JA, Sakai H;
PI
XX WPI; 2003-553970/52.
DR
XX P-PSDB; ABO44375.
XX
XX Novel isolated polynucleotide encoding a polypeptide comprising C-8,7
PT sterol isomerase activity, useful in the production of a transformed host
PT cell and in the production of a transgenic plant.
XX
XX Disclosure; Col 63-64; 42pp; English.
XX
XX The invention relates to an isolated polynucleotide comprising a sequence
CC encoding a polypeptide having C-8,7 sterol isomerase activity. The
CC polynucleotide is useful for transforming a cell and producing a
CC transgenic plant. The polynucleotide is useful in the production of
CC altered levels of sterol biosynthetic enzyme in a transformed host cell.
CC Nucleic acid fragments of the polynucleotide are useful to create
CC transgenic plants in which sterol biosynthetic enzymes are present at
CC higher or lower levels than normal or in cell types or developmental
CC stages in which they are not normally found. The nucleic acid fragments
CC are also useful as probes for genetically and physically mapping the
CC genes that they are a portion of and as markers for traits linked to
CC those genes. Such information is useful in plant breeding to develop
CC lines with desired phenotypes. The nucleic acid fragments are also useful
CC as restriction fragment length polymorphism (RFLP) markers, for physical
CC mapping and in direct fluorescence in situ hybridisation (FISH) mapping.
CC The present sequence represents cDNA encoding a plant steroid 22-alpha
CC hydroxylase
XX
XX Sequence 616 BP; 149 A; 148 C; 180 G; 125 T; 0 U; 14 Other;

Query Match      83.3%; Score 15; DB 9; Length 616;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCACCGGAAGTTGAG 17
   |||||
Db 376 CCACCGGAAGTTGAG 362

Query Match      83.3%; Score 15; DB 9; Length 600;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCACCGGAAGTTGAG 17
   |||||
Db 164 CCACCGGAAGTTGAG 150
```

```
RESULT 41
ACHO3757/c
ID ACH03757 standard; cDNA; 673 BP.
XX
XX ACH03757;
AC
XX 26-SEP-2003 (first entry)
XX
XX Corn steroid 22-alpha hydroxylase #3 cDNA.
DE
XX Steroid 22-alpha hydroxylase; transgenic; plant; sterol biosynthesis;
KW plant breeding; ss; gene.
XX
XX Zea mays.
OS
XX US6545200-B1.
XX
XX 08-APR-2003.
PD
XX 15-DEC-1999; 99US-00464535.
PF
XX 16-DEC-1998; 98US-0112555P.
PR
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
PA
XX Cahoon RE, Famodu OO, Mcgonigle B, Rafalski JA, Sakai H;
PI
XX WPI; 2003-553970/52.
DR
XX P-PSDB; ABO44374.
XX
XX Novel isolated polynucleotide encoding a polypeptide comprising C-8,7
PT sterol isomerase activity, useful in the production of a transformed host
PT cell and in the production of a transgenic plant.
XX
XX Disclosure; Col 61-62; 42pp; English.
XX
XX The invention relates to an isolated polynucleotide comprising a sequence
CC encoding a polypeptide having C-8,7 sterol isomerase activity. The
CC polynucleotide is useful for transforming a cell and producing a
CC transgenic plant. The polynucleotide is useful in the production of
CC altered levels of sterol biosynthetic enzyme in a transformed host cell.
CC Nucleic acid fragments of the polynucleotide are useful to create
CC transgenic plants in which sterol biosynthetic enzymes are present at
CC higher or lower levels than normal or in cell types or developmental
CC stages in which they are not normally found. The nucleic acid fragments
CC are also useful as probes for genetically and physically mapping the
CC genes that they are a portion of and as markers for traits linked to
CC those genes. Such information is useful in plant breeding to develop
CC lines with desired phenotypes. The nucleic acid fragments are also useful
CC as restriction fragment length polymorphism (RFLP) markers, for physical
CC mapping and in direct fluorescence in situ hybridisation (FISH) mapping.
CC The present sequence represents cDNA encoding a plant steroid 22-alpha
CC hydroxylase
XX
XX Sequence 673 BP; 160 A; 164 C; 197 G; 135 T; 0 U; 17 Other;

Query Match      83.3%; Score 15; DB 9; Length 673;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCACCGGAAGTTGAG 17
   |||||
Db 362 CCACCGGAAGTTGAG 348

RESULT 42
AAH65402/c
ID AAH65402 standard; DNA; 1863 BP.
XX
XX AAH65402;
AC
XX
```


PF 23-MAR-2001; 2001WO-US009231.
 XX
 PR 23-MAR-2000; 2000US-0191637P.
 PR 11-JUL-2000; 2000US-00614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR WPI; 2001-656860/75.
 DR P-PSDB; ABB60849.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PT interactions.
 XX
 PS Claim 1; SEQ ID NO 9338; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 52872 BP; 15532 A; 11487 C; 10803 G; 15050 T; 0 U; 0 Other;
 Query Match 83.3%; Score 15; DB 4; Length 52872;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 CACCGGAAGTTGAGT 18
 DB 19409 CACCGGAAGTTGAGT 19395
 RESULT 45
 AAH68525/C
 ID AAH68525 standard; DNA; 349980 BP.
 XX
 AC AAH68525;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE C Glutamicum coding sequence fragment SEQ ID NO: 7060.
 XX
 KW Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
 KW organic acid synthesis; ds.
 XX
 OS Corynebacterium glutamicum.
 XX
 PN EP1108790-A2.
 XX
 PD 20-JUN-2001.
 XX
 PF 18-DEC-2000; 2000EP-00127688.
 XX
 PR 16-DEC-1999; 95JP-00377484.
 PR 07-APR-2000; 2000JP-00159162.
 PR 03-AUG-2000; 2000JP-00280988.
 XX
 PA (KYOWA) KYOWA HAKKO KOGYO KK.
 XX
 PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
 PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
 XX
 DR WPI; 2001-376931/40.
 XX
 PT Novel polynucleotides derived from Coryneform bacteria, for identifying

PT mutation point of a gene, measuring expression of a gene, analyzing
 PT expression profile or pattern of a gene and identifying homologous gene.
 XX
 PS Disclosure; SEQ ID NO 7060; 246pp + Sequence Listing; English.
 XX
 CC The present invention provides a number of nucleotide and protein
 CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These
 CC are useful for identifying the mutation point of a gene derived from a
 CC mutant of coryneform bacterium, measuring expression amount and analysing
 CC the expression profile or expression pattern of a gene derived from
 CC Coryneform bacterium, and identifying a homologue of a gene derived from
 CC coryneform bacterium. Coryneform bacteria are useful for producing amino
 CC acids, nucleic acids, vitamins, saccharides and organic acids,
 CC particularly L-lysine. The present sequence is a nucleic acid described
 CC in the exemplification of the invention. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from the European Patent Office
 XX
 SQ Sequence 349980 BP; 80289 A; 91081 C; 97378 G; 81232 T; 0 U; 0 Other;
 Query Match 83.3%; Score 15; DB 5; Length 349980;
 Best Local Similarity 100.0%; Pred. No. 7.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 CCACCGGAAGTTGAG 17
 DB 111416 CCACCGGAAGTTGAG 111402
 RESULT 46
 ACD72382/C
 ID ACD72382 standard; DNA; 100 BP.
 XX
 AC ACD72382;
 XX
 DT 18-SEP-2003 (first entry)
 XX
 DE E. coli K12 MG1655 biochip probe SEQ ID 3652.
 XX
 KW Biochip; gene expression; gut; diagnostic; detection; probe; ss.
 XX
 OS Escherichia coli.
 XX
 PN EP1260592-A1.
 XX
 PD 27-NOV-2002.
 XX
 PF 17-MAY-2001; 2001EP-00112179.
 XX
 PR 17-MAY-2001; 2001EP-00112179.
 XX
 PA (MWGB-) MWGB-BIOFTECH AG.
 XX
 PI Donner H, Drescher B, Huber A, Weber J;
 XX
 DR WPI; 2003-241155/24.
 XX
 PT Biochip containing probes complementary with open reading frames in
 PT Escherichia coli K12, useful for detecting gene expression and expression
 PT patterns.
 XX
 PS Claim 3; Page 576; 2004pp; German.
 XX
 CC This invention describes a novel biochip comprising probe spots, each
 CC containing many identical probes. The probes are nucleotide sequences of
 CC 30-80 bases, are prepared ex situ from synthetic oligonucleotides and at
 CC least one includes a segment of at least 20 bases identical with, or
 CC complementary to, a segment of an open reading frame (orf) of Escherichia
 CC coli K12. The biochip is used for specific detection of gene expression
 CC in K12 and for determining the gene expression pattern, e.g. for
 CC diagnostic determination of which E. coli strains are present in the gut,
 CC and to determine the effects of e.g. growth media on gene expression. The
 CC biochip provides as comprehensive as possible detection of the K12

CC genome, with simultaneous analysis of many different genes with a single
 CC device, and comparison of gene expression between K12 and its mutants or
 CC other *E. coli* strains in a single experiment. Apart from qualitative and
 CC quantitative information about gene expression, it also allows
 CC measurements of population densities for the various strains. The use of
 CC synthetic oligonucleotides for preparation of probes allows free
 CC variation in probe length and ensures high purity (and thus selectivity,
 CC reactivity and reproducibility); also synthetic probes are generally
 CC shorter than probes prepared by polymerase chain reaction. ACD68731 to
 CC ACD81540 represent oligonucleotide probes used with the biochip described
 CC in the invention

SQ Sequence 100 BP; 23 A; 29 C; 26 G; 22 T; 0 U; 0 Other;

Query Match 82.2%; Score 14.8; DB 8; Length 100;

Best Local Similarity 88.9%; Pred. No. 3.6e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGTTGAGT 18

DB 58 CGGCACCGGAGATGAGT 41

RESULT 47

ACD72383/c

ID ACD72383 standard; DNA; 100 BP.

XX ACD72383;

AC 18-SEP-2003 (first entry)

DE *E. coli* K12 MG1655 biochip probe SEQ ID 3653.

XX Biochip; gene expression; gut; diagnostic; detection; probe; ss.

XX *Escherichia coli*.

OS EP1260592-A1.

XX 27-NOV-2002.

PD 17-MAY-2001; 2001EP-00112179.

PF 17-MAY-2001; 2001EP-00112179.

XX (MWGB-) MWG-BIOTECH AG.

XX Donner H, Drescher B, Huber A, Weber J;

PI WPI; 2003-241155/24.

DR Biochip containing probes complementary with open reading frames in
 PT *Escherichia coli* K12, useful for detecting gene expression and expression
 PT patterns.

PS Claim 3; Page 576; 2004pp; German.

XX This invention describes a novel biochip comprising probe spots, each
 CC containing many identical probes. The probes are nucleotide sequences of
 CC 30-80 bases, are prepared ex situ from synthetic oligonucleotides and at
 CC least one includes a segment of at least 20 bases identical with, or
 CC complementary to, a segment of an open reading frame (orf) of *Escherichia*
 CC *coli* K12. The biochip is used for specific detection of gene expression
 CC in K12 and for determining the gene expression pattern, e.g. for
 CC diagnostic determination of which *E. coli* strains are present in the gut,
 CC and to determine the effects of e.g. growth media on gene expression. The
 CC biochip provides as comprehensive as possible detection of the K12
 CC genome, with simultaneous analysis of many different genes with a single
 CC device, and comparison of gene expression between K12 and its mutants or
 CC other *E. coli* strains in a single experiment. Apart from qualitative and
 CC quantitative information about gene expression, it also allows
 CC measurements of population densities for the various strains. The use of
 CC synthetic oligonucleotides for preparation of probes allows free

CC variation in probe length and ensures high purity (and thus selectivity,
 CC reactivity and reproducibility); also synthetic probes are generally
 CC shorter than probes prepared by polymerase chain reaction. ACD68731 to
 CC ACD81540 represent oligonucleotide probes used with the biochip described
 CC in the invention

SQ Sequence 100 BP; 23 A; 29 C; 26 G; 22 T; 0 U; 0 Other;

Query Match 82.2%; Score 14.8; DB 8; Length 100;

Best Local Similarity 88.9%; Pred. No. 3.6e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGTTGAGT 18

DB 58 CGGCACCGGAGATGAGT 41

RESULT 48

ADQ16356/c

ID ADQ16356 standard; DNA; 363 BP.

XX AC ADQ16356;

XX 09-SEP-2004 (first entry)

XX Nucleotide sequence of a *Bordetella* variable 16S rRNA gene region.

XX fragmentation-based method; mass spectrometric method;

XX nucleic acid polymorphism; nucleic acid mutation; genetic disease;

XX chromosome abnormality; obesity; atherosclerosis; cancer; haplotype; ss;

XX rRNA gene.

XX *Bordetella* sp.; strain SHA-1.

XX WO2004050839-A2.

XX 17-JUN-2004.

XX 26-NOV-2003; 2003WO-US037931.

XX 27-NOV-2002; 2002US-0429895P.

XX (SEQU-) SEQUENOM INC.

XX Van Den Boom D, Becker S;

XX WPI; 2004-487567/46.

XX Use of fragmentation-based methods and systems, e.g. mass spectrometric
 PT methods for the analysis of sequence variations including nucleic acid
 PT polymorphisms and mutations.

PS Example 4; SEQ ID NO 33; 198pp; English.

XX The specification describes the use of fragmentation-based methods and
 CC systems including mass spectrometric methods for the analysis of sequence
 CC variations including nucleic acid polymorphisms and mutations. The
 CC fragmentation-based methods and systems of the invention are useful for
 CC the analysis of sequence variations including nucleic acid polymorphisms
 CC and mutations. The methods are useful for identifying a genetic disease
 CC or chromosome abnormality; identifying a predisposition to a disease or
 CC condition including obesity, atherosclerosis, or cancer; identifying an
 CC infection by an infectious agent; providing information relating to
 CC identity, heredity, or histocompatibility; identifying pathogens; or
 CC determining haplotypes. ADQ16353-ADQ16361 represent *Bordetella* variable
 CC 16S rRNA gene regions. Amplicons from this region were used to demonstrate
 CC the invention. They were used to demonstrate a method for bacterial
 CC typing by base-specific fragmentation.

SQ Sequence 363 BP; 86 A; 92 C; 119 G; 66 T; 0 U; 0 Other;

Query Match 82.2%; Score 14.8; DB 12; Length 363;

Best Local Similarity 88.9%; Pred. No. 4.2e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGTTGAGT 18
 DB 143 CGCCACCGGAGTTGAGT 126

RESULT 49
 ADQ16357/C
 ID ADQ16357 standard; DNA; 363 BP.

XX AC ADQ16357;
 XX DT 09-SEP-2004 (first entry)
 XX DE Nucleotide sequence of a Bordetella variable 16S rRNA gene region.
 XX KW fragmentation-based method; mass spectrometric method;
 KW nucleic acid polymorphism; nucleic acid mutation; genetic disease;
 KW chromosome abnormality; obesity; atherosclerosis; cancer; haplotype; ss;
 KW rRNA gene.
 XX OS Bordetella sp.; strain SHA-110.
 XX PN WO2004050839-A2.
 XX PD 17-JUN-2004.
 XX PF 26-NOV-2003; 2003WO-US037931.
 XX PR 27-NOV-2002; 2002US-0429895P.
 XX PA (SEQU-) SEQUENOM INC.
 XX PI Van Den Boom D, Boecker S;
 XX DR WPI; 2004-487567/46.

XX PT Use of fragmentation-based methods and systems, e.g. mass spectrometric
 PT methods for the analysis of sequence variations including nucleic acid
 PT polymorphisms and mutations.

XX PS Example 4; SEQ ID NO 34; 198pp; English.

XX CC The specification describes the use of fragmentation-based methods and
 CC systems including mass spectrometric methods for the analysis of sequence
 CC variations including nucleic acid polymorphisms and mutations. The
 CC fragmentation-based methods and systems of the invention are useful for
 CC the analysis of sequence variations including nucleic acid polymorphisms
 CC and mutations. The methods are useful for identifying a genetic disease
 CC or chromosome abnormality; identifying a predisposition to a disease or
 CC condition including obesity, atherosclerosis, or cancer; identifying an
 CC infection by an infectious agent; providing information relating to
 CC identity, heredity, or histocompatibility; identifying pathogens; or
 CC determining haplotypes. ADQ16353-ADQ16361 represent Bordetella variable
 CC 16S rRNA gene regions. Amplicons from this region were used to demonstrate
 CC the invention. They were used to demonstrate a method for bacterial
 CC typing by base-specific fragmentation.

XX SQ Sequence 363 BP; 90 A; 89 C; 116 G; 68 T; 0 U; 0 Other;

Query Match 82.2%; Score 14.8; DB 12; Length 363;
 Best Local Similarity 88.9%; Pred. No. 4.2e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGTTGAGT 18
 DB 143 CGCCACCGGAGTTGAGT 126

RESULT 50
 AAF64813/C
 ID AAF64813 standard; cDNA; 389 BP.

XX AC AAF64813;
 XX DT 09-APR-2001 (first entry)
 XX DE Novel human polynucleotide, SEQ ID NO: 569.
 XX KW Human; cytostatic; gene therapy; colon cancer; prostate cancer;
 KW breast cancer; lung cancer; cancer detection; ss.
 XX OS Homo sapiens.
 XX PN WO200102568-A2.
 XX PD 11-JAN-2001.
 XX PF 30-JUN-2000; 2000WO-US018374.
 XX PR 02-JUL-1999; 99US-0142310P.
 XX PR 02-JUL-1999; 99US-0142311P.
 XX PA (CHIR) CHIRON CORP.
 PA (HYSE-) HYSEQ INC.
 XX PI Williams LT, Escobedo J, Innis MA, Garcia PD, Klinger J;
 PI Kassam A, Reinhard C, Randazzo F, Kennedy GC, Pot D, Lamson G;
 PI Drmanac R, Crkenjakov R, Drmanac S, Dickson M, Labat I;
 PI Leshkowitz D, Kita D, Garcia V, Jones LW, Strache-Crain B;
 XX DR WPI; 2001-091805/10.
 XX PT Library of polynucleotides for diagnosing a cancerous state of a
 PT mammalian cell and detecting cancer, particularly of the colon or
 PT prostate, comprises 3351 human polynucleotide sequences.
 XX PS Claim 9; Page 626; 1046pp; English.

XX CC The present sequence is one of 3351 sequences in a library of human
 CC polynucleotides. The library is used to detect differentially expressed
 CC genes correlated with a cancerous state of a mammalian cell and can
 CC detect colon, prostate, breast and lung cancer. The library can be used
 CC to produce probes for detection of mRNA and to produce additional copies
 CC of the polynucleotides. The probes can be used for chromosome mapping of
 CC the polynucleotide and for detection of transcription levels. Ribozymes
 CC or antisense oligonucleotides can be generated. The polynucleotides and
 CC their gene products are used as genetic or biochemical markers (e.g. in
 CC blood or tissues) that will detect the earliest changes along the
 CC carcinogenesis pathway and/or monitor the efficacy of therapies and
 CC preventive interventions. The polynucleotides, polypeptides and
 CC antibodies against them can be used in pharmaceutical compositions to
 CC treat the cancers and proliferative disorders such as neoplasia,
 CC dysplasia and hyperplasia

XX SQ Sequence 389 BP; 65 A; 139 C; 110 G; 75 T; 0 U; 0 Other;

Query Match 82.2%; Score 14.8; DB 5; Length 389;
 Best Local Similarity 88.9%; Pred. No. 4.3e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGTTGAGT 18
 DB 266 CGCCACCGGAGTTGAGT 249

Search completed: March 25, 2005, 11:14:36
 Job time : 226.857 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 25, 2005, 10:41:57 ; Search time 1341 Seconds
(without alignments)
510.930 Million cell updates/sec

Title: US-10-688-489-64

Perfect score: 18
Sequence: 1 cggccaccggaagttagt 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_hic: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gsa1: *
9: gb_gsa2: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	17	94.4	737	8	BH794414 ME MBa000
C 2	17	94.4	895	7	CF824029 ESTT701411
C 3	16.4	91.1	514	8	AO492895 HS 5126.A
C 4	16.4	91.1	576	2	BE994137
C 5	16.4	91.1	598	5	BP117402
C 6	16.4	91.1	1331	3	CR665917
C 7	16	88.9	480	5	BQ559427 H4058B07-
C 8	16	88.9	539	6	CA542435 C0618H12-
C 9	16	88.9	587	7	CF895091 AO143H02-
C 10	16	88.9	602	2	AW338466 xw78h03.x
C 11	16	88.9	604	8	AQ47015
C 12	16	88.9	607	7	CO430950 UT-M-HXO-
C 13	16	88.9	612	2	AW173515
C 14	16	88.9	614	2	AW173560 xJ08a06.x
C 15	16	88.9	626	2	AW168911 xJ15b06.x
C 16	16	88.9	627	2	AW172834 xJ04d03.x
C 17	16	88.9	697	1	AI871886 wms3a05.x
C 18	16	88.9	707	1	AI884543 wms3a04.x
C 19	16	88.9	736	6	CB244514 UT-M-FYO-
C 20	16	88.9	823	9	CNS0088X
C 21	16	88.9	897	9	CNS00C0Q
C 22	16	88.9	4339	3	AK040525 Mus muscu
C 23	15.4	85.6	83	9	CG474564 OST2570 M
C 24	15.4	85.6	138	9	CW510696 Cot678.D1

98	15	83.3	404	8	CC072920	CSU-K33r.	C 171	14.8	82.2	550	2	BE488657	WHE1053_C
99	15	83.3	419	2	BB770230	BB770230	172	14.8	82.2	551	7	CN614415	TGESTzyM7
100	15	83.3	422	6	CA294158	SCGLV101	173	14.8	82.2	552	4	BJ125488	BJ125488
101	15	83.3	423	8	CC011670	PUDHQ39TD	174	14.8	82.2	553	4	BJ763853	BJ763853
102	15	83.3	436	6	CA704862	wk1c.pk0	C 175	14.8	82.2	555	2	BE581874	Kq54F07.Y
103	15	83.3	457	8	CC333035	CGSAL86TV	C 176	14.8	82.2	556	4	BE226157	Kq18A10.Y
104	15	83.3	506	5	BQ243992	Tae15006D	C 177	14.8	82.2	557	4	BJ759822	BJ759822
105	15	83.3	516	7	CF637839	ZNRW00.0	C 178	14.8	82.2	558	4	BM176817	TGESTzya9
106	15	83.3	565	8	AZ245878	RPCI-23-B	179	14.8	82.2	560	4	BJ108116	BJ108116
107	15	83.3	571	8	AZ269364	RPCI-23-1	180	14.8	82.2	567	4	AU205903	AU205903
108	15	83.3	582	9	CL962487	OsIFCC007	181	14.8	82.2	572	1	BJ107270	BJ107270
109	15	83.3	591	7	CO898907	Mgfrt3055	182	14.8	82.2	577	4	BJ122447	BJ122447
110	15	83.3	625	5	BQ619714	TaLr1172C	183	14.8	82.2	581	4	BJ104448	BJ104448
111	15	83.3	629	7	CF574030	MCSA079B1	184	14.8	82.2	582	4	BJ109803	BJ109803
112	15	83.3	643	8	AZ509564	IM0352M04	185	14.8	82.2	583	4	BJ698887	BJ698887
113	15	83.3	651	1	AV836130	AV836130	C 186	14.8	82.2	585	4	AZ356373	IM0097L22
114	15	83.3	675	9	CL1159759	H91_60_EO	187	14.8	82.2	590	8	AV859812	AV859812
115	15	83.3	685	6	CD211397	H91_60_EO	C 188	14.8	82.2	592	4	BJ113330	BJ113330
116	15	83.3	698	1	AI569959	t-90C09.X	C 189	14.8	82.2	593	1	AV537605	AV537605
117	15	83.3	703	7	CO902852	Mgfrt3059	C 190	14.8	82.2	593	4	BJ123585	BJ123585
118	15	83.3	717	7	CF530757	UI-M-FY0	C 191	14.8	82.2	593	4	BJ762659	BJ762659
119	15	83.3	765	6	CA275632	SCBFS0103	C 192	14.8	82.2	594	4	BJ768227	BJ768227
120	15	83.3	803	9	CG095738	PUIHD45TD	C 193	14.8	82.2	596	4	BJ752838	BJ752838
121	15	83.3	829	7	CV198371	CGF100397	C 194	14.8	82.2	596	4	BJ754964	BJ754964
122	15	83.3	895	4	BI199621	602761295	C 195	14.8	82.2	599	4	BJ773886	BJ773886
123	15	83.3	929	9	CG235378	OG3AM30TH	C 196	14.8	82.2	611	4	BJ760094	BJ760094
124	15	83.3	1028	8	CC219896	CH261-99H	197	14.8	82.2	612	2	BE784693	601473570
125	15	83.3	1101	9	CNS00FPH	AL070811	198	14.8	82.2	616	4	BJ767201	BJ767201
126	14.8	82.2	139	8	CC326021	RPF451_Ba	C 199	14.8	82.2	617	5	BM216301	BM216301
127	14.8	82.2	246	8	BH802497	BH802497	C 200	14.8	82.2	619	4	BJ754368	BJ754368
128	14.8	82.2	271	2	BB402484	BB402484	C 201	14.8	82.2	625	5	BM209946	BM209946
129	14.8	82.2	273	4	BI042640	RC5-OT010	C 202	14.8	82.2	629	1	AU205198	AU205198
130	14.8	82.2	273	8	BZ123536	CH230-404	C 203	14.8	82.2	630	8	BH680077	BOMXB23TR
131	14.8	82.2	302	1	AV529859	AV529859	C 204	14.8	82.2	631	4	AV840985	AV840985
132	14.8	82.2	320	5	BY363149	BY363149	205	14.8	82.2	631	4	BJ117107	BJ117107
133	14.8	82.2	335	9	CC534852	CH240_413	C 206	14.8	82.2	635	1	AV856003	AV856003
134	14.8	82.2	355	1	AV828582	AV828582	207	14.8	82.2	638	5	BM400929	BM400929
135	14.8	82.2	360	6	C67113	C67113_Yuji	C 208	14.8	82.2	638	6	CB499589	88a16rxc0
136	14.8	82.2	360	6	C69905	C69905_Yuji	C 209	14.8	82.2	642	6	CB499875	CDA1-H03
137	14.8	82.2	374	6	C43301	C43301_Yuji	C 210	14.8	82.2	647	6	CB262303	66-E9779-
138	14.8	82.2	377	6	C67728	C67728	C 211	14.8	82.2	648	5	BM250276	BM250276
139	14.8	82.2	401	2	BE072588	ETESTee14	C 212	14.8	82.2	651	7	CF735199	UI-M-HB0-
140	14.8	82.2	409	7	CF182599	UI-M-EY0-	C 213	14.8	82.2	652	8	AQ325382	nbx0012F
141	14.8	82.2	415	8	B78264	T32A16TF_TA	C 214	14.8	82.2	654	7	CN459311	UI-M-HNO-
142	14.8	82.2	426	5	BY391950	BY391950	C 215	14.8	82.2	657	7	CF446478	EST682823
143	14.8	82.2	428	4	BJ799551	BJ799551	216	14.8	82.2	662	8	BZ540936	OGAFG32TC
144	14.8	82.2	441	7	D27310	CELK011FYF	217	14.8	82.2	663	9	CG975273	MBEFG84TF
145	14.8	82.2	444	4	BM321629	BM321629	218	14.8	82.2	669	5	BM075684	BM075684
146	14.8	82.2	445	2	BE580405	Kq41a08.Y	C 219	14.8	82.2	670	2	BE489235	WHE1075_C
147	14.8	82.2	449	8	BZ764041	SALK_1232	C 220	14.8	82.2	671	5	BM338494	BM338494
148	14.8	82.2	461	2	BB834942	BB834942	C 221	14.8	82.2	678	7	CN112621	EC2CAA38D
149	14.8	82.2	465	5	BP765351	BP765351	C 222	14.8	82.2	679	5	BM236399	BM236399
150	14.8	82.2	475	1	AI152886	ue01a07.r	C 223	14.8	82.2	684	8	AZ874951	2M0189F16
151	14.8	82.2	477	5	BM153608	BM153608	C 224	14.8	82.2	689	8	BZ008956	oej73b09
152	14.8	82.2	479	1	AL510170	AL510170	C 225	14.8	82.2	691	9	CL923835	OA_ABA002
153	14.8	82.2	480	2	BB860708	BB860708	C 226	14.8	82.2	694	6	CD522527	AGENCOURT
154	14.8	82.2	491	4	BI962014	Q1209_1a	C 227	14.8	82.2	699	4	BM013177	603638064
155	14.8	82.2	491	4	BJ760475	BJ760475	C 228	14.8	82.2	700	7	CN525506	UI-M-HNO-
156	14.8	82.2	496	5	BM283132	BM283132	C 229	14.8	82.2	708	8	BZ047632	lkf32c04
157	14.8	82.2	504	4	BM361219	A00551-R	C 230	14.8	82.2	712	1	AA928785	AA928785
158	14.8	82.2	507	4	BG553757	dac37e04	C 231	14.8	82.2	712	5	BM485504	BM485504
159	14.8	82.2	514	4	BM361218	A00551-F	C 232	14.8	82.2	713	5	BM393159	BM393159
160	14.8	82.2	518	1	AL638977	AL638977	C 233	14.8	82.2	715	9	AG545816	AG545816
161	14.8	82.2	518	4	BJ115823	BJ115823	C 234	14.8	82.2	715	5	BM476592	BM476592
162	14.8	82.2	520	1	AU199410	AU199410	C 235	14.8	82.2	719	5	BM018907	BM018907
163	14.8	82.2	520	1	AA396914	AA396914	C 236	14.8	82.2	721	8	BZ071759	BZ071759
164	14.8	82.2	526	4	BJ805486	BJ805486	C 237	14.8	82.2	722	5	BM018210	BM018210
165	14.8	82.2	538	8	AQ410418	HS_5125_A	C 238	14.8	82.2	734	8	AZ707788	RPCI-23-2
166	14.8	82.2	540	4	BJ102272	BJ102272	C 239	14.8	82.2	741	8	BH605882	BOGUT86TR
167	14.8	82.2	546	5	BM528892	BM528892	C 240	14.8	82.2	741	9	AG563765	AG563765
168	14.8	82.2	547	1	AU207859	AU207859	C 241	14.8	82.2	742	7	CF728116	UI-M-HNO-
169	14.8	82.2	548	2	BE488506	WHE1058_C	C 242	14.8	82.2	750	7	CN458381	UI-M-HNO-
170	14.8	82.2	549	4	BM189625	TGESTzyB4	C 243	14.8	82.2				

c 244	14.8	82.2	752	7	CO434442	UI-M-HX0-	CO434442	UI-M-HX0-	c 317	14.8	82.2	1256	3	CR671014	Tetraodon
c 245	14.8	82.2	761	2	BE739840	601593122	BE739840	601593122	c 318	14.8	82.2	1257	3	CR669602	Tetraodon
c 246	14.8	82.2	767	8	BZ571409	msb2_1872	BZ571409	msb2_1872	c 319	14.8	82.2	1260	3	CR659741	Tetraodon
c 247	14.8	82.2	769	7	CP710150	CCAG053TF	CP710150	CCAG053TF	c 320	14.8	82.2	1262	3	CR665207	Tetraodon
c 248	14.8	82.2	770	9	CL658179	PR10130C	CL658179	PR10130C	c 321	14.8	82.2	1262	3	CR674922	Tetraodon
c 249	14.8	82.2	771	7	CF818659	EST96041	CF818659	EST96041	c 322	14.8	82.2	1263	3	CR671585	Tetraodon
c 250	14.8	82.2	772	2	BF538276	602053757	BF538276	602053757	c 323	14.8	82.2	1264	3	CR664109	Tetraodon
c 251	14.8	82.2	774	5	BM464150	BM464150	BM464150	BM464150	c 324	14.8	82.2	1270	3	CR668244	Tetraodon
c 252	14.8	82.2	780	5	BM390264	BM390264	BM390264	BM390264	c 325	14.8	82.2	1270	3	CR670804	Tetraodon
c 253	14.8	82.2	780	8	BZ070063	lkf64c03	BZ070063	lkf64c03	c 326	14.8	82.2	1270	3	CR699010	Tetraodon
c 254	14.8	82.2	783	6	CA216701	SCC8T3C1	CA216701	SCC8T3C1	c 327	14.8	82.2	1270	3	CR679976	Tetraodon
c 255	14.8	82.2	795	7	CO110027	GR_EB004	CO110027	GR_EB004	c 328	14.8	82.2	1279	3	CR678540	Tetraodon
c 256	14.8	82.2	800	4	BI666056	603287225	BI666056	603287225	c 329	14.8	82.2	1282	3	CR668717	Tetraodon
c 257	14.8	82.2	801	6	CB246377	UI-M-FIO-	CB246377	UI-M-FIO-	c 330	14.8	82.2	1288	3	CR667596	Tetraodon
c 258	14.8	82.2	803	7	CN455488	UI-M-HNO-	CN455488	UI-M-HNO-	c 331	14.8	82.2	1289	3	CR678123	Tetraodon
c 259	14.8	82.2	808	7	CF682852	CCAGU4ATF	CF682852	CCAGU4ATF	c 332	14.8	82.2	1289	3	CR661996	Tetraodon
c 260	14.8	82.2	811	7	CO028051	EST906435	CO028051	EST906435	c 333	14.8	82.2	1294	3	CR669151	Tetraodon
c 261	14.8	82.2	822	7	CV125676	OSTF30043	CV125676	OSTF30043	c 334	14.8	82.2	1297	3	CR666151	Tetraodon
c 262	14.8	82.2	827	7	CN526319	UI-M-HNO-	CN526319	UI-M-HNO-	c 335	14.8	82.2	1300	3	CR677752	Tetraodon
c 263	14.8	82.2	845	9	CG126505	PUIJBV73TB	CG126505	PUIJBV73TB	c 336	14.8	82.2	1301	3	CR675285	Tetraodon
c 264	14.8	82.2	845	9	CG126506	PUIJBV73TD	CG126506	PUIJBV73TD	c 337	14.8	82.2	1302	3	CR666747	Tetraodon
c 265	14.8	82.2	872	2	BE905758	601495778	BE905758	601495778	c 338	14.8	82.2	1304	3	CR678826	Tetraodon
c 266	14.8	82.2	873	8	BZ571354	msb2_1848	BZ571354	msb2_1848	c 339	14.8	82.2	1304	3	CR679580	Tetraodon
c 267	14.8	82.2	875	8	BZ578064	msb2_5704	BZ578064	msb2_5704	c 340	14.8	82.2	1311	3	CR659664	Tetraodon
c 268	14.8	82.2	875	9	CR169876	Reverse s	CR169876	Reverse s	c 341	14.8	82.2	1317	3	CR660552	Tetraodon
c 269	14.8	82.2	882	4	BI598367	AGENCOURT	BI598367	AGENCOURT	c 342	14.8	82.2	1317	3	CR677639	Tetraodon
c 270	14.8	82.2	882	6	CD251956	AGENCOURT	CD251956	AGENCOURT	c 343	14.8	82.2	1326	3	CR678383	Tetraodon
c 271	14.8	82.2	900	2	BF104921	601822654	BF104921	601822654	c 344	14.8	82.2	1332	3	CR677618	Tetraodon
c 272	14.8	82.2	909	7	CF721573	CCAS714TO	CF721573	CCAS714TO	c 345	14.8	82.2	1339	3	CNS0A633	Arabidops
c 273	14.8	82.2	930	4	BG331325	602432061	BG331325	602432061	c 346	14.8	82.2	1339	3	CR674011	Tetraodon
c 274	14.8	82.2	932	9	CG025460	CG025460	CG025460	ZMBBbC056	c 347	14.8	82.2	1341	3	CR664146	Tetraodon
c 275	14.8	82.2	932	9	CG165928	CG165928	CG165928	PUIGH91TD	c 348	14.8	82.2	1346	3	CR657169	Tetraodon
c 276	14.8	82.2	942	4	CNS06XW	T7 end of	AL419898	T7 end of	c 349	14.8	82.2	1357	8	BZ580189	msb2_982
c 277	14.8	82.2	946	4	BG106647	602290476	BG106647	602290476	c 350	14.8	82.2	1371	3	CNS0A50B	Arabidops
c 278	14.8	82.2	948	8	BZ568174	pac82-164	BZ568174	pac82-164	c 351	14.8	82.2	1371	3	CNS0A61I	Arabidops
c 279	14.8	82.2	958	7	CF822320	EST700302	CF822320	EST700302	c 352	14.8	82.2	1390	3	CNS0A4PE	Arabidops
c 280	14.8	82.2	984	2	BF793038	BF793038	BF793038	AGENCOURT	c 353	14.8	82.2	1390	3	CNS0A5XQ	Arabidops
c 281	14.8	82.2	991	9	CNS06XST	AL420147	T7 end of	AL420147	c 354	14.8	82.2	1511	3	CR662153	Tetraodon
c 282	14.8	82.2	992	7	CO020078	EST816171	CO020078	EST816171	c 355	14.8	82.2	1537	3	CR670911	Tetraodon
c 283	14.8	82.2	1001	9	CNS07A3W	CH261-84D	AL436098	T7 end of	c 356	14.8	82.2	1869	3	CR734403	Tetraodon
c 284	14.8	82.2	1007	8	CF245614	CH261-84D	CF245614	CH261-84D	c 357	14.8	82.2	5739	9	AV412184	Mus muscu
c 285	14.8	82.2	1012	7	CF680690	CF680690	CF680690	CCACK95TO	c 358	14.4	80.0	176	2	AW101948	sd81b05.y
c 286	14.8	82.2	1013	4	BM469895	AGENCOURT	BM469895	AGENCOURT	c 359	14.4	80.0	179	9	BX949575	Arabidops
c 287	14.8	82.2	1018	8	BZ563083	pac82-164	BZ563083	pac82-164	c 360	14.4	80.0	213	8	AZ311450	1M0026H20
c 288	14.8	82.2	1024	9	CG165925	PUIGH91TB	CG165925	PUIGH91TB	c 361	14.4	80.0	218	8	CC056654	SALK_1104
c 289	14.8	82.2	1029	8	BZ569608	pac82-164	BZ569608	pac82-164	c 362	14.4	80.0	235	2	B8048331	BB048331
c 290	14.8	82.2	1069	3	CR664976	Tetraodon	CR664976	Tetraodon	c 363	14.4	80.0	239	1	AV010618	AV010618
c 291	14.8	82.2	1081	6	CD506094	CD506094	CD506094	CDA77-D01	c 364	14.4	80.0	244	7	H51023	Y035909.rl
c 292	14.8	82.2	1093	9	CNS05RGO	AL337569	Tetraodon	AL337569	c 365	14.4	80.0	248	2	AW436988	77654 MAR
c 293	14.8	82.2	1098	8	CL237118	ZMBBb058	CL237118	ZMBBb058	c 366	14.4	80.0	249	7	CV415924	RC3-CT041
c 294	14.8	82.2	1101	8	BZ563108	pac82-164	BZ563108	pac82-164	c 367	14.4	80.0	257	7	CO756234	MdfrC3046
c 295	14.8	82.2	1107	3	CR667312	Tetraodon	CR667312	Tetraodon	c 368	14.4	80.0	265	1	AV238596	AV238596
c 296	14.8	82.2	1109	5	BQ679999	AGENCOURT	BQ679999	AGENCOURT	c 369	14.4	80.0	271	1	AI448830	msb43g02.x
c 297	14.8	82.2	1190	3	CR669720	Tetraodon	CR669720	Tetraodon	c 370	14.4	80.0	274	2	BB430321	BB430321
c 298	14.8	82.2	1196	8	BZ569607	pac82-164	BZ569607	pac82-164	c 371	14.4	80.0	285	2	BB370666	BB370666
c 299	14.8	82.2	1200	3	CR659993	Tetraodon	CR659993	Tetraodon	c 372	14.4	80.0	289	2	BB721062	BB721062
c 300	14.8	82.2	1202	3	CR729671	Tetraodon	CR729671	Tetraodon	c 373	14.4	80.0	290	9	AL937634	Arabidops
c 301	14.8	82.2	1205	3	CR669317	Tetraodon	CR669317	Tetraodon	c 374	14.4	80.0	293	2	BF399133	UI-R-CAL-
c 302	14.8	82.2	1205	3	CR726698	Tetraodon	CR726698	Tetraodon	c 375	14.4	80.0	294	2	BB310902	BB310902
c 303	14.8	82.2	1210	3	CR725907	Tetraodon	CR725907	Tetraodon	c 376	14.4	80.0	298	7	CF504172	USDA-FP_1
c 304	14.8	82.2	1213	8	BZ577635	msb2_5503	BZ577635	msb2_5503	c 377	14.4	80.0	299	2	AW307146	sf53d03.y
c 305	14.8	82.2	1215	3	CR657983	Tetraodon	CR657983	Tetraodon	c 378	14.4	80.0	306	2	BB518094	BB518094
c 306	14.8	82.2	1221	3	CR730718	Tetraodon	CR730718	Tetraodon	c 379	14.4	80.0	306	6	BY654785	BY654785
c 307	14.8	82.2	1225	3	CR724213	Tetraodon	CR724213	Tetraodon	c 380	14.4	80.0	307	4	BI398022	NKPV_113
c 308	14.8	82.2	1235	3	CR678259	Tetraodon	CR678259	Tetraodon	c 381	14.4	80.0	311	2	AW909428	uf48f01.x
c 309	14.8	82.2	1237	3	CR678825	Tetraodon	CR678825	Tetraodon	c 382	14.4	80.0	312	1	AV101708	AV101708
c 310	14.8	82.2	1240	3	CR680688	Tetraodon	CR680688	Tetraodon	c 383	14.4	80.0	312	1	BF014710	ro27d08.y
c 311	14.8	82.2	1242	3	CR659500	Tetraodon	CR659500	Tetraodon	c 384	14.4	80.0	315	6	AV318797	AV318797
c 312	14.8	82.2	1247	3	CR670847	Tetraodon	CR670847	Tetraodon	c 385	14.4	80.0	315	6	BY617834	BY617834
c 313	14.8	82.2	1248	3	CR679229	Tetraodon	CR679229	Tetraodon	c 386	14.4	80.0	321	1	AV333596	AV333596
c 314	14.8	82.2	1252	3	CR658850	Tetraodon	CR658850	Tetraodon	c 387	14.4	80.0	321	1	BF013532	ro14h08.y
c 315	14.8	82.2	1255	3	CR680065	Tetraodon	CR680065	Tetraodon	c 388	14.4	80.0	325	2	AW244788	BR-END12F
c 316	14.8	82.2	1256	3	CR667004	Tetraodon	CR667004	Tetraodon	c 389	14.4	80.0	329	9	CL360898	RPC144_34

C 390 14.4 80.0 330 5 BQ300900
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 C 471 14.4 80.0 408 5 B6201617
 C 472 14.4 80.0 409 6 B639482
 C 473 14.4 80.0 410 2 B6137740
 C 474 14.4 80.0 410 6 B626680
 C 475 14.4 80.0 410 6 B649624
 C 476 14.4 80.0 411 6 B621613
 C 477 14.4 80.0 412 6 B624537
 C 478 14.4 80.0 413 8 A2078804
 C 479 14.4 80.0 414 2 AV956455
 C 480 14.4 80.0 414 6 B632689
 C 481 14.4 80.0 415 6 B587679
 C 482 14.4 80.0 415 6 B643163
 C 483 14.4 80.0 416 2 AW985721
 C 484 14.4 80.0 419 9 CG646157
 C 485 14.4 80.0 420 5 B391970
 C 486 14.4 80.0 420 6 B616643
 C 487 14.4 80.0 420 6 B616643
 C 488 14.4 80.0 420 6 B631991
 C 489 14.4 80.0 421 5 B6597878
 C 490 14.4 80.0 421 5 CK739785
 C 491 14.4 80.0 424 6 B699642
 C 492 14.4 80.0 425 2 B6950407
 C 493 14.4 80.0 426 6 B648660
 C 494 14.4 80.0 427 2 B6559829
 C 495 14.4 80.0 427 2 B6557723
 C 496 14.4 80.0 429 2 B6058144
 C 497 14.4 80.0 429 7 CK382785
 C 498 14.4 80.0 430 2 B6716809
 C 499 14.4 80.0 430 7 W57057
 C 500 14.4 80.0 431 2 AW743725

ALIGNMENTS

RESULT 1
 BH794414/C
 LOCUS BH794414.1
 DEFINITION ME MBA0002N14r Manihot esculenta Manihot esculenta genomic clone
 ACCESSION BH794414.1
 VERSION BH794414.1
 KEYWORDS GSS
 SOURCE Manihot esculenta (cassava)
 ORGANISM Manihot esculenta
 Manihot esculenta
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Malpighiales; Euphorbiaceae; Crotonoideae;
 Manihoteae; Manihot.
 1 (bases 1 to 737)
 REFERENCE Tomkins,J.P., Fregene,M., Main,D., Goicoechea,J.L., Blackmon,B.,
 Atkins,M., Tohme,J. and Wing,R.A.
 New Genomic Resources for Cassava (Manihot esculenta): Development
 of a Deep-Coverage BAC Library and Preliminary STC Analysis
 JOURNAL Unpublished (2002)
 COMMENT Contact: Tomkins J
 Clemson University
 100 Jordan Hall,
 Clemson University, Clemson, SC 29634, USA
 Tel: 864 656 6419
 Fax: 864 656 4293
 Email: jtmkns@clemson.edu
 Total High Quality bases = 383
 Seq primer: TAATACGACTCATATAGGG
 Class: BAC ends

High quality sequence start: 130
High quality sequence stop: 737.

FEATURES

source

1. .737
/organism="Manihot esculenta"
/mol_type="genomic DNA"
/strain="MECW72"
/db_xref="taxon:3983"
/clone="ME_MBa0002N14r"
/tissue_type="Leaf"
/lab_host="E. coli"
/clone_lib="Manihot esculenta"
/note="Vector: pCUBAC-1; Site 1: HindIII; Site 2: NotI;
For more details on library preparation and sequence
analysis see
http://www.genome.clemson.edu/projects/stc/cassava/ME_MBa
To order clones from this library see
http://www.genome.clemson.edu/orders "

ORIGIN

Query Match 94.4%; Score 17; DB 8; Length 737;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACCGGAAGTTGAG 17

Db 254 GCCACCGGAAGTTGAG 238
|||||

RESULT 2

LOCUS

CF824029 895 bp mRNA linear EST 01-APR-2004
DEFINITION EST701411 Coccidioides posadasii saprobic phase cDNA library, 2 to 4 kb Coccidioides posadasii cDNA clone CIDAP04 5' end, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Coccidioides posadasii
Coccidioides posadasii
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; Mitosporic Onygenales; Coccidioides.

REFERENCE

AUTHORS

TITLE

Gardner, M.J. and Cole, G.T.
Analysis of gene expression in Coccidioides posadasii mycelia and
spherules via expressed sequence tags

JOURNAL

COMMENT

Other ESTs: EST701410
Contact: Gardner MJ
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208

Email: gardner@tigr.org

Seq primer: M13 Reverse.

FEATURES

source

1. .895
/organism="Coccidioides posadasii"
/mol_type="mRNA"
/strain="C735"
/db_xref="taxon:199306"
/clone="CIDAP04"
/dev_stage="saprobic phase (mycelia)"
/lab_host="E. coli DH10B, T1 phage resistant"
/clone_lib="Coccidioides posadasii saprobic phase cDNA
library, 2 to 4 kb"
/note="Vector: pExpress 1; Site 1: Not I; Site 2: Eco RV;
Coccidioides posadasii saprobic phase cDNA library, size
fractionated cDNA 2 to 4 kb"

ORIGIN

Query Match 94.4%; Score 17; DB 7; Length 895;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;

Matches

QY

2 GCCACCGGAAGTTGAGT 18
|||||

Db

829 GCCACCGGAAGTTGAGT 845
|||||

RESULT 3

LOCUS

AQ492895/c 514 bp DNA linear GSS 28-APR-1999
DEFINITION HS_5126_A2_C06_T7A_RPCI-11 Human Male BAC Library Homo sapiens
Genomic Clone Plate=702 Col=12 Row=E, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AQ492895.1 GI:4691753
Homo sapiens (human)
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 514)

REFERENCE
AUTHORS Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
Hood, L.

Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome

Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589

JOURNAL

MEDLINE

PUBMED

COMMENT

10449764
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Research Genetics (info@resgen.com). BAC end Web Server:
http://www.htac.washington.edu
Plate: 702 row: E column: 12
Seq primer: T7
Class: BAC ends
High quality sequence stop: 514.

FEATURES

source

1. 514
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="plate=702 Col=12 Row=E"
/sex="male"
/clone_lib="RPCI-11 Human Male BAC Library"
/note="Vector: pBACE3.6; Site 1: EcoRI; Site 2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACE3.6 vector at EcoRI sites"

ORIGIN

Query Match 91.1%; Score 16.4; DB 8; Length 514;
Best Local Similarity 94.4%; Pred. No. 6.5e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCACCGGAAGTTGAGT 18

Db 298 GCCACCGGAAGTTGAGT 281
|||||

RESULT 4

LOCUS

BE994137 576 bp mRNA linear EST 29-APR-2002
DEFINITION UI-M-CG0p-bih-d-02-0-UI.s1 NIH_BMAP_Ret4_s2 Mus musculus cDNA clone

UI-M-CG0p-bih-d-02-0-UI 3', mRNA sequence.
 BE994137
 VERSION BE994137.1 GI:10677076
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 576)
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 PubMed 8889548
 COMMENT Contact: Chin, H
 National Institute of Mental Health
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
 20892-9643, USA
 Tel: 301 443 1706
 Fax: 301 443 9890
 Email: mES@mail.nih.gov
 Oligo-dt track not found, Not I site shown in beginning of sequence
 is likely internal to the message. cDNA Library Preparation: M.B.
 Soares Lab Clone distribution: Researchers may obtain BMAP cDNA
 clones from RESEARCH GENETICS. It should be noted that Bento Soares
 is generating a small number of additional specialized
 non-redundant arrays of BMAP cDNAs whose availability will be
 considered under appropriate and limited collaborative arrangements
 The tissue for this library was contributed by Dr. Xin-Yuan Fu,
 Yale University School of Medicine
 Seq primer: M13 Forward
 POLYA=No.

FEATURES
 source
 1..576
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strains="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UI-M-CG0p-bih-d-02-0-UI"
 /lab_host="DH10B (life Technologies)"
 /clone_lib="NIH BMAP Ret4 S2"
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; The
 NIH BMAP Ret4 S2 library is a subcloned library,
 ultimately derived from mouse retina tissue libraries at
 various stages of development. For a detailed description
 of the library from which this clone was derived, please
 visit our web site at brainest.eng.uiowa.edu. The tissue
 for this library was contributed by Dr. Xin-Yuan Fu, Yale
 University School of Medicine
 TAG_SEQ=None found"

ORIGIN
 Query Match 91.1%; Score 16.4; DB 2; Length 576;
 Best Local Similarity 94.4%; Pred. No. 6.5e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CGCCACCGGAGTTGAGT 18
 |||||
 Db 163 CGCCACCGGAGTTGAGT 146
 |||||

RESULT 5
 BP117402/C
 LOCUS BP117402 698 bp mRNA linear EST 03-APR-2003
 DEFINITION BP117402 ce-- Bombyx mori cDNA clone ce--0261, mRNA sequence.
 ACCESSION BP117402
 VERSION BP117402.1 GI:29535560
 KEYWORDS EST.
 SOURCE Bombyx mori (domestic silkworm)
 ORGANISM Bombyx mori
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Query Match 91.1%; Score 16.4; DB 3; Length 1331;
 Best Local Similarity 94.4%; Pred. No. 6.7e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CGCCACCGGAGTTGAGT 18
 |||||
 Db 685 CGCCACCGGAGTTGAGT 668
 |||||

Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 Bombycoidea; Bombycidae; Bombyx.

REFERENCE 1 (bases 1 to 698)
 AUTHORS Mita,K., Morimyo,M., Shimada,T., Okano,K. and Maeda,S.
 TITLE Bombyx mori cDNA (Mita,K. 2003)
 JOURNAL Unpublished (2003)
 COMMENT Contact: Mita K
 Genome Research Group
 National Institute of Agrobiological Sciences
 Otsu 1-2, Tsukuba, Ibaraki 305-8634, Japan
 Email: kmita@nias.affrc.go.jp
 method:uni-directional, sequence direction:sequenced from T3 primer
 (5' -> 3').

FEATURES
 Location/Qualifiers
 1..698
 /organism="Bombyx mori"
 /mol_type="mRNA"
 /db_xref="taxon:7091"
 /clone="ce--0261"
 /tissue_type="compound eye"
 /clone_lib="ce--"
 /note="mixed stages from 5th instar larva to pupa"

ORIGIN
 Query Match 91.1%; Score 16.4; DB 5; Length 698;
 Best Local Similarity 94.4%; Pred. No. 6.6e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CGCCACCGGAGTTGAGT 18
 |||||
 Db 678 CGCCACCGGAGTTGAGT 661
 |||||

RESULT 6
 CR665917/c
 LOCUS CR665917 1331 bp mRNA linear HTC 18-AUG-2004
 DEFINITION Tetraodon nigroviridis full-length cDNA.
 ACCESSION CR665917
 VERSION CR665917.1 GI:51162362
 KEYWORDS HTC; cDNA; full-length; Tetraodon nigroviridis.
 SOURCE Tetraodon nigroviridis
 ORGANISM Tetraodon nigroviridis
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
 Tetraodontidae; Tetraodontidae; Tetraodon.

REFERENCE 1 (bases 1 to 1331)
 Genoscope.
 Direct Submission
 Submitted (10-AUG-2004) Genoscope - Centre National de Sequencage -
 : 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
 The sequences are based on single pass reads.
 More information available at
 http://www.genoscope.cns.fr/tetraodon.

FEATURES
 Location/Qualifiers
 1..1331
 /organism="Tetraodon nigroviridis"
 /mol_type="mRNA"
 /db_xref="taxon:99883"
 /tissue_type="Muscle"

ORIGIN
 Query Match 91.1%; Score 16.4; DB 3; Length 1331;
 Best Local Similarity 94.4%; Pred. No. 6.7e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CGCCACCGGAGTTGAGT 18
 |||||
 Db 685 CGCCACCGGAGTTGAGT 668
 |||||

RESULT 7

LOCUS	BQ559427	480 bp	linear	EST 20-JUN-2002
DEFINITION	H4058B07-5	NIA Mouse 7.4K cDNA Clone Set	Mus musculus	cDNA clone
VERSION	H4058B07	5', mRNA sequence.		
ACCESSION	BQ559427			
KEYWORDS	BQ559427.1	GI:21460312		
SOURCE	EST.			
ORGANISM	Mus musculus	(house mouse)		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 480)			
AUTHORS	VanBuren,V., Piao,Y., Dudekula,D.B., Qian,Y., Carter,M.G., Martin,P.R., Stagg,C.A., Bassey,U., Aiba,K., Hamatani,T., Kargul,G.J., Luo,A.G., Kelo,J., Hide,W. and Ko,M.S.H.			
TITLE	Assembly, verification, and initial annotation of NIA 7.4K mouse cDNA clone set			
JOURNAL	Genome Res. 12 (12), 1999-2003 (2002)			
MEDLINE	22354164			
PUBMED	12466305			
COMMENT	Other ESTs: H4058B07-3 Contact: Yong Qian Laboratory of Genetics National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA Email: cdna@lgun.grc.nia.nih.gov This clone set has been freely distributed to the community. Please visit http://lgun.grc.nia.nih.gov/cDNA/NIA_7_4k.html for details. Plate: H4058 row: B column: 07 Seq primer: -21M13 Reverse High quality sequence stop: 480 POLYA=No.			

```

FEATURES                                Location/Qualifiers
source                                  1..480
    /organism="Mus musculus"
    /mol_type="cDNA"
    /strain="C57BL/6"
    /db_xref="niaEST:H4058B07-5"
    /db_xref="taxon:10090"
    /clone="H4058B07"
    /sex="mixed"
    /dev_stage="mixed"
    /lab_host="DH10B"
    /clone_lib="NIA Mouse 7.4K cDNA Clone Set"
    /notes="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; This
clone is among a rearranged set of 7,407 clones from more
than 20 cDNA libraries."

ORIGIN

Query Match      88.9%; Score 16; DB 5; Length 480;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

TITLE Systematic Analyses of N1A Mouse Trophoblast Stem Cell cDNA Library (Long)

JOURNAL Unpublished (2001)

COMMENT Other ESTs: C0618H12-3
 Contact: Dawood B. Dudekula
 Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
 Email: cdna@lgsun.grc.nia.nih.gov
 Plate: C0618 row: H column: 12
 Seq primer: M13 Reverse
 High quality sequence stop: 539
 POLYA-No.

FEATURES Location/Qualifiers

1..539

 /organism="Mus musculus"

 /mol_type="mRNA"

 /strain="B57/EGFP transgenic ICR mice"

 /db_xref="niaEST:C0618H12-5N"

 /db_xref="taxon:10090"

 /clone="NIA:C0618H12 IMAGE:30021983"

 /issue_type="Trophoblast stem cell"

 /dev_stage="3.5-dpc"

 /lab_host="DH10B"

 /clone_lib="NIA Mouse Trophoblast Stem Cell cDNA Library (Long)"

 /notes="Vector: pSPORT1 (Invitrogen); Site.1: SalI; Site.2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (<http://lgsun.grc.nia.nih.gov/cdna>). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001)). (PMID: 11544199)}. Total RNAs were obtained from Dr. Janet Rossant and Tilo Kunath (Samuel Lunenfeld Research Institute, Canada). Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen].

5'-pGACTAGTTCTAGATCGAGCGCGCCCTTTTTTTTTTTT-3') from 4 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-SalI, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.6 kb. The library was constructed by Yulan Piao (NIA)".

```

ORIGIN                                     by Ivan Fiso (NIA).
Query Match      88.9%; Score 16; DB 6; Length 539;
Best Local Similarity 100.0%; Pred No. 1.le+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GCCACCGGAAGTTGAG 17
          |||||
Db       440 GCCACCGGAAGTTGAG 425

RESULT 9
CF895091/c
LOCUS
DEFINITION    CF895091 linear EST 04-NOV-2003
               A0143H02-5 NIA Mouse Undifferentiated ES Cell cDNA Library (Long 1)
Mus musculus CDNA clone NIA:A0143H02 IMAGE:30727765 5', mRNA
sequence.
ACCESSION     CF895091
VERSION       CF895091.1 GI:38162140
KEYWORDS      EST.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

REFERENCE
AUTHORS
TITLE
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 587)
Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.
Construction of long-transcript enriched cDNA libraries from
submicrogram amounts of total RNAs by a universal PCR amplification
method
Genome Res. 11 (9), 1553-1558 (2001)
21429098
11544199
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@geun.grc.nia.nih.gov
Plate: A0143 row: H column: 02
Seq primer: M13 Reverse
High quality sequence stop: 587
POLYA=No.

FEATURES
source
1. 587
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129/Sv x 129/Sv-Cp"
/db_xref="niaEST:A0143H02-5"
/db_xref="taxon:10090"
/clone="NIA:A0143H02 IMAGE:30727765"
/dev_stage="E1 ES cells"
/lab_host="DH10B"
/clone_lib="NIA Mouse Undifferentiated ES Cell cDNA
Library (long 1)"
/notes="Vector: pCMV-SPORT6 (Invitrogen); Site 1: Sali;
Site 2: NotI; Mouse cDNA project by the Laboratory of
Genetics, National Institute on Aging (NIA), Intramural
Research Program, NIH (http://igsum.grc.nia.nih.gov/cDNA).
This is a long-transcript enriched cDNA library (Ref.
Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total
RNAs were obtained from Dr. Kenneth R. Boheler (National
Institute on Aging, USA). ES cells were cultured without
feeder cells in the presence of LIF and BRL-conditioned
media. Double-stranded cDNAs were synthesized with an
Oligo(dT) primer [Invitrogen:
5'-pGACTAGTCTAGATCGGAGCGCCCTTTT-3'] from
14.2 ug of total RNA, treated with T4 DNA polymerase, and
purified by ethanol-precipitation. The cDNAs were ligated
to Lona-linker IL-Sal4, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Taq polymerase (Takara) with a primer Sal4-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with Sali and NotI enzymes
and cloned into Sali/NotI site of pCMV-SPORT6 plasmid
vector. The DH10B E. coli host was transformed with the
ligation mixture by the standard chemical method. The
average insert size is about 2.4 Kb. The library was
constructed by Yulan Piao."

ORIGIN
Query Match 88.9%; Score 16; DB 7; Length 587;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCACCGGAAGTTGAG 17
|||||
Db 214 GCCACCGGAAGTTGAG 199

RESULT 10
AW338466/c
LOCUS
DEFINITION
xw78h03.x1 NCI CGAP Panl Homo sapiens cDNA clone IMAGE:2834165 3'
similar to SW:ACDV HUMAN P49748 ACYL-COA DEHYDROGENASE,
VERY-LONG-CHAIN SPECIFIC PRECURSOR ;contains Alu repetitive
element;; mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AW338466
AW338466.1 GI:6835092
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 602)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 359.

FEATURES
source
1. 602
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2834165"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/clone_lib="NCI CGAP Panl"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: Sali;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"

ORIGIN
Query Match 88.9%; Score 16; DB 2; Length 602;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCACCGGAAGTTGAGT 18
|||||
Db 564 CCACCGGAAGTTGAGT 549

RESULT 11
AQ447015/c
LOCUS
DEFINITION
mgxb0002M12f CUGI Rice Blast BAC Library Magnaporthe grisea genomic
clone mgxb0002M12f, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AQ447015 604 bp DNA linear GSS 08-APR-1999
clone mgxb0002M12f, genomic survey sequence.
GSS.
Magnaporthe grisea (anamorph: Pyricularia grisea)
Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
1 (bases 1 to 604)
Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
Genome
Unpublished (1998)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: Dean RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seq primer: TAATACGACTCACTATAGG
Class: BAC ends
High quality sequence start: 61

High quality sequence stop: 455.

FEATURES source

```
1. .604
/organism="Magnaporthe grisea"
/mol_type="genomic DNA"
/strain="70-15"
/db_xref="taxon:148305"
/clone="mgxb0002M12f"
/tissue_type="Protoplasts"
/lab_host="E. coli DH10B"
/clone_lib="CUGI Rice Blast RAC Library"
/note="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII;
Rice blast is one of the most devastating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction. In
order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
kbp was constructed. This library represents greater
than 25X genome coverage. High density colony filters
are available upon request."
```

ORIGIN

```
Query Match      88.9%; Score 16; DB 8; Length 604;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCACCGGAAGTTGAGT 18
|||||
Db 558 CCACCGGAAGTTGAGT 543
```

RESULT 12

```
LOCUS      CO430950/c
DEFINITION UI-M-HXO-csc-e-14-0-UI.r1 NIH BMAP_HXO Mus musculus cDNA clone
IMAGE:30685069 5', mRNA sequence.
ACCESSION  CO430950
VERSION     CO430950.1 GI:49677244
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 607)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
```

FEATURES source

```
Seq primer: pYX-5,
Location/Qualifiers
1. .607
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30685069"
/tissue_type="whole eye"
/dev_stage="newborn (1, 5, 15 days) and embryonic (15, 16,
17, 18 dpc)"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH BMAP_HXO"
/note="Organ: Eye; Vector: pYX-Asc; Site_1: EcoR I;
```

Site_2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag is AATAATTACG. This library was created for the polyA tail sequence located between the Not I site and the polyA tail is AATAATTACG. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH)."

ORIGIN

```
Query Match      88.9%; Score 16; DB 7; Length 607;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCACCGGAAGTTGAG 17
|||||
Db 101 GCCACCGGAAGTTGAG 86
```

RESULT 13

```
LOCUS      AW173515/c
DEFINITION xj08a06.x1 NCI CGAP Ut2 Homo sapiens cDNA clone IMAGE:2656594 3',
similar to SW-ACDV HUMAN P49748 ACYL-COA DEHYDROGENASE,
VERY-LONG-CHAIN SPECIFIC PRECURSOR ;, mRNA sequence.
ACCESSION  AW173515
VERSION     AW173515.1 GI:6439463
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 612)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 416.
Location/Qualifiers
1. .612
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2656594"
/tissue_type="moderately-differentiated endometrial
adenocarcinoma, 3 pooled tumors"
/lab_host="DH10B"
/clone_lib="NCI CGAP Ut2"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.85 kb. Life Technologies catalog #:
11539-012"
```

FEATURES source

ORIGIN

```
Query Match      88.9%; Score 16; DB 2; Length 612;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      3 CCACCGGAAGTTGAGT 18
Db      571 CCACCGGAAGTTGAGT 556

RESULT 14
AW173560/c
LOCUS   xj08906.x1 NCI_CGAP Ut2 Homo sapiens cDNA clone IMAGE:2656666 3,
DEFINITION similar to SW:ACDV_HUMAN P49748 ACYL-COA DEHYDROGENASE,
VERY-LONG-CHAIN SPECIFIC PRECURSOR ;, mRNA sequence.
ACCESSION AW173560
VERSION   AW173560.1 GI:6439508
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 614)
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 415.
Location/Qualifiers
1..614
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2656666"
/tissue_type="moderately-differentiated endometrial
adenocarcinoma, 3 pooled tumors"
/lab_host="DH10B"
/clone_lib="NCI_CGAP Ut2"
/Note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.85 kb. Life Technologies catalog #:
11539-012"

FEATURES
source
Query Match 88.9%; Score 16; DB 2; Length 614;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 CCACCGGAAGTTGAGT 18
Db      570 CCACCGGAAGTTGAGT 555

RESULT 15
AW168911/c
LOCUS   xj15b06.x1 NCI_CGAP Ut2 Homo sapiens cDNA clone IMAGE:2657267 3,
DEFINITION similar to SW:ACDV_HUMAN P49748 ACYL-COA DEHYDROGENASE,
VERY-LONG-CHAIN SPECIFIC PRECURSOR ;, mRNA sequence.
ACCESSION AW168911
VERSION   AW168911.1 GI:6400436
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 626)
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 425.
Location/Qualifiers
1..626
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2657267"
/tissue_type="moderately-differentiated endometrial
adenocarcinoma, 3 pooled tumors"
/lab_host="DH10B"
/clone_lib="NCI_CGAP Ut2"
/Note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.85 kb. Life Technologies catalog #:
11539-012"

ORIGIN
Query Match 88.9%; Score 16; DB 2; Length 626;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 CCACCGGAAGTTGAGT 18
Db      565 CCACCGGAAGTTGAGT 550

RESULT 16
AW172834/c
LOCUS   xj04d03.x1 NCI_CGAP Ut2 Homo sapiens cDNA clone IMAGE:2656229 3,
DEFINITION similar to SW:ACDV_HUMAN P49748 ACYL-COA DEHYDROGENASE,
VERY-LONG-CHAIN SPECIFIC PRECURSOR ;, mRNA sequence.
ACCESSION AW172834
VERSION   AW172834.1 GI:6438782
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 627)
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 401.

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FEATURES
source
  Location/Qualifiers
    1. .627
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="IMAGE:2656229"
      /tissue_type="moderately-differentiated endometrial
adenocarcinoma, 3 pooled tumors"
      /lab_host="DH10B"
      /clone_lib="NCI CGAP Ut2"
      /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.85 kb. Life Technologies catalog #:
11539-012"

ORIGIN
Query Match      88.9%; Score 16; DB 2; Length 627;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCACCGGAAGTTGAGT 18
|||||
Db 562 CCACCGGAAGTTGAGT 547

RESULT 17
AI871886/c
LOCUS
DEFINITION
  AI871886 697 bp mRNA linear EST 07-MAR-2000
  wm53a05.x1 NCI CGAP Ut2 Homo sapiens cDNA clone IMAGE:2439632 3'
  similar to SW:ACDV_HUMAN P49748 ACYL-COA DEHYDROGENASE,
  VERY-LONG-CHAIN SPECIFIC PRECURSOR ;, mRNA sequence.
ACCESSION
  AI871886
VERSION
  AI871886.1 GI:5545935
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 697)
AUTHORS
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
JOURNAL
  Unpublished (1997)
COMMENT
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-r@mail.nih.gov
  Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
  Emmert-Buck, M.D., Ph.D.
  cDNA Library Preparation: Life Technologies, Inc.
  DNA Sequencing by: Washington University Genome Sequencing Center
  Clone distribution: NCI-CGAP clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  www-bio.llnl.gov/bbrp/image/image.html
  Insert Length: 1198 Std Error: 0.00
  Seq primer: -40UP from Gibco
  High quality sequence stop: 414.
  Location/Qualifiers
    1. .697
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="IMAGE:2439632"
      /tissue_type="moderately-differentiated endometrial
adenocarcinoma, 3 pooled tumors"
      /lab_host="DH10B"
      /clone_lib="NCI CGAP Ut2"
      /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.85 kb. Life Technologies catalog #:
11539-012"

ORIGIN
Query Match      88.9%; Score 16; DB 1; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FEATURES
source
  Location/Qualifiers
    1. .627
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="IMAGE:2439632"
      /tissue_type="moderately-differentiated endometrial
adenocarcinoma, 3 pooled tumors"
      /lab_host="DH10B"
      /clone_lib="NCI CGAP Ut2"
      /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.85 kb. Life Technologies catalog #:
11539-012"

ORIGIN
Query Match      88.9%; Score 16; DB 1; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FEATURES
source
  Location/Qualifiers
    1. .627
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="IMAGE:2439632"
      /tissue_type="moderately-differentiated endometrial
adenocarcinoma, 3 pooled tumors"
      /lab_host="DH10B"
      /clone_lib="NCI CGAP Ut2"
      /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.85 kb. Life Technologies catalog #:
11539-012"

ORIGIN
Query Match      88.9%; Score 16; DB 1; Length 707;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCACCGGAAGTTGAGT 18
|||||
Db 568 CCACCGGAAGTTGAGT 553

RESULT 19
CB244514/c
LOCUS
DEFINITION
  CB244514 736 bp mRNA linear EST 09-JUL-2003
  UI-M-FY0-cdq-1-20-0-UI.r1 NIH BMAP_FY0 Mus musculus cDNA clone
  IMAGE:6833085 5', mRNA sequence.
ACCESSION
  CB244514
VERSION
  CB244514.1 GI:28366158
KEYWORDS
  EST.
SOURCE
  Mus musculus (house mouse)

```

```

FEATURES
source
  Location/Qualifiers
    1. .627
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="IMAGE:2439632"
      /tissue_type="moderately-differentiated endometrial
adenocarcinoma, 3 pooled tumors"
      /lab_host="DH10B"
      /clone_lib="NCI CGAP Ut2"
      /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.85 kb. Life Technologies catalog #:
11539-012"

ORIGIN
Query Match      88.9%; Score 16; DB 1; Length 707;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCACCGGAAGTTGAGT 18
|||||
Db 564 CCACCGGAAGTTGAGT 549

RESULT 18
AI884543/c
LOCUS
DEFINITION
  AI884543 707 bp mRNA linear EST 07-MAR-2000
  wm34a04.x1 NCI CGAP Ut4 Homo sapiens cDNA clone IMAGE:2437806 3'
  similar to SW:ACDV_HUMAN P49748 ACYL-COA DEHYDROGENASE,
  VERY-LONG-CHAIN SPECIFIC PRECURSOR ;, mRNA sequence.
ACCESSION
  AI884543
VERSION
  AI884543.1 GI:5589707
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 707)
AUTHORS
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
JOURNAL
  Unpublished (1997)
COMMENT
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-r@mail.nih.gov
  Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
  Emmert-Buck, M.D., Ph.D.
  cDNA Library Preparation: Life Technologies, Inc.
  DNA Sequencing by: Washington University Genome Sequencing Center
  Clone distribution: NCI-CGAP clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  www-bio.llnl.gov/bbrp/image/image.html
  Insert Length: 1252 Std Error: 0.00
  Seq primer: -40UP from Gibco
  High quality sequence stop: 410.
  Location/Qualifiers
    1. .707
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="IMAGE:2437806"
      /tissue_type="serous papillary carcinoma, high grade, 2
pooled tumors"
      /lab_host="DH10B"
      /clone_lib="NCI CGAP Ut4"
      /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.48 kb. Life Technologies catalog #:
11542-016"

ORIGIN
Query Match      88.9%; Score 16; DB 1; Length 707;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCACCGGAAGTTGAGT 18
|||||
Db 568 CCACCGGAAGTTGAGT 553

RESULT 19
CB244514/c
LOCUS
DEFINITION
  CB244514 736 bp mRNA linear EST 09-JUL-2003
  UI-M-FY0-cdq-1-20-0-UI.r1 NIH BMAP_FY0 Mus musculus cDNA clone
  IMAGE:6833085 5', mRNA sequence.
ACCESSION
  CB244514
VERSION
  CB244514.1 GI:28366158
KEYWORDS
  EST.
SOURCE
  Mus musculus (house mouse)

```

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 736)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strauberg, Ph.D.
Email: gsapbs@email.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer: pYX-5.

FEATURES
source

Location/Qualifiers

1..736
/organism="Mus musculus"
/mol_type="mrna"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6833085"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,15.5,17.5dpc"
/lab_host="DH10B (TI phage resistant)"
/clone_lib="NIH BMAP_FY0"
/notes="Organ: Brain; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to BonaIto, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is ACCGACACG. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Heming Chin, Ph.D., program coordinator."

ORIGIN

Query Match 88.9%; Score 16; DB 6; Length 736;
Best Local Similarity 100.0%; Pred. NO. 1.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GCCACCGGAAGTTGAG 17
|||||
Db 438 GCCACCGGAAGTTGAG 423

RESULT 20
CNS0088X/c
LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR16G18 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Drosophila melanogaster (fruit fly)
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 823)
Genoscope.
Direct Submission

REFERENCE
AUTHORS
TITLE

JOURNAL

COMMENT

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : secref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammose in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source

Location/Qualifiers
1..823
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR16G18"
/clone_lib="RPCI-98"
/note="end : TET3"

ORIGIN

Query Match 88.9%; Score 16; DB 9; Length 823;
Best Local Similarity 100.0%; Pred. NO. 1.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGCCACCGGAAGTTGA 16
|||||
Db 418 CGCCACCGGAAGTTGA 403

RESULT 21

CNS00CQ0

LOCUS

DEFINITION

Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR24G05 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Drosophila melanogaster (fruit fly)
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 897)
Genoscope.
Direct Submission

REFERENCE

AUTHORS

TITLE

JOURNAL

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : secref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammose in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

Location/Qualifiers


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source
1. .897
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/mol_type="genomic DNA"
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/clonelib="BACR24G05"
/clonelib="RPCL-98"
/note="end : TET3"

ORIGIN
Query Match      88.9%; Score 16; DB 9; Length 897;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGA 16
Db 372 CGCCACCGGAAGTTGA 387

RESULT 22
AK040525/c
LOCUS
DEFINITION
Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched
library, clone:A430105D10 product:hypothetical protein, full insert
sequence.
ACCESSION
AK040525
VERSION
AK040525.1 GI:26087907
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
PUBMED
10349636
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
PUBMED
11042159
3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kusunagi, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
PUBMED
11076861
4
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 695-690 (2001)
5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 4639)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Oheato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUN-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration and Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,
URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/

FEATURES
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1. .4639
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM DB:A430105D10"
/db_xref="taxon:10090"
/clonelib="A430105D10"
/tissue_type="thymus"
/clonelib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="0 day neonate"
1. .4639
/note="hypothetical protein (evidence: rscds)"

ORIGIN
Query Match      88.9%; Score 16; DB 3; Length 4639;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCACCGGAAGTTGAG 17
Db 830 GCCACCGGAAGTTGAG 815

RESULT 23
CG474564/c
LOCUS
DEFINITION
Mus musculus 129Sv/Ev Mus musculus cDNA clone OST2570, mRNA
sequence.
ACCESSION
CG474564
VERSION
CG474564.1 GI:37225453
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 83)
Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,
Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,
Key, B.W., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,
Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,
Zhu, Q., Person, C. and Sands, A.T.
Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
Contact: Zambrowicz BP

```

OmniBank
 Lexicon Genetics Incorporated
 4000 Research Forest Drive, The Woodlands, TX 77381, USA
 Email: materials@lexgen.com
 Gene trap sequence tag generated by 3' RACE from mouse ES cells as
 described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
 Class: Gene Trap.

FEATURES

source
 Location/Qualifiers
 1..83
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="129Sv/Ev"
 /db_xref="taxon:10090"
 /clone="OST2570"
 /cell_type="embryonic stem cell"
 /clone_lib="Mus musculus 129Sv/Ev"

ORIGIN

Query Match 85.6%; Score 15.4; DB 9; Length 83;
 Best Local Similarity 94.1%; Pred. No. 2.2e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17
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 Db 36 CGTCACCGGAAGTTGAG 20

RESULT 24

CW510696 138 bp DNA linear GSS 06-OCT-2004
 LOCUS Cot678.D17.077.G1.Ta001 Triticum aestivum High-cot Triticum
 DEFINITION aestivum genomic, genomic survey sequence.
 ACCESSION CW510696
 VERSION CW510696.1 GI:53840202
 KEYWORDS GSS.

SOURCE Triticum aestivum (bread wheat)

ORGANISM
 Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Triticum.

REFERENCE 1 (bases 1 to 138)

AUTHORS Gao, W. and Bennetzen, J. L.
 TITLE High Cot sequence analysis of the wheat genome
 JOURNAL Unpublished (2004)
 COMMENT Contact: Bennetzen JL
 Department of Genetics
 University of Georgia
 1057 Green Street, Athens, GA 30602, USA
 Tel: 706 542 9729
 Fax: 706 583 0972
 Email: maize@uga.edu
 Class: High-Cot.

FEATURES

source
 Location/Qualifiers
 1..138
 /organism="Triticum aestivum"
 /mol_type="genomic DNA"
 /cultivar="Chinese Spring"
 /db_xref="taxon:4565"
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 /note="Organ: Seedling; Vector: PCR4-TOPO; Wheat genomic
 DNA was Sheared to fragments averaging about 1.8 kb,
 denatured and then reassociated in phosphate buffer at
 650C. After a given Cot value was reached, aliquots were
 run through a hydroxyapatite (HAP) column in order to
 separate single stranded DNA from double stranded DNA. The
 single stranded DNA was then converted to a double
 stranded form with one round of Klenow DNA polymerase
 treatment with random 6-mer primers. The double-stranded
 fragments were then further size-selected through a column
 and cloned into the PCR4-TOPO vector"

ORIGIN

Query Match 85.6%; Score 15.4; DB 9; Length 138;

Best Local Similarity 94.1%; Pred. No. 2.2e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17
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 Db 21 CGCCACCGGAAGTTGAG 37

RESULT 25

CW510353 140 bp DNA linear GSS 06-OCT-2004
 LOCUS Cot678.D17.077.b1.Ta001 Triticum aestivum High-cot Triticum
 DEFINITION aestivum genomic, genomic survey sequence.
 ACCESSION CW510353
 VERSION CW510353.1 GI:53839859
 KEYWORDS GSS.

SOURCE Triticum aestivum (bread wheat)

ORGANISM
 Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Triticum.

REFERENCE 1 (bases 1 to 140)

AUTHORS Gao, W. and Bennetzen, J. L.
 TITLE High Cot sequence analysis of the wheat genome
 JOURNAL Unpublished (2004)
 COMMENT Contact: Bennetzen JL
 Department of Genetics
 University of Georgia
 1057 Green Street, Athens, GA 30602, USA
 Tel: 706 542 9729
 Fax: 706 583 0972
 Email: maize@uga.edu
 Class: High-Cot.

FEATURES

source
 Location/Qualifiers
 1..140
 /organism="Triticum aestivum"
 /mol_type="genomic DNA"
 /cultivar="Chinese Spring"
 /db_xref="taxon:4565"
 /clone_lib="Triticum aestivum High-cot"
 /note="Organ: Seedling; Vector: PCR4-TOPO; Wheat genomic
 DNA was Sheared to fragments averaging about 1.8 kb,
 denatured and then reassociated in phosphate buffer at
 650C. After a given Cot value was reached, aliquots were
 run through a hydroxyapatite (HAP) column in order to
 separate single stranded DNA from double stranded DNA. The
 single stranded DNA was then converted to a double
 stranded form with one round of Klenow DNA polymerase
 treatment with random 6-mer primers. The double-stranded
 fragments were then further size-selected through a column
 and cloned into the PCR4-TOPO vector"

ORIGIN

Query Match 85.6%; Score 15.4; DB 9; Length 140;
 Best Local Similarity 94.1%; Pred. No. 2.2e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17
 ||| ||||| ||||| |||||
 Db 106 CGCCACCGGAAGTTGAG 90

RESULT 26

BW540688/c 258 bp mRNA linear EST 31-AUG-2004
 LOCUS BW540688 Yutaka Satou unpublished cDNA library (cstb) Clona
 DEFINITION savigny cDNA clone cstb013k24 5', mRNA sequence.
 ACCESSION BW540688
 VERSION BW540688.1 GI:51720539
 KEYWORDS EST.

SOURCE Clona savignyi

ORGANISM
 Clona savignyi
 Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;

```

REFERENCE
1 (bases 1 to 258)
AUTHORS
Satou, Y. and Satoh, N.
TITLE
Expressed genes in Ciona savignyi
JOURNAL
Unpublished (2004)
COMMENT
Contact: Yutaka Satou
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto 606-8502, Japan
Tel: 81-75-753-4095
Fax: 81-75-705-1113
Email: yutaka@ascidian.zool.kyoto-u.ac.jp.

FEATURES
source
Location/Qualifiers
1..258
/organism="Ciona savignyi"
/mol_type="mRNA"
/db_xref="taxon:51511"
/clone="cstb013k24"
/dev_stage="tailbud stage"
/clone_lib="Yutaka Satou unpublished cDNA library (cstb)"

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Best Local Similarity 94.1%; Pred. No. 2.2e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17
|||||
Db 203 CGCCACCGGAAGTTGAG 187

RESULT 27
BM500789
LOCUS
332 bp mRNA linear EST 14-FEB-2002
DEFINITION
PAC000000000174 Pioneer AF-1 array Zea mays cDNA, mRNA sequence.
ACCESSION
BM500789
VERSION
BM500789.1 GI:18666297
KEYWORDS
EST.
SOURCE
Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 332)
Hunter, B.G., Beatty, M., Singletary, G., Hamaker, B., Larkins, B.A. and
Jung, R.

TITLE
Maize opaque endosperm mutations create extensive changes in
patterns of gene expression
JOURNAL
Unpublished (2002)
COMMENT
Contact: Jung R
Trait and Technology Development, Food and Feed Research
Pioneer Hi-Bred International, Inc.
7300 NW 62nd Ave., P.O. Box 1004, Johnston, IA 50131-1004, USA
Tel: 515 270 5934
Fax: 515 254 2619
Email: rudolf.jung@pioneer.com.

FEATURES
source
Location/Qualifiers
1..332
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="taxon:4577"
/clone_lib="Pioneer AF-1 array"

ORIGIN
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Best Local Similarity 94.1%; Pred. No. 2.2e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17
|||||
Db 279 CGCCACCGGAAGTTGAG 295

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RESULT 28
BY660181/c
LOCUS
DEFINITION
Rathke's pouches Mus musculus cDNA clone K720001K04 3', mRNA
sequence.
ACCESSION
BY660181
VERSION
BY660181.1 GI:27028659
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 357)
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,
Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,
Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,
Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,
Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,
Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,
Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,
Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,
Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
Wells, C., Wilming, L.G., Wyshaw-Boris, A., Yanagisawa, M., Yang, I.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
22354683
12456851
Contact: Yoshihide Hayashizaki
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The Institute of Physical and Chemical Research (RIKEN)
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
Hayashizaki, Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken

```

Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Michelle Brinkmeier and Sally Camper (Dept. Human Genetics University of Michigan Medical School 4301 MSRB 3 1500 W. Medical Center Dr. Ann Arbor, MI 48109-0638 USA) whose assistance we gratefully acknowledge.
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES

source

Location/Qualifiers

1..357

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="K72000LK04"

/tissue_type="Rathke's pouches"

/dev_stage="14.5 days embryo RP+/+"

/clone_lib="RIKEN full-length enriched, 14.5 days embryo RP+/+ Rathke's pouches"

ORIGIN

Query Match 85.6%; Score 15.4; DB 6; Length 357;

Best Local Similarity 94.1%; Pred. NO. 2.2e+03;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGTTGAG 17

Db 138 CGCCACTGGAGTTGAG 122

RESULT 29

D69844

LOCUS

DEFINITION CELK09209F Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA clone yk9299 5', mRNA sequence.

ACCESSION D69844

VERSION D69844.1

KEYWORDS EST.

SOURCE Caenorhabditis elegans

ORGANISM Caenorhabditis elegans

REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Pelodierinae; Caenorhabditis.

AUTHORS Kohara.Y., Mitsuki.H., Nishigaki.A., Motohashi.T., Sugimoto.A. and Tabara.H.

TITLE Toward an expression map of the C.elegans genome

JOURNAL Unpublished (1994)

COMMENT Contact: Yuji Kohara

Genome Biology Lab.

National Institute of Genetics

Yata 1111, Mishima, Shizuoka 411, Japan

Tel: 81-559-81-6854

Fax: 81-559-81-6855

Email: ykohara@lab.nig.ac.jp.

FEATURES

source

Location/Qualifiers

1..360

/organism="Caenorhabditis elegans"

/mol_type="mRNA"

/strain="CB1489 him-8(e1489)"

/db_xref="taxon:6239"

/clone="yk9299"

/sex="hermaphrodite, male"

/tissue_type="whole animal"

/dev_stage="varied"

/clone_lib="Yuji Kohara unpublished cDNA"

ORIGIN

Query Match 85.6%; Score 15.4; DB 7; Length 360;

Best Local Similarity 88.9%; Pred. NO. 2.2e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGTTGAGT 18

|||||

Db 323 CGCCACCGGAGCTGAGT 340

RESULT 30

CK119645/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

1 (bases 1 to 371)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Birgit Kersten

Plant Protein Chip Group, Department Lehrach

Max-Planck-Institute for Molecular Genetics

Innestr. 73 D-14195 Berlin, Germany

Tel: +49(0)30/84131648

Fax: +49(0)30/84131128

Email: Kersten@molgen.mpg.de

Insert Length: 371 Std Error: 0.00

Plate: 211 row: F column: 22

Seq primer: PQE65

Location/Qualifiers

1..371

/organism="Arabidopsis thaliana"

/mol_type="mRNA"

/ecotype="Columbia"

/db_xref="GABI:953887"

/db_xref="taxon:3702"

/clone="MPMGp2011P22211"

/tissue_type="inflorescence meristem"

/dev_stage="about one week after bolting"

/lab_host="E. coli SCS-1/pSE111"

/clone_lib="AtcM1"

/note="Vector: PQE-3ONAST-attB (AV386205); Site_1: SalI;

Site_2: NotI; About 1 week after bolting, cDNA synthesis

using SuperscriptTM-System (Invitrogen) with an

oligo(dT)-primer containing NotI restriction site and a

SalI adapter. The main library (plate numbers begin with

1) of 38,000 clones was rearrayed into the sublibrary

(plate numbers begin with 201) containing 5,000 putative

expression clones. Average insert size is 1 kb. Note: The

rearrayed sublibrary (plate numbers begin with 201) was

sequenced. Library generation and sequencing was granted

in context of GABI-LAPP; data are also accessible at

<https://gabi.rzpd.de>

ORIGIN

Query Match

Best Local Similarity

Matches

QY

Db

RESULT 31

BY612625/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

1 (bases 1 to 371)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Birgit Kersten

Plant Protein Chip Group, Department Lehrach

Max-Planck-Institute for Molecular Genetics

Innestr. 73 D-14195 Berlin, Germany

Tel: +49(0)30/84131648

Fax: +49(0)30/84131128

Email: Kersten@molgen.mpg.de

Insert Length: 371 Std Error: 0.00

Plate: 211 row: F column: 22

Seq primer: PQE65

Location/Qualifiers

1..371

/organism="Arabidopsis thaliana"

/mol_type="mRNA"

/ecotype="Columbia"

/db_xref="GABI:953887"

/db_xref="taxon:3702"

/clone="MPMGp2011P22211"

/tissue_type="inflorescence meristem"

/dev_stage="about one week after bolting"

/lab_host="E. coli SCS-1/pSE111"

/clone_lib="AtcM1"

/note="Vector: PQE-3ONAST-attB (AV386205); Site_1: SalI;

Site_2: NotI; About 1 week after bolting, cDNA synthesis

using SuperscriptTM-System (Invitrogen) with an

oligo(dT)-primer containing NotI restriction site and a

SalI adapter. The main library (plate numbers begin with

1) of 38,000 clones was rearrayed into the sublibrary

(plate numbers begin with 201) containing 5,000 putative

expression clones. Average insert size is 1 kb. Note: The

rearrayed sublibrary (plate numbers begin with 201) was

sequenced. Library generation and sequencing was granted

in context of GABI-LAPP; data are also accessible at

<https://gabi.rzpd.de>

KEYWORDS

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 388)
 Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaide, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brueic, V., Chochia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., Mckenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 22354683
 12466851
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/
 Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission
 Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Tissues were provided by Michela Fagioli and Takao K. Hensch (Laboratory for Neuronal Circuit Development Brain Science Institute RIKEN 2-1 Hiroawa, Wako-shi, Saitama 351-0198 Japan) whose assistance we gratefully acknowledge.
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for

further details.

FEATURES source

Location/Qualifiers
 1..388
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="K23033P10"
 /tissue type="visual cortex"
 /clone_lib="RIKEN full-length enriched, visual cortex"

ORIGIN

Query Match 85.6%; Score 15.4; DB 6; Length 388;
 Best Local Similarity 94.1%; Pred. NO. 2.2e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CGCCACCGAAGTTGAG 17
 DB 172 CGCCACTGGAAGTTGAG 156

RESULT 32

CV240627/c

LOCUS

CV240627
 WS0251.B21.O12 PT-MB-N-A-15 Populus balsamifera subsp. trichocarpa
 cDNA clone WS0251_O12 3', mRNA sequence.

ACCESSION

CV240627

VERSION

CV240627.1 GI:52493602

KEYWORDS

EST.

SOURCE

Populus balsamifera subsp. trichocarpa (Populus trichocarpa)

ORGANISM

Populus balsamifera subsp. trichocarpa

REFERENCE

Ralph, S., Cooper, D., Kolosova, N., Oddy, C., Butterfield, Y., Kirkpatrick, R., Liu, J., Palmquist, D., Scott, J., Barber, S., Yang, G., Babakaiff, R., Brown-John, M., Chand, S., Featherstone, R., Masson, A., Mayo, M., Moran, J., Olson, T., Wong, D., Ritland, C.E., Siddiqui, A., Holt, R., Jones, S., Marra, M., Ellis, B.E., Douglas, C., Ritland, K. and Bohlmann, J.
 The poplar transcriptome: Analysis of expressed sequence tags from multiple cDNA libraries
 Unpublished (2004)
 Contact: Joerg Bohlmann
 Genome BC forest genomics program
 University of British Columbia
 UBC Biotechnology Laboratory, 6174 University Boulevard, Rm. 237,
 Vancouver, British Columbia, Canada, V6T 1Z3
 Tel: 1-604-822-0282
 Fax: 1-604-822-6097
 Email: bohlmann@interchange.ubc.ca
 Plate: WS0251 row: O column: 12
 High quality sequence stop: 392
 POLYA=Yes.

TITLE

The poplar transcriptome: Analysis of expressed sequence tags from multiple cDNA libraries

JOURNAL

Unpublished (2004)

COMMENT

Contact: Joerg Bohlmann

Genome BC forest genomics program

University of British Columbia

UBC Biotechnology Laboratory, 6174 University Boulevard, Rm. 237,

Vancouver, British Columbia, Canada, V6T 1Z3

Tel: 1-604-822-0282

Fax: 1-604-822-6097

Email: bohlmann@interchange.ubc.ca

Plate: WS0251 row: O column: 12

High quality sequence stop: 392

POLYA=Yes.

FEATURES

source

Location/Qualifiers
 1..392
 /organism="Populus balsamifera subsp. trichocarpa"
 /mol_type="mRNA"
 /cultivar="Wild clone"
 /sub_species="trichocarpa"
 /db_xref="taxon:3694"
 /clone="WS0251_O12"
 /sex="Male"
 /lab_host="E. coli DH10B T1 phage resistant cells"
 /clone_lib="PT-MB-N-A-15"
 /note=vector: pBluescript II SK (+) XR; Site 1: EcoRI (5' end of cDNA); Site 2: XhoI (3' end of cDNA); Terminal
 vegetative buds from 20 year old trees harvested near
 Corvallis, Oregon on September 19th, 2001. cDNA was
 prepared from 5 micrograms of mRNA and directionally
 ligated into the pBluescript II SK (+) XR vector using the
 pBluescript II XR cDNA Library Construction Kit according

to manufacturer's instructions with modifications (Stratagene). Plasmid DNA was then transformed by electroporation into DH10B cells (Invitrogen) for propagation. Normalization was applied according to Published methods [Bonaldo M.F. et al. (1996) Genome Research 6(9):791] in order to reduce the abundance of highly expressed transcripts."

ORIGIN

Query Match 85.6%; Score 15.4; DB 7; Length 392;
 Best Local Similarity 94.1%; Pred. No. 2.2e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17
 |||||
 Db 355 CGCCACCGGAAGTTGAG 339

RESULT 33
 CA662270/c

LOCUS

DEFINITION

CA662270 400 bp mRNA linear EST 24-NOV-2002
 wlmk1.pk0013.h6 wlmk1 Triticum aestivum cDNA clone wlmk1.pk0013.h6
 5' end, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Triticum aestivum (bread wheat)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Triticum.

REFERENCE

AUTHORS

Tingley, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z.,
 Miao, G., Caraher, N. and Hanafey, M.K.

TITLE

JOURNAL

COMMENT

DuPont Wheat cDNA Sequence
 Unpublished (2002)
 Contact: Scott V. Tingley
 Crop Genetics
 E. I. DuPont de Nemours and Company
 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
 Tel: 302-631-2602
 Fax: 302-631-2607
 Email: Scott.V.Tingley@USA.dupont.com
 Seq primer: M13.

FEATURES

Location/Qualifiers

1..400
 /organism="Triticum aestivum"
 /mol_type="mRNA"
 /cultivar="Stephens"
 /db_xref="taxon:4565"
 /clone="wlmk1.pk0013.h6"
 /tissue_type="leaf"
 /clone_lib="wlmk1"
 /note="Vector: Lambda Zap; Site 1: EcoRI; Site 2: XhoI;
 wheat (Triticum aestivum L.) seedlings 1 hr after
 inoculation with Erysiphe graminis f. sp tritici and
 treatment with
 6-iodo-3-propyl-2-propyloxy-4(3H)-quinazolinone"

ORIGIN

Query Match 85.6%; Score 15.4; DB 6; Length 400;
 Best Local Similarity 88.9%; Pred. No. 2.2e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18
 |||||
 Db 333 CGCCACCGGAAGTTGAGT 316

RESULT 34
 AV798486

LOCUS

DEFINITION

CA662270 430 bp mRNA linear EST 29-MAR-2002
 wlmk1.pk0013.h6 wlmk1 Triticum aestivum cDNA clone wlmk1.pk0013.h6
 5' end, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Triticum aestivum (bread wheat)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Triticum.

REFERENCE

AUTHORS

Tingley, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z.,
 Miao, G., Caraher, N. and Hanafey, M.K.

TITLE

JOURNAL

COMMENT

DuPont Wheat cDNA Sequence
 Unpublished (2002)
 Contact: Scott V. Tingley
 Crop Genetics
 E. I. DuPont de Nemours and Company
 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
 Tel: 302-631-2602
 Fax: 302-631-2607
 Email: Scott.V.Tingley@USA.dupont.com
 Seq primer: M13.

FEATURES

Location/Qualifiers

1..430
 /organism="Triticum aestivum"
 /mol_type="mRNA"
 /db_xref="taxon:4565"
 /clone="wlmk1.pk0013.h6"
 /dev_stage="plants at various developmental stages from
 germination to mature seeds"
 /lab_host="DH10B"
 /clone_lib="RAFL9"
 /note="Site 1: BamHI; Site 2: SalI; subjected to
 dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24
 hr) treatments"

ORIGIN

Query Match 85.6%; Score 15.4; DB 1; Length 430;
 Best Local Similarity 94.1%; Pred. No. 2.3e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17
 |||||
 Db 262 CGCCACCGGAAGTTGAG 278

RESULT 35
 CE271971

LOCUS

DEFINITION

tigr-gss-dog-17000333558770 Dog Library Canis familiaris genomic,
 genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Canis familiaris (dog)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE

AUTHORS

Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
 Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
 Venter, J.C.

TITLE

JOURNAL

MEDLINE

The dog genome: survey sequencing and comparative analysis
 Science 301 (5641), 1898-1903 (2003)
 22875432

mRNA sequence.

AV798486

AV798486.1 GI:19832469

EST.

Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosid II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE

AUTHORS

Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,
 Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,
 Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.
 and Shinozaki, K.

TITLE

JOURNAL

COMMENT

Large scale analysis of Arabidopsis full-length cDNA (2002b)
 Unpublished (2002)

Contact: Motoaki Seki
 Plant Functional Genomics Research Group
 RIKEN Genomic Sciences Center
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: 81-298-36-4359
 Fax: 81-298-36-9060
 Email: msekic@rken.go.jp

An Arabidopsis full-length cDNA library was constructed essentially
 as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
 and XhoI was ligated to modified Lambda FLIC-1 vector (Carninci et
 al., submitted for publication) digested with BamHI and SalI. This
 clone is in a modified pBluescript vector. Please visit our web
 site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
 details.

FEATURES

Location/Qualifiers

1..430
 /organism="Arabidopsis thaliana"
 /mol_type="mRNA"
 /db_xref="taxon:3702"
 /clone="RAFL09-16-G21"
 /dev_stage="plants at various developmental stages from
 germination to mature seeds"
 /lab_host="DH10B"
 /clone_lib="RAFL9"
 /note="Site 1: BamHI; Site 2: SalI; subjected to
 dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24
 hr) treatments"

ORIGIN

Query Match 85.6%; Score 15.4; DB 1; Length 430;
 Best Local Similarity 94.1%; Pred. No. 2.3e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17
 |||||
 Db 262 CGCCACCGGAAGTTGAG 278

RESULT 35
 CE271971

LOCUS

DEFINITION

tigr-gss-dog-17000333558770 Dog Library Canis familiaris genomic,
 genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Canis familiaris (dog)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE

AUTHORS

Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
 Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
 Venter, J.C.

TITLE

JOURNAL

MEDLINE

The dog genome: survey sequencing and comparative analysis
 Science 301 (5641), 1898-1903 (2003)
 22875432

14512627
 PUBMED
 COMMENT
 Contact: Kirkness EF
 The Institute for Genomic Research
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
 Rockville, MD 20850, USA
 Tel: 301-838-0200
 Fax: 301-838-0208
 Email: ekirknes@tigr.org
 Class: shotgun.

FEATURES
 source
 1..432
 /organism="Canis familiaris"
 /mol_type="genomic DNA"
 /strain="Standard Poodle"
 /db_xref="taxon:9615"
 /clone_lib="Dog Library"
 /notes="Site 1: BstXI; Libraries were prepared from
 peripheral blood"

ORIGIN
 Query Match 85.6%; Score 15.4; DB 9; Length 432;
 Best Local Similarity 94.1%; Pred. No. 2.3e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17
 |||||
 Db 219 CGCCCGCGGAAGTTGAG 235

RESULT 36
 AZ738118/c
 LOCUS
 DEFINITION
 RPCI-24-102J15.TVB RPCI-24 Mus musculus genomic clone
 RPCI-24-102J15, genomic survey sequence.

ACCESSION
 AZ738118
 VERSION
 AZ738118.1 GI:12506903
 KEYWORDS
 GSS.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 446)
 Zhao, S., Nieman, W., Malek, J., Shatsman, S., Akinret, B., Levins, M.,
 Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E.,
 Russell, D., de Jong, P., and Fraser, C.M.
 Mouse BAC End Sequences from Library RPCI-24
 Unpublished (1999)
 Other_GSSs: RPCI-24-102J15.TVB
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the mouse BAC library RPCI-24. For BAC
 library availability, please contact Pieter de Jong
 {pdejong@mail.cho.org}. Clones may be purchased from BACPAC
 Resources (<http://www.choi.org/bacpac/orderingframe.htm>). BAC end
 page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
 Plate: 102 row: J column: 15
 Seq primer: T7
 Class: BAC ends.

FEATURES
 source
 1..446
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone_lib="RPCI-24-102J15"
 /sex="Male"
 /cell_type="Spleen/Brain"
 /clone_lib="RPCI-24"

/note="Vector: pTARBAC1; Site 1: BamHI; Site 2: BamHI;
 RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
 library was cloned in the pTARBAC1 cloning vector at the
 BamHI sites using MboI partially digested male C57BL/6J
 DNA."

ORIGIN
 Query Match 85.6%; Score 15.4; DB 8; Length 446;
 Best Local Similarity 94.1%; Pred. No. 2.3e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCACCGGAAGTTGAGT 18
 |||||
 Db 333 GCCACCTGAAGTTGAGT 317

RESULT 37
 CD986497/c
 LOCUS
 DEFINITION
 QAN22e08.Yg QAN Zea mays CDNA clone QAN22e08, mRNA sequence.
 ACCESSION
 CD986497
 VERSION
 CD986497.1 GI:32846816
 KEYWORDS
 EST.
 SOURCE
 Zea mays
 ORGANISM
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 451)
 Genoplate.
 AUTHORS
 Genoplate, a major partnership french program in plant genomics
 TITLE
 Unpublished (2003)
 JOURNAL
 COMMENT
 Contact: Genoplate
 Genoplate
 93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00
 Fax: 33 1 69 47 54 10
 This sequence has been generated in the framework of the french
 plant genomics programme 'Genoplate' (<http://www.genoplate.com>
 and <http://genoplate-info.infobiogen.fr>).

FEATURES
 source
 1..451
 /organism="Zea mays"
 /mol_type="mRNA"
 /cultivar="P2"
 /db_xref="taxon:4577"
 /clone="QAN22e08"
 /tissue_type="pericarp"
 /clone_lib="QAN"

ORIGIN
 Query Match 85.6%; Score 15.4; DB 6; Length 451;
 Best Local Similarity 94.1%; Pred. No. 2.3e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17
 |||||
 Db 311 CGCCTCCGGAAGTTGAG 295

RESULT 38
 CD573266
 LOCUS
 DEFINITION
 labs_Zea mays CDNA, mRNA sequence.
 ACCESSION
 CD573266
 VERSION
 CD573266.1 GI:31664086
 KEYWORDS
 EST.
 SOURCE
 Zea mays
 ORGANISM
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.

```

REFERENCE
AUTHORS      1 (bases 1 to 453)
TITLE        Walbot, V.
COMMENT      Maize ESTs from various cDNA libraries sequenced at Stanford
            University
            Unpublished (1999)
            Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 3529.1.119.1 row: E column: 10.
FEATURES
source      Location/Qualifiers
            1..453
            /organism="Zea mays"
            /mol_type="mRNA"
            /cultivar="B73"
            /db_xref="taxon:4577"
            /tissue_type="ear"
            /dev_stage="2 mm"
            /lab_host="E. coli XL0LR"
            /clone_lib="3529 - 2 mm ear tissue from Schmidt and Hake
            labs"
            /notes="Organ: ear; Vector: PAD-GAL4-2.1; Site 1: EcoRI;
            Site 2: XhoI; RNA isolated by Hake lab. 1 million pfu
            amplified. Ampicillin is the selection marker."
ORIGIN
Query Match      85.6%; Score 15.4; DB 6; Length 453;
Best Local Similarity 94.1%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGCCACCGGAGTTGAG 17
        |||||
Db      400 CGCCCCCGGAGTTGAG 416

RESULT 39
BE345714/c
LOCUS      BE345714      481 bp mRNA linear EST 17-JUL-2000
DEFINITION      946025D07.y2 946 - tassell primordium prepared by Schmidt lab Zea
mays cDNA, mRNA sequence.
ACCESSION      BE345714
VERSION        BE345714.1 GI:9255246
KEYWORDS       EST.
SOURCE         Zea mays
ORGANISM       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 481)
Walbot V.
Maize ESTs from various cDNA libraries sequenced at Stanford
University
Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 946025 row: D column: 07.
FEATURES
source      Location/Qualifiers
            1..481
            /organism="Zea mays"
            /mol_type="mRNA"
            /cultivar="OH43"
            /db_xref="taxon:4577"
            /tissue_type="tassels"
            /dev_stage="just after the transition from vegetative to
            inflorescence development"

```

```

/lab_host="XL0LR"
/clone_lib="946 - tassell primordium prepared by Schmidt
lab"
/note="Organ: tassels; Vector: HybriZAP; Site 1: EcoRI;
Site 2: XhoI; George Chuck dissected immature tassels
between 1mm and 3mm. Sharon Stanfield prepared the cDNA
library in HybriZAP. Sample insert size range was 350 bp
to 3 Kb with a 1 Kb average."
ORIGIN
Query Match      85.6%; Score 15.4; DB 2; Length 481;
Best Local Similarity 94.1%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGCCACCGGAGTTGAG 17
        |||||
Db      180 CGCCCCCGGAGTTGAG 164

RESULT 40
AI664820
LOCUS      AI664820      485 bp mRNA linear EST 02-FEB-2000
DEFINITION      605002A06.x1 605 - Endosperm cDNA library from Schmidt lab Zea mays
cDNA, mRNA sequence.
ACCESSION      AI664820
VERSION        AI664820.1 GI:4775815
KEYWORDS       EST.
SOURCE         Zea mays
ORGANISM       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 485)
Walbot, V.
Maize ESTs from various cDNA libraries sequenced at Stanford
University
Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 605002 row: A column: 06.
FEATURES
source      Location/Qualifiers
            1..485
            /organism="Zea mays"
            /mol_type="mRNA"
            /cultivar="Ohio43"
            /db_xref="taxon:4577"
            /tissue_type="nucellar, embryo, and endosperm"
            /dev_stage="10-14 days post-pollination"
            /lab_host="DH5(alpha)"
            /clone_lib="605 - Endosperm cDNA library from Schmidt lab"
            /note="Organ: Kernel; Vector: PAD-GAL4-2; Site 1: EcoRI;
            Site 2: XhoI; Kernel endosperm cDNA library from Schmidt
            lab"
ORIGIN
Query Match      85.6%; Score 15.4; DB 1; Length 485;
Best Local Similarity 94.1%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGCCACCGGAGTTGAG 17
        |||||
Db      430 CGCCCCCGGAGTTGAG 446

RESULT 41
AV544944
LOCUS      AV544944      499 bp mRNA linear EST 20-FEB-2004
DEFINITION      Arabidopsis thaliana roots Columbia Arabidopsis thaliana

```



```

CDNA clone RZ64h05F 3', mRNA sequence.
AV544944
VERSION AV544944.1 GI:8716358
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 499)
AUTHORS Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
TITLE A large scale analysis of cDNA in Arabidopsis thaliana: Generation
of 12,028 non-redundant expressed sequence tags from normalized and
size-selected cDNA libraries
JOURNAL DNA Res. 7 (3), 175-180 (2000)
MEDLINE 20363093
PUBMED 10907847
COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
FEATURES
    source
        1..499
            /organism="Arabidopsis thaliana"
            /mol_type="mRNA"
            /ecotype="Columbia"
            /db_xref="taxon:3702"
            /clone="RZ64h05F"
            /tissue_type="roots"
            /clone_lib="Arabidopsis thaliana roots Columbia"
            /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
            XhoI"
ORIGIN
    Query Match      85.6%; Score 15.4; DB 1; Length 499;
    Best Local Similarity 94.1%; Pred. No. 2.3e+03;
    Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CGCCACCGGAGTTGAG 17
    |||||
Db 204 CGCCACCGGAGTTGAG 220
    |||||
RESULT 42
CA148045/c
LOCUS CA148045 512 bp mRNA linear EST 24-SEP-2003
DEFINITION SCEZRZ1016C02.g R21 Saccharum officinarum cDNA clone SCEZRZ1016C02
5', mRNA sequence.
ACCESSION CA148045
VERSION CA148045.1 GI:35048690
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
complex.
REFERENCE 1 (bases 1 to 512)
AUTHORS Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.
TITLE The libraries that made SUCEST
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bccccenter.fcav.unesp.br
Plate: 016 row: C column: 02
Seq primer: T7 Promoter Primer.
Location/Qualifiers
1..512
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCEZRZ1016C02"
/lab_host="DH10B"
/clone_lib="R21"
/note="Organ: Shoot-root transition zone from young plants
(large insert library); Vector: pSport1; Site_1: SalI;
Site_2: NotI; An unidirectional cDNA library generated
from [Shoot-root transition zone from young plants (large
insert library)]. cDNA was prepared from poly(A+ mRNA
using SuperScript Plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CL-2B 40cm-columns and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at http://sucest.iad.ic.unicamp.br/public"
FEATURES
    source
        85.6%; Score 15.4; DB 6; Length 512;
        Query Match
        Best Local Similarity 94.1%; Pred. No. 2.3e+03;
        Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CGCCACCGGAGTTGAG 17
    |||||
Db 47 CGCCACCGGAGTTGAG 31
    |||||
RESULT 43
BI097902/c
LOCUS BI097902 529 bp mRNA linear EST 26-JUN-2001
DEFINITION IP1_29_E03.g1_A002 Immature pannicle 1 (IP1) Sorghum bicolor cDNA,
mRNA sequence.
ACCESSION BI097902
VERSION BI097902.1 GI:14569484
KEYWORDS EST.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE 1 (bases 1 to 529)
AUTHORS Klein, R.R., Cordonnier-Pratt, M.-M., Gingle, A., Sudman, M. and
Pratt, L.H.
TITLE An EST database from Sorghum: developing preanthesis pannicles
JOURNAL Unpublished (2001)
COMMENT Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for high quality sequence is
20. Three-prime sequences, which are obtained with PolyTMix or T7
sequencing primer, are presented as the reverse complement.
Seq primer: T7
High quality sequence start: 125
High quality sequence stop: 529
POLVA=Yes.
FEATURES
    source
        Location/Qualifiers
        1..529
            /organism="Sorghum bicolor"
            /mol_type="mRNA"
            /cultivar="BTx623"
            /db_xref="taxon:4558"
            /clone_lib="Immature pannicle 1 (IP1)"
            /note="Organ: Developing preanthesis pannicles; Vector:
            pBluescript II SK(-) from Lambda Zap II; Site_1: XhoI;

```

Site 2: EcoRI. The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision."

ORIGIN

Query Match 85.6%; Score 15.4; DB 4; Length 529;
Best Local Similarity 94.1%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17
|||||
Db 62 CGCCCCCGGAAGTTGAG 46

RESULT 44
BI211550/c

LOCUS BI211550 531 bp mRNA linear EST 11-JUL-2001
DEFINITION IP1_59_A04_g1_A002 Immature pannicle 1 (IP1) Sorghum bicolor cDNA, mRNA sequence.

ACCESSION BI211550

VERSION BI211550

KEYWORDS BI211550.1 GI:14689274

SOURCE Sorghum bicolor (sorghum)

ORGANISM Sorghum bicolor

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 531)

Klein, R.R., Cordonnier-Pratt, M.-M., Gingle, A., Sudman, M. and Pratt, L.H.

TITLE An EST database from Sorghum: developing preanthesis pannicles

JOURNAL Unpublished (2001)

COMMENT Contact: Cordonnier-Pratt MM

Laboratory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Tel: 706 542 1860

Fax: 706 583 0210

Email: mmpratt@uga.edu

Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for high quality sequence is 20. Three-prime sequences, which are obtained with PolyTWix or T7 sequencing primer, are presented as the reverse complement.

Seq primer: T7

High quality sequence start: 5

High quality sequence stop: 531

POLYA=Yes.

FEATURES

source

1..531
Location/Qualifiers
/organism="Sorghum bicolor"
/mol_type="mRNA"
/cultivar="BTx623"
/db_xref="taxon:4558"
/clone_lib="Immature pannicle 1 (IP1)"
/note="Organ: Developing preanthesis pannicles; Vector: pBluescript II SK(-) from Lambda zap II; Site 1: XhoI; Site 2: EcoRI. The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision."

ORIGIN

Query Match 85.6%; Score 15.4; DB 4; Length 531;
Best Local Similarity 94.1%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17

|||||

Db 65 CGCCCCCGGAAGTTGAG 49

RESULT 45

BI2139519/c

LOCUS BI2139519

533 bp mRNA linear EST 02-NOV-2002

DEFINITION

BI2139519 Nori Satoh unpublished cDNA library, gastrula and neurula

Ciona intestinalis cDNA clone rcign053a17 3', mRNA sequence.

ACCESSION BI2139519

VERSION BI2139519.1

KEYWORDS GI:24495918

SOURCE EST.

ORGANISM Ciona intestinalis

Ciona intestinalis

Ciona intestinalis

REFERENCE 1 (bases 1 to 533)

AUTHORS Satou, Y., Shin-i, T., Kohara, Y. and Satoh, N.

TITLE Expressed genes in Ciona intestinalis (2002c)

JOURNAL Unpublished (2002)

COMMENT Contact: Nori Satoh

Department of Zoology

Kyoto University

Sakyo-Ku, Kyoto, Kyoto 606-8502, Japan

Tel: 81-75-753-4081

Fax: 81-75-705-1113

Email: satoh@ascidian.zool.kyoto-u.ac.jp.

Location/Qualifiers

1..533

/organism="Ciona intestinalis"

/mol_type="mRNA"

/db_xref="taxon:7719"

/clone_lib="rcign053a17"

/tissue_type="whole body"

/dev_stages="gastrula and neurula"

/clone_lib="Nori Satoh unpublished cDNA library, gastrula and neurula"

ORIGIN

Query Match 85.6%; Score 15.4; DB 5; Length 533;

Best Local Similarity 94.1%; Pred. No. 2.3e+03;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17

|||||

Db 28 CGCCACCGGAAGTTGCG 12

RESULT 46

BI2166340

LOCUS BI2166340

DEFINITION 1000090D03.x1 1000 - Unigene I from Maize Genome Project Zea mays

CDNA, mRNA sequence.

ACCESSION BI2166340

VERSION BI2166340.1

KEYWORDS GI:12969396

EST.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 534)

AUTHORS Walbot, V.

TITLE Maize ESTs from various cDNA libraries sequenced at Stanford

JOURNAL University

COMMENT Unpublished (1999)

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 1000090 row: D column: 03.

Location/Qualifiers

1..534

/organism="Zea mays"

/mol_type="mRNA"

/db_xref="dbEST:606038C11.x1"

/db_xref="taxon:4577"

/clone_lib="1000 - Unigene I from Maize Genome Project"
/notes="This library represents the unique ESTs found in
the first round of EST sequencing at Stanford University
for the maize genome project. Sequences are present from
libraries 486, 487, 496, 603, 605, 606, 614, 618, 660,
683, 687, 707, and 945. Contigs were assembled using
TIGR's CAP program and a representative EST from each
contig was selected for the Unigene set. All singletons were
also selected."

ORIGIN

Query Match 85.6%; Score 15.4; DB 4; Length 534;
Best Local Similarity 94.1%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17
|||||
Db 480 CGCCCCCGGAAGTTGAG 496

RESULT 47

BF145790
LOCUS
DEFINITION
WHE1840_F12_L24ZS Secale cereale anther cDNA library Secale cereale
CDNA clone WHE1840_F12_L24, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BF145790 542 bp mRNA linear EST 26-OCT-2000
WHE1840_F12_L24ZS Secale cereale anther cDNA library Secale cereale
CDNA clone WHE1840_F12_L24, mRNA sequence.

REFERENCE

AUTHORS
Anderson, O.D., Butler, E., Chao, S., Choi, D.W., Close, T.J.,
Fenton, R.D., Gustafson, J.P., Han, P.S., Hsia, C.C., Kang, Y.-I.,
Lazo, G.R., Miller, R., Rausch, C.J., Ross, K., Seaton, C.L. and
Tong, J.C.

TITLE
The structure and function of the expressed portion of the wheat
genomes - Anther cDNA library from rye

JOURNAL

COMMENT
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818

Email: oanderson@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: StrataGene SK primer.

FEATURES

Source

Location/Qualifiers
1..542
/organism="Secale cereale"
/mol_type="mRNA"
/cultivar="Blanco"
/db_xref="taxon:4550"
/clone="WHE1840_F12_L24"
/tissue_type="Anther"
/dev_stage="Adult plant before anthesis"
/lab_host="E. coli SOLR"
/clone_lib="Secale cereale anther cDNA library"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site 1: EcoRI; Site 2: XhoI; Plants were grown in the
greenhouse. Anthers were harvested and pooled from early
meiosis to late meiosis. The tissue, total RNA, and
poly(A) RNA were prepared (Butler, Ross and Gustafson) at
University of Missouri, Columbia. A cDNA library was
made, and the cDNA clones were in vivo excised to give
phagescript phagemids in the TJ Close lab (Choi, Close,
Fenton) at the University of California, Riverside.
Plasmid DNA preparations and DNA sequencing were performed
in the OD Anderson lab (all other authors)."

ORIGIN

Query Match 85.6%; Score 15.4; DB 2; Length 542;
Best Local Similarity 94.1%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17
|||||
Db 34 CGCCACCGGAAGATGAG 50

RESULT 48

BI245760/c
LOCUS
DEFINITION
IP1_64_A04_g1_A002 Immature pannicle 1 (IP1) Sorghum bicolor cDNA,
mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BI245760 544 bp mRNA linear EST 17-JUL-2001
IP1_64_A04_g1_A002 Immature pannicle 1 (IP1) Sorghum bicolor cDNA,
mRNA sequence.

REFERENCE

AUTHORS
Klein, R.R., Cordonnier-Pratt, M.-M., Gingle, A., Sudman, M. and
Pratt, L.H.

TITLE
An EST database from Sorghum: developing preanthesis pannicles
Unpublished (2001)

JOURNAL

COMMENT
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210

Email: mmpratt@uga.edu

Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for high quality sequence is
20. Three-prime sequences, which are obtained with PolyTmix or T7
sequencing primer, are presented as the reverse complement.

Seq primer: T7

High quality sequence start: 11

High quality sequence stop: 544

POLYA=Yes.

FEATURES
source

Location/Qualifiers
1..544
/organism="Sorghum bicolor"
/mol_type="mRNA"
/cultivar="BTx623"
/db_xref="taxon:4558"
/clone_lib="Immature pannicle 1 (IP1)"
/note="Organ: Developing preanthesis pannicles; Vector:
phagescript II SK(-) from Lambda Zap II; Site 1: XhoI;
Site 2: EcoRI; The library was made from poly-A RNA in the
cloning vector lambda ZAP II. Clones to be sequenced were
prepared by mass excision."

ORIGIN

Query Match 85.6%; Score 15.4; DB 4; Length 544;
Best Local Similarity 94.1%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17
|||||
Db 77 CGCCCCCGGAAGTTGAG 61

RESULT 49

BG266709
LOCUS
DEFINITION
1000100E03.x3 1000 - Unigene I from Maize Genome Project Zea mays
cDNA, mRNA sequence.

ACCESSION

BG266709

```

VERSION      BG266709.1  GI:12969892
KEYWORDS
SOURCE
ORGANISM     Zea mays
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
              clade; Panicoideae; Andropogoneae; Zea.
REFERENCE    1 (bases 1 to 547)
AUTHORS      Walbot, V.
TITLE        Maize ESTs from various cDNA libraries sequenced at Stanford
              University
JOURNAL
COMMENT      Contact: Walbot V
              Department of Biological Sciences
              Stanford University
              855 California Ave, Palo Alto, CA 94304, USA
              Tel: 650 723 2227
              Fax: 650 725 8221
              Email: walbot@stanford.edu
              Plate: 100100 row: E column: 03.

FEATURES
  source
    1..547
    Location/Qualifiers
      /organism="Zea mays"
      /mol_type="mRNA"
      /db_xref="dbEST:60502H07.x1"
      /db_xref="taxon:4577"
      /clone_lib="1000 - Unigene I from Maize Genome Project"
      /note="This library represents the unique ESTs found in
the first round of EST sequencing at Stanford University
for the maize genome project. Sequences are present from
libraries 486, 487, 496, 603, 605, 606, 614, 618, 660,
683, 687, 707, and 945. Contigs were assembled using
TIGR's CAP program and a representative EST from each
contig was selected for the Unigene set. All singlets were
also selected."

ORIGIN
  Query Match      85.6%; Score 15.4; DB 4; Length 547;
  Best Local Similarity 94.1%; Pred. No. 2.3e+03;
  Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

  QY 1 CGCCACCGGAAGTTGAG 17
      ||| ||||| ||||| |||||
  Db 459 CGCCCCCGGAAGTTGAG 475

RESULT 50
BG948081/c
LOCUS
DEFINITION   IP1_9_B08.g1.A002 Immature pannicle 1 (ip1) Sorghum bicolor cDNA,
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VERSION
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REFERENCE    1 (bases 1 to 549)
AUTHORS      Klein, R.R., Cordonnier-Pratt, M.-M., Gingle, A., Sudman, M. and
              Pratt, L.H.
TITLE        An EST database from Sorghum: developing preanthesis pannicles
              Unpublished (2001)
JOURNAL
COMMENT      Contact: Cordonnier-Pratt MM
              Laboratory for Genomics and Bioinformatics
              The University of Georgia, Department of Plant Biology
              Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
              Tel: 706 542 1860
              Fax: 706 583 0210
              Email: mmpratt@uga.edu
              Sequences have been trimmed to exclude PolyA, vector and regions
              below Phred quality 16. The threshold for high quality sequence is

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20. Three-prime sequences, which are obtained with PolyTWix or T7 sequencing primer, are presented as the reverse complement.

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Site 2: EcoRI; The library was made from poly-A RNA in the
cloning vector lambda Zap II. Clones to be sequenced were
prepared by mass excision."

ORIGIN

Query Match 85.6%; Score 15.4; DB 4; Length 549;
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Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 97 CGCCCCCGGAAGTTGAG 81

Search completed: March 25, 2005, 12:32:57
Job time : 1406 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 25, 2005, 10:59:21 ; Search time 58.7143 Seconds

(without alignments)
501.632 Million cell updates/sec

Title: US-10-688-489-64

Perfect score: 18
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Scoring table: IDENTITY NUC
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Searched: 1202784 seqs, 81813359 residues

Total number of hits satisfying chosen parameters: 2405568

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Post-processing: Minimum Match 0%
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Listing first 500 summaries

Database : Issued Patents NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C	96	13.8	76.7	4964	4	US-09-949-016-15131	Sequence 15131, A
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c 110	13.8	76.7	323820	4	US-09-949-016-14139	Sequence 14139, A	183	13.2	73.3	1364	4	US-09-949-016-464	Sequence 464, App
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c 138	13.4	74.4	3774	4	US-09-252-991A-719	Sequence 719, App	c 211	13.2	73.3	1722	4	US-09-489-847-93	Sequence 93, Appl
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c 142	13.4	74.4	11613	3	US-09-453-702B-42	Sequence 42, Appl	c 215	13.2	73.3	1936	3	US-09-032-365A-59	Sequence 1, Appl
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c 156	13.2	73.3	601	4	US-09-949-016-47505	Sequence 47505, A	c 229	13.2	73.3	1956	3	US-08-993-170A-55	Sequence 55, Appl
c 157	13.2	73.3	601	4	US-09-949-016-47506	Sequence 47506, A	c 230	13.2	73.3	1956	3	US-08-993-170A-57	Sequence 57, Appl
c 158	13.2	73.3	601	4	US-09-949-016-87133	Sequence 87133, A	c 231	13.2	73.3	1956	3	US-08-993-775B-51	Sequence 51, Appl
c 159	13.2	73.3	601	4	US-09-949-016-204217	Sequence 204217, A	c 232	13.2	73.3	1956	3	US-08-993-775B-55	Sequence 55, Appl
c 160	13.2	73.3	601	4	US-09-949-016-204906	Sequence 204906, A	c 233	13.2	73.3	1956	4	US-09-427-770-51	Sequence 51, Appl
c 161	13.2	73.3	606	4	US-09-252-991A-6866	Sequence 6866, Ap	c 234	13.2	73.3	1956	4	US-09-427-770-55	Sequence 55, Appl
c 162	13.2	73.3	640	4	US-09-513-999C-829	Sequence 829, App	c 235	13.2	73.3	1956	4	US-09-427-770-57	Sequence 57, Appl
c 163	13.2	73.3	702	4	US-09-902-540-2058	Sequence 2058, Ap	c 236	13.2	73.3	1956	4	US-09-427-770-57	Sequence 57, Appl
c 164	13.2	73.3	708	4	US-09-270-767-11725	Sequence 11725, A	c 237	13.2	73.3	1956	4	US-09-427-769-51	Sequence 51, Appl
c 165	13.2	73.3	753	4	US-09-902-540-2320	Sequence 2320, Ap	c 238	13.2	73.3	1956	4	US-09-427-769-55	Sequence 55, Appl
c 166	13.2	73.3	783	4	US-09-902-540-6140	Sequence 6140, Ap	c 239	13.2	73.3	1956	4	US-09-427-769-57	Sequence 57, Appl
c 167	13.2	73.3	862	4	US-09-270-767-9860	Sequence 9860, Ap	c 240	13.2	73.3	1959	3	US-08-996-441B-1	Sequence 1, Appl
c 168	13.2	73.3	885	4	US-09-583-110-1079	Sequence 1079, Ap	c 241	13.2	73.3	1959	3	US-08-996-441B-3	Sequence 3, Appl
c 169	13.2	73.3	891	4	US-09-711-164-156	Sequence 156, App	c 242	13.2	73.3	1959	3	US-08-996-441B-5	Sequence 5, Appl
c 170	13.2	73.3	900	3	US-08-961-527-332	Sequence 332, App	c 243	13.2	73.3	1959	3	US-08-996-441B-7	Sequence 7, Appl
c 171	13.2	73.3	900	4	US-09-252-991A-465	Sequence 465, App	c 244	13.2	73.3	1959	3	US-08-996-441B-9	Sequence 9, Appl
c 172	13.2	73.3	948	4	US-09-107-433-518	Sequence 518, App	c 245	13.2	73.3	1959	3	US-08-996-441B-11	Sequence 11, Appl
c 173	13.2	73.3	972	4	US-09-252-991A-404	Sequence 404, App	c 246	13.2	73.3	1959	3	US-08-996-441B-13	Sequence 13, Appl


```

RESULT 2
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match      88.9%; Score 16; DB 3; Length 4411529;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2  GCCACCGGAAGTTGAG 17
Db      1450409  GCCACCGGAAGTTGAG 1450394
|||||
|||||

RESULT 3
US-09-464-535-13/c
; Sequence 13, Application US/09464535
; Patent No. 6545200
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Sakai, Hajime
; APPLICANT: McGonigle, Brian
; APPLICANT: Rafalski, J. Antoni
; TITLE OF INVENTION: STEROL BIOSYNTHETIC ENZYMES
; FILE REFERENCE: BB1306 US NA
; CURRENT APPLICATION NUMBER: US/09/464,535
; CURRENT FILING DATE: 1999-12-15
; EARLIER APPLICATION NUMBER: 60/112,555
; EARLIER FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
; LENGTH: 436
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-09-464-535-13

Query Match      83.3%; Score 15; DB 4; Length 436;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3  CCACCGGAAGTTGAG 17
Db      157  CCACCGGAAGTTGAG 143
|||||
|||||

RESULT 4
US-09-464-535-39/c
; Sequence 39, Application US/09464535
; Patent No. 6545200
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.

```

```

; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Sakai, Hajime
; APPLICANT: McGonigle, Brian
; APPLICANT: Rafalski, J. Antoni
; TITLE OF INVENTION: STEROL BIOSYNTHETIC ENZYMES
; FILE REFERENCE: BB1306 US NA
; CURRENT APPLICATION NUMBER: US/09/464,535
; CURRENT FILING DATE: 1999-12-15
; EARLIER APPLICATION NUMBER: 60/112,555
; EARLIER FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 39
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-09-464-535-39

Query Match      83.3%; Score 15; DB 4; Length 600;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3  CCACCGGAAGTTGAG 17
Db      164  CCACCGGAAGTTGAG 150
|||||
|||||

RESULT 5
US-09-464-535-33/c
; Sequence 33, Application US/09464535
; Patent No. 6545200
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Sakai, Hajime
; APPLICANT: McGonigle, Brian
; APPLICANT: Rafalski, J. Antoni
; TITLE OF INVENTION: STEROL BIOSYNTHETIC ENZYMES
; FILE REFERENCE: BB1306 US NA
; CURRENT APPLICATION NUMBER: US/09/464,535
; CURRENT FILING DATE: 1999-12-15
; EARLIER APPLICATION NUMBER: 60/112,555
; EARLIER FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 33
; LENGTH: 616
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (387)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (415)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (489)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (491)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (544)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (551)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (558)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (562)

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; FEATURE:
; NAME/KEY: unsure
; LOCATION: (567)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (569)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (592)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (600)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (611)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (616)
US-09-464-535-33

```

Query Match 83.3%; Score 15; DB 4; Length 616;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 3 CCACCGGAAGTTGAG 17
    |||||
Db 376 CCACCGGAAGTTGAG 362
    |||||

```

```

RESULT 6
US-09-464-535-31/c
; Sequence 31, Application US/09464535
; Patent No. 6545200
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Sakai, Hajime
; APPLICANT: McGonigle, Brian
; APPLICANT: Rafalski, J. Antoni
; TITLE OF INVENTION: STEROL BIOSYNTHETIC ENZYMES
; FILE REFERENCE: BB1306 US NA
; CURRENT APPLICATION NUMBER: US/09/464,535
; EARLIER FILING DATE: 1999-12-15
; EARLIER FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 31
; LENGTH: 673
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (3)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (41)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (95)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (227)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (385)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (388)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (390)
; FEATURE:

```

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; NAME/KEY: unsure
; LOCATION: (487)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (491)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (554)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (557)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (560)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (626)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (634)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (650)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (664)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (668)
US-09-464-535-31

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Query Match 83.3%; Score 15; DB 4; Length 673;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 3 CCACCGGAAGTTGAG 17
    |||||
Db 362 CCACCGGAAGTTGAG 348
    |||||

```

```

RESULT 7
US-08-976-259-27/c
; Sequence 27, Application US/08976259
; Patent No. 6316609
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Choi, Gil H.
; APPLICANT: Welch, Rodney A.
; TITLE OF INVENTION: Nucleotide Sequence of Escherichia coli
; Patent No. 6316609
; NUMBER OF SEQUENCES: 142
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Ave, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,259
; FILING DATE: Herewith
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/031,626 AND US 60/061,953
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0740002/EKS/CBM

```

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 1118 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-976-259-27

Query Match 82.2%; Score 14.8; DB 3; Length 1118;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18
||||| |||||
Db 1054 CGCCACGAGGTTGAGT 1037

RESULT 8

US-09-956-004-27/c
Sequence 27, Application US/09956004
Patent No. 6787643
GENERAL INFORMATION:
APPLICANT: Patrick J. Dillon et al.
TITLE OF INVENTION: Nucleotide Sequences of Escherichia coli Pathogenicity Islands
FILE REFERENCE: PB324D1
CURRENT APPLICATION NUMBER: US/09/956,004
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: 08/976,259
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/061,953
PRIOR FILING DATE: 1997-10-14
PRIOR APPLICATION NUMBER: 60/031,626
PRIOR FILING DATE: 1996-11-22
NUMBER OF SEQ ID NOS: 142
SOFTWARE: PatentIn version 3.1
SEQ ID NO 27

LENGTH: 1118
TYPE: DNA
ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: misc feature
LOCATION: (142)..(142)
OTHER INFORMATION: n equals a, t, g, or c
NAME/KEY: misc feature
LOCATION: (228)..(228)
OTHER INFORMATION: n equals a, t, g, or c
NAME/KEY: misc feature
LOCATION: (261)..(261)
OTHER INFORMATION: n equals a, t, g, or c
NAME/KEY: misc feature
LOCATION: (693)..(693)
OTHER INFORMATION: n equals a, t, g, or c
US-09-956-004-27

Query Match 82.2%; Score 14.8; DB 4; Length 1118;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18
||||| |||||
Db 1054 CGCCACGAGGTTGAGT 1037

RESULT 9

US-09-252-991A-14725
Sequence 14725, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 14725
LENGTH: 1203
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-14725

Query Match 82.2%; Score 14.8; DB 4; Length 1203;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18
||||| |||||
Db 277 CGCCACCGGAGTTGATT 294

RESULT 10

US-09-252-991A-14603
Sequence 14603, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 14603
LENGTH: 1233
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-14603

Query Match 82.2%; Score 14.8; DB 4; Length 1233;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18
||||| |||||
Db 266 CGCCACCGGAGTTGATT 283

RESULT 11

US-09-252-991A-15026/c
Sequence 15026, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 15026
LENGTH: 1329

```
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-15026

Query Match      82.2%; Score 14.8; DB 4; Length 1329;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGCCACCGGAAGTTGAGT 18
   ||||| ||||| |||||
Db 1005 CGCCACCGGAAGTTGATT 988

RESULT 12
US-09-252-991A-15978/c
; Sequence 15978, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 15978
; LENGTH: 1806
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-15978

Query Match      82.2%; Score 14.8; DB 4; Length 1806;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGCCACCGGAAGTTGAGT 18
   ||||| ||||| |||||
Db 536 CGCCACCGGAAGCCGAGT 519

RESULT 13
US-09-252-991A-16301
; Sequence 16301, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 16301
; LENGTH: 2289
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16301

Query Match      82.2%; Score 14.8; DB 4; Length 2289;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGCCACCGGAAGTTGAGT 18
   ||||| ||||| |||||
Db 1994 CGCCACCGGAAGCCGAGT 2011
```

```
RESULT 14
US-09-543-681A-3437
; Sequence 3437, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543.681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 3437
; LENGTH: 5151
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-3437

Query Match      82.2%; Score 14.8; DB 4; Length 5151;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGCCACCGGAAGTTGAGT 18
   ||||| ||||| ||||| |||||
Db 5069 CGCCTCCGCAAGTTGAGT 5086

RESULT 15
US-09-949-016-17417
; Sequence 17417, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949.016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17417
; LENGTH: 77772
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(77772)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17417

Query Match      82.2%; Score 14.8; DB 4; Length 77772;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGCCACCGGAAGTTGAGT 18
   ||||| ||||| ||||| |||||
Db 921 CGCCACCGGAAGTTGAGT 938

RESULT 16
US-09-949-016-12249
; Sequence 12249, Application US/09949016
; Patent No. 6812339
```

GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001307
 CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 12249
 LENGTH: 77997
 TYPE: DNA
 ORGANISM: Human
 FEATURE:
 NAME/KEY: misc.feature
 LOCATION: (1)...(77997)
 OTHER INFORMATION: n = A, T, C or G
 US-09-949-016-12249

Query Match 82.2%; Score 14.8; DB 4; Length 77997;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18
 DB 925 CGCCACCGGAAGTTGAGT 942

RESULT 17
 US-09-634-238-154
 Sequence 154, Application US/09634238
 Patent No. 6544772
 GENERAL INFORMATION:
 APPLICANT: Glenn, Matthew
 APPLICANT: Havukkala, Ilkka J.
 APPLICANT: Bloksberg, Leonard, N.
 APPLICANT: Lubbers, Mark W.
 APPLICANT: Dekker, James
 APPLICANT: Christensen, Anna C.
 APPLICANT: Holland, Ross
 APPLICANT: O'Toole, Paul W.
 APPLICANT: Reid, Julian R.
 APPLICANT: Coolbear, Timothy
 TITLE OF INVENTION: Polynucleotides, materials incorporating
 them and methods for using them.
 FILE REFERENCE: 11000.1043U1
 CURRENT APPLICATION NUMBER: US/09/634,238
 CURRENT FILING DATE: 2000-08-08
 NUMBER OF SEQ ID NOS: 422
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 154
 LENGTH: 435
 TYPE: DNA
 ORGANISM: Lactobacillus rhamnosus
 FEATURE:
 NAME/KEY: misc.feature
 LOCATION: (1)...(435)
 OTHER INFORMATION: n = A, T, C or G
 US-09-634-238-154

Query Match 80.0%; Score 14.4; DB 4; Length 435;
 Best Local Similarity 93.8%; Pred. No. 2.4e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGA 16
 DB 420 CGCCACCGGAAGTTGA 435

RESULT 18
 US-09-949-016-142247
 Sequence 142247, Application US/09949016
 Patent No. 6812339
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001307
 CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 142247
 LENGTH: 601
 TYPE: DNA
 ORGANISM: Human
 US-09-949-016-142247

Query Match 80.0%; Score 14.4; DB 4; Length 601;
 Best Local Similarity 93.8%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCCACCGGAAGTTGAG 17
 DB 449 GCCACCGGAAGTTGAG 464

RESULT 19
 US-09-549-848B-5/c
 Sequence 5, Application US/09549848B
 Patent No. 6541259
 GENERAL INFORMATION:
 APPLICANT: Lassner, Michael
 APPLICANT: Post-Beittenmiller, Dusty
 APPLICANT: Savidge, Beth
 APPLICANT: Weiss, James
 TITLE OF INVENTION: Nucleic Acid Sequences Involved in
 Tumor Promotion and Tumor Inhibition
 FILE REFERENCE: 17133/02/US
 CURRENT APPLICATION NUMBER: US/09/549,848B
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/129,899
 PRIOR FILING DATE: 1999-04-15
 PRIOR APPLICATION NUMBER: 60/146,461
 PRIOR FILING DATE: 1999-07-30
 NUMBER OF SEQ ID NOS: 94
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 5
 LENGTH: 1296
 TYPE: DNA
 ORGANISM: Arabidopsis sp
 US-09-549-848B-5

Query Match 80.0%; Score 14.4; DB 4; Length 1296;
 Best Local Similarity 93.8%; Pred. No. 2.8e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCCACCGGAAGTTGAG 17
 DB 1238 GCCACCGGAAGTTGAG 1223

RESULT 20
 US-08-704-966-3/c

Fri Mar 25 15:14:16 2005

us-10-688-489-64.rni

```

; Sequence 3, Application US/08704966
; Patent No. 6013523
; GENERAL INFORMATION:
; APPLICANT: Adams, Michael J.
; APPLICANT: Rocheleau, Thomas A.
; APPLICANT: Merlo, Donald
; APPLICANT: Murray, Elizabeth E.
; TITLE OF INVENTION: Synthetic Insecticidal Crystal Protein
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 1000 Legion Place, Suite 1750
; CITY: Orlando
; STATE: Florida
; COUNTRY: USA
; ZIP: 32801
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 29-AUG-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/704,966
; FILING DATE: 29-AUG-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/369,839
; FILING DATE: 06-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,191
; FILING DATE: 03-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,844
; FILING DATE: 28-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/242,482
; FILING DATE: 09-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Lloyd, Jeff
; REGISTRATION NUMBER: 35,589
; REFERENCE/DOCKET NUMBER: MPS 8-88AFD3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 407-426-7500
; TELEFAX: 407-839-8589
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1833 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-704-966-3

Query Match      80.0%; Score 14.4; DB 3; Length 1833;
Best Local Similarity 93.8%; Pred. No. 3e+02; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 CCACCGGAAGTTGAGT 18
DB      1402 CCAACGGAAGTTGAGT 1387

RESULT 21
US-08-705-438-3/c
; Sequence 3, Application US/08705438
; Patent No. 6015891
; GENERAL INFORMATION:
; APPLICANT: Adams, Michael J.
; APPLICANT: Rocheleau, Thomas A.
; APPLICANT: Merlo, Donald
; APPLICANT: Murray, Elizabeth E.
; TITLE OF INVENTION: 'Synthetic Insecticidal Crystal Protein

```

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; TITLE OF INVENTION: Gene
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 1000 Legion Place, Suite 1750
; CITY: Orlando
; STATE: Florida
; COUNTRY: USA
; ZIP: 32801
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/705,438
; FILING DATE: 29-AUG-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/369,839
; FILING DATE: 06-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,191
; FILING DATE: 03-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,844
; FILING DATE: 28-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/242,482
; FILING DATE: 09-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Lloyd, Jeff
; REGISTRATION NUMBER: 35,589
; REFERENCE/DOCKET NUMBER: MPS 8-88AFD4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 407-426-7500
; TELEFAX: 407-839-8589
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1833 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-705-438-3

Query Match      80.0%; Score 14.4; DB 3; Length 1833;
Best Local Similarity 93.8%; Pred. No. 3e+02; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 CCACCGGAAGTTGAGT 18
DB      1402 CCAACGGAAGTTGAGT 1387

RESULT 22
US-09-549-848B-93/c
; Sequence 93, Application US/09549848B
; Patent No. 6541259
; GENERAL INFORMATION:
; APPLICANT: Lasner, Michael
; APPLICANT: Post-Beittenmiller, Dusty
; APPLICANT: Savidge, Beth
; APPLICANT: Weiss, James
; TITLE OF INVENTION: Tocopherol Synthesis
; FILE REFERENCE: 17133/02/US
; CURRENT APPLICATION NUMBER: US/09/549,848B
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/129,899
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/146,461
; PRIOR FILING DATE: 1999-07-30

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; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 2850
; TYPE: DNA
; ORGANISM: Arabidopsis sp
; US-0549-8488-93

Query Match      80.0%; Score 14.4; DB 4; Length 2850;
Best Local Similarity 93.8%; Pred. No. 3.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GCACCGGAAGTTGAG 17
      |||||
Db      2371 GCACCGGAGTTGAG 2356

RESULT 23
US-09-949-016-14257
; Sequence 14257, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14257
; LENGTH: 29321
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-14257

Query Match      80.0%; Score 14.4; DB 4; Length 29321;
Best Local Similarity 93.8%; Pred. No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GCACCGGAAGTTGAG 17
      |||||
Db      9179 GCACCGGAAGTTGAG 9194

RESULT 24
US-09-949-016-14258
; Sequence 14258, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14258
; LENGTH: 29321
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-14258

Query Match      80.0%; Score 14.4; DB 4; Length 29321;
Best Local Similarity 93.8%; Pred. No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GCACCGGAAGTTGAG 17
      |||||
Db      9179 GCACCGGAAGTTGAG 9194

RESULT 25
US-09-949-016-11758
; Sequence 11758, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11758
; LENGTH: 32798
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-11758

Query Match      80.0%; Score 14.4; DB 4; Length 32798;
Best Local Similarity 93.8%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 CCACCGGAAGTTGAGT 18
      |||||
Db      11464 CCACCGGAAGTTGAGT 11479

RESULT 26
US-09-949-016-17366
; Sequence 17366, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17366
; LENGTH: 32798
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-17366

Query Match      80.0%; Score 14.4; DB 4; Length 32798;
Best Local Similarity 93.8%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 CCACCGGAAGTTGAGT 18
      |||||
Db      11464 CCACCGGAAGTTGAGT 11479

RESULT 26
US-09-949-016-17366
; Sequence 17366, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17366
; LENGTH: 32798
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-17366

Query Match      80.0%; Score 14.4; DB 4; Length 32798;
Best Local Similarity 93.8%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CCACCGAAGTTGAGT 18
 |||||
 Db 11464 CCACCGAAGTAGAGT 11479

RESULT 27
 US-09-949-016-11932/c
 ; Sequence 11932, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 11932
 ; LENGTH: 41522
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-016-11932

Query Match 80.0%; Score 14.4; DB 4; Length 41522;
 Best Local Similarity 93.8%; Pred. No. 4.5e-02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCCACCGAAGTTGAG 17
 |||||
 Db 4350 GCCACGGAAGTTGAG 4335

RESULT 28
 US-09-949-016-15764/c
 ; Sequence 15764, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 15764
 ; LENGTH: 41523
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-016-15764

Query Match 80.0%; Score 14.4; DB 4; Length 41523;
 Best Local Similarity 93.8%; Pred. No. 4.5e-02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCCACCGAAGTTGAG 17
 |||||
 Db 4350 GCCACGGAAGTTGAG 4335

RESULT 29
 US-09-491-356C-1
 ; Sequence 1, Application US/09491356C
 ; Patent No. 6566061
 ; GENERAL INFORMATION:
 ; APPLICANT: Philibert, Robert A.
 ; APPLICANT: Ginns, Edward I.
 ; APPLICANT: Delisi, Lynn
 ; TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13
 ; FILE REFERENCE: 9465.6US11
 ; CURRENT APPLICATION NUMBER: US/09/491,356C
 ; CURRENT FILING DATE: 2000-01-26
 ; PRIOR APPLICATION NUMBER: PCT/US99/09365
 ; PRIOR FILING DATE: 1999-04-29
 ; PRIOR APPLICATION NUMBER: 60/083,465
 ; PRIOR FILING DATE: 1998-04-29
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 55298
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (485)..(485)
 ; OTHER INFORMATION: n is not determined
 ; NAME/KEY: misc feature
 ; LOCATION: (838)..(838)
 ; OTHER INFORMATION: n is not determined
 ; NAME/KEY: misc feature
 ; LOCATION: (16728)..(16728)
 ; OTHER INFORMATION: n is not determined
 ; NAME/KEY: misc feature
 ; LOCATION: (22750)..(22750)
 ; OTHER INFORMATION: n is not determined
 ; NAME/KEY: misc feature
 ; LOCATION: (22756)..(22756)
 ; OTHER INFORMATION: n is not determined
 ; NAME/KEY: misc feature
 ; LOCATION: (28519)..(28519)
 ; OTHER INFORMATION: n is not determined
 ; NAME/KEY: misc feature
 ; LOCATION: (44804)..(44804)
 ; OTHER INFORMATION: n is not determined
 ; NAME/KEY: misc feature
 ; LOCATION: (45002)..(45002)
 ; OTHER INFORMATION: n is not determined
 ; NAME/KEY: misc feature
 ; LOCATION: (54049)..(54049)
 ; OTHER INFORMATION: n is not determined
 ; NAME/KEY: misc feature
 ; LOCATION: (54226)..(54226)
 ; OTHER INFORMATION: n is not determined
 ; US-09-491-356C-1

Query Match 80.0%; Score 14.4; DB 4; Length 55298;
 Best Local Similarity 93.8%; Pred. No. 4.7e-02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCCACCGAAGTTGAG 17
 |||||
 Db 34613 GCCACCGAAGTTGAG 34628

RESULT 30
 US-09-949-016-15794
 ; Sequence 15794, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED


```
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15794
; LENGTH: 123513
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(123513)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15794

Query Match      80.0%; Score 14.4; DB 4; Length 123513;
Best Local Similarity 93.8%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 CCACCGGAAGTTGAGT 18
      |||
Db      118414 CCACCGGAAGTTGACT 118429

RESULT 31
US-09-270-767-14483
; Sequence 14483, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 14483
; LENGTH: 443
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-14483

Query Match      77.8%; Score 14; DB 4; Length 443;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GCACCGGAAGTTG 15
      |||
Db      334 GCACCGGAAGTTG 347

RESULT 32
US-09-902-540-8535/c
; Sequence 8535, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
```

```
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 8535
; LENGTH: 2850
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-8535

Query Match      77.8%; Score 14; DB 4; Length 2850;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGCCACCGGAAGTT 14
      |||
Db      1752 CGCCACCGGAAGTT 1739

RESULT 33
US-09-949-016-12296
; Sequence 12296, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12296
; LENGTH: 2913
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12296

Query Match      77.8%; Score 14; DB 4; Length 2913;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGCCACCGGAAGTT 14
      |||
Db      758 CGCCACCGGAAGTT 771

RESULT 34
US-09-902-540-899
; Sequence 899, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 899
; LENGTH: 8518
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-899

Query Match      77.8%; Score 14; DB 4; Length 8518;
```

Best Local Similarity 100.0%; Pred. No. 6.1e+02; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0;

QY 1 GCCACCGGAAGTT 14
Db 6766 CGCACCGGAAGTT 6779

RESULT 35

US-09-085-199B-30
; Sequence 30, Application US/09085199B
; Patent No. 6235879

; GENERAL INFORMATION:

; APPLICANT: Hayden, Michael R.
; APPLICANT: Hackam, Abigail
; APPLICANT: Hug, A.H.M. Mahbubul
; APPLICANT: Chopra, Vikramjit Singh
; APPLICANT: Kalchman, Michael

; TITLE OF INVENTION: Apoptosis Modulators That Interact with the

; NUMBER OF SEQUENCES: 44

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Oppedahl & Larson

; STREET: PO Box 5270

; CITY: Frlisco

; STATE: CO

; COUNTRY: USA

; ZIP: 80443-5270

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Kb storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: MS DOS 5.0

; SOFTWARE: WordPerfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/085,199B

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Larson, Marina T.

; REGISTRATION NUMBER: 32038

; REFERENCE/DOCKET NUMBER: UBC.P-013US2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (970) 668-2050

; TELEFAX: (970) 668-2052

; INFORMATION FOR SEQ ID NO: 30:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 359

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: genomic DNA

; HYPOTHETICAL: no

; ANTI-SENSE: no

; ORIGINAL SOURCE:

; ORGANISM: human

; FEATURE:

; OTHER INFORMATION: exon 15 of HIP1

US-09-085-199B-30

Query Match

Best Local Similarity 76.7%; Score 13.8; DB 3; Length 359;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCCACCGGAAGTTGAGT 18

Db 231 GCCACCGGAAGTTGAGT 247

RESULT 36

US-09-513-999C-20187/c

; Sequence 20187, Application US/09513999C

; Patent No. 6783961

; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Duclert, A.

; APPLICANT: Giordano, J.Y.

; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

; Patent No. 6783961

; FILE REFERENCE: 59 US2 REG

; CURRENT APPLICATION NUMBER: US/09/513,999C

; CURRENT FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/122,487

; PRIOR FILING DATE: 1999-02-26

; NUMBER OF SEQ ID NOS: 36681

; SOFTWARE: Patent.pm

; SEQ ID NO 20187

; LENGTH: 420

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-513-999C-20187

Query Match

Best Local Similarity 76.7%; Score 13.8; DB 4; Length 420;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCCACCGGAAGTTGAGT 18

Db 111 GCCACCGGAAGTTGAGT 95

RESULT 37

US-09-270-767-4798/c

; Sequence 4798, Application US/09270767

; Patent No. 6703491

; GENERAL INFORMATION:

; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

; FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270,767

; CURRENT FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 4798

; LENGTH: 483

; TYPE: DNA

; ORGANISM: Drosophila melanogaster

US-09-270-767-4798

Query Match

Best Local Similarity 76.7%; Score 13.8; DB 4; Length 483;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCCACCGGAAGTTGAGT 18

Db 211 GCCACCGGAAGTTGAGT 195

RESULT 38

US-09-270-767-20080/c

; Sequence 20080, Application US/09270767

; Patent No. 6703491

; GENERAL INFORMATION:

; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

; FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270,767

; CURRENT FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 20080

; LENGTH: 483

; TYPE: DNA

; ORGANISM: Drosophila melanogaster

US-09-270-767-20080

Query Match

Best Local Similarity 76.7%; Score 13.8; DB 4; Length 483;

Best Local Similarity 88.2%; Pred. No. 5.3e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 15; Conservative 0;

QY 2 GCCATCGGAAGTTGAGT 18
|||||
Db 211 GCCATCGGAAGTTGAGT 195

RESULT 39
US-09-949-016-89710/c
; Sequence 89710, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89710
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-89710

Query Match 76.7%; Score 13.8; DB 4; Length 601;
Best Local Similarity 88.2%; Pred. No. 5.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCACCGGAAGTTGAGT 17
|||||
Db 200 CCCACCGGAAGTTGAGT 184

RESULT 40
US-08-998-416-51
; Sequence 51, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippsen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jurgen
; APPLICANT: Knechtle, Philipp
; APPLICANT: Rebschung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPHII
; AND USES THEREOF
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6239264artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 632 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: PAG1013UP
US-08-998-416-51

Query Match 76.7%; Score 13.8; DB 3; Length 632;
Best Local Similarity 88.2%; Pred. No. 5.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 17
|||||
Db 24 CGCCACCGGAAGTTGAGT 40

RESULT 41
US-09-134-000C-32
; Sequence 32, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 32
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-32

Query Match 76.7%; Score 13.8; DB 4; Length 720;
Best Local Similarity 88.2%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCCACCGGAAGTTGAGT 18
|||||
Db 141 GCCACCGGAAGTTGAGT 157

RESULT 42
US-09-791-540-5/c
; Sequence 5, Application US/09791540
; Patent No. 6824782
; GENERAL INFORMATION:
; APPLICANT: WHITLOW, MARC
; SHORR, ROBERT G.L.
; FILPULA, DAVID R.
; LEE, LIHSYNG S.
; TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN
; POLYPEPTIDES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/791,540
FILING DATE: 26-Feb-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/069,842
FILING DATE: 1998-04-30
APPLICATION NUMBER: US 60/050,472
FILING DATE: 23-JUN-1997
APPLICATION NUMBER: US 60/063,074
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: US 60/067,341
FILING DATE: 02-DEC-1997

ATTORNEY/AGENT INFORMATION:

NAME: JORGE A. GOLDSTEIN
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.1840002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 723 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both

FEATURE:

NAME/KEY: CDS
LOCATION: 1..723
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-791-540-5

Query Match 76.7%; Score 13.8; DB 4; Length 723;
Best Local Similarity 88.2%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGTTGAG 17
Db 358 CGCTACCGGAGTAGAG 342

RESULT 43

US-08-392-338A-12/c
Sequence 12, Application US/08392338A
Patent No. 5869620
GENERAL INFORMATION:
APPLICANT: Whitlow, Marc
APPLICANT: Wood, James F.
APPLICANT: Hardman, Karl
APPLICANT: Bird, Robert
APPLICANT: Filpula, David
TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, NW
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/392,338A
FILING DATE: 22-FEB-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/989,846
FILING DATE: 20-NOV-1992
APPLICATION DATA:
APPLICATION NUMBER: US 07/796,936
FILING DATE: 25-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.

REFERENCE/DOCKET NUMBER: 29,021

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:
LENGTH: 744 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both

FEATURE:

NAME/KEY: CDS
LOCATION: 1..732
US-08-392-338A-12

Query Match

Best Local Similarity 88.2%; Score 13.8; DB 2; Length 744;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGTTGAG 17
Db 358 CGCTACCGGAGTAGAG 342

RESULT 44

US-09-166-750-12/c
Sequence 12, Application US/09166750
Patent No. 6025165
GENERAL INFORMATION:
APPLICANT: Whitlow, Marc
APPLICANT: Wood, James F.
APPLICANT: Hardman, Karl
APPLICANT: Bird, Robert
APPLICANT: Filpula, David
APPLICANT: Rollence, Michelle
TITLE OF INVENTION: Methods for Producing Multivalent Antigen-Binding
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, NW
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/166,750
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/392,338
FILING DATE: 22-FEB-1995

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/989,846
;; FILING DATE: 20-NOV-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/796,936
;; FILING DATE: 25-NOV-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Goldstein, Jorge A.
;; REGISTRATION NUMBER: 29,021
;; REFERENCE/DOCKET NUMBER: 0977.003000C
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 371-2600
;; TELEFAX: (202) 371-2540
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 744 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: both
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..732
US-09-166-750-12

Query Match 76.7%; Score 13.8; DB 3; Length 744;
Best Local Similarity 88.2%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17
Db 358 CGCTACCGGAAGTAGAG 342

RESULT 45
US-09-166-093-12/c
; Sequence 12, Application US/09166093
; Patent No. 6027725
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Wood, James F.
; APPLICANT: Hardman, Karl
; APPLICANT: Bird, Robert
; APPLICANT: Filpula, David
; APPLICANT: Rollence, Michelle
; TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/166,093
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/392,338
; FILING DATE: 22-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/989,846
; FILING DATE: 20-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,936
; FILING DATE: 25-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.003000D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 744 base pairs
; TYPE: nucleic acid

;; REGISTRATION NUMBER: 29,021
;; REFERENCE/DOCKET NUMBER: 0977.003000B
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 371-2600
;; TELEFAX: (202) 371-2540
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 744 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: both
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..732
US-09-166-093-12

Query Match 76.7%; Score 13.8; DB 3; Length 744;
Best Local Similarity 88.2%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17
Db 358 CGCTACCGGAAGTAGAG 342

RESULT 46
US-09-172-019-12/c
; Sequence 12, Application US/09172019
; Patent No. 6103889
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Hardman, Karl
; APPLICANT: Bird, Robert
; APPLICANT: Filpula, David
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Single-Chain
; TITLE OF INVENTION: Antigen-Binding Proteins (As Amended)
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/172,019
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/392,338
; FILING DATE: 22-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/989,846
; FILING DATE: 20-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,936
; FILING DATE: 25-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.003000D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 744 base pairs
; TYPE: nucleic acid

STRANDEDNESS: both
TOPOLOGY: both
NAME/KEY: CDS
LOCATION: 1..732
US-09-172-019-12

Query Match 76.7%; Score 13.8; DB 3; Length 744;
Best Local Similarity 88.2%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17
DB 358 CGCTACCGGAGTAGAG 342

RESULT 47
US-09-166-094-12/c
Sequence 12, Application US/09166094
Patent No. 6121424
GENERAL INFORMATION:
APPLICANT: Whitlow, Marc
APPLICANT: Wood, James F.
APPLICANT: Hardman, Karl
APPLICANT: Bird, Robert
APPLICANT: Filpula, David
APPLICANT: Rollence, Michelle
TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, NW
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09166,094
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/392,338
FILING DATE: 22-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/989,846
FILING DATE: 20-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,936
FILING DATE: 25-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.003000A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 744 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
FEATURE:
NAME/KEY: CDS
LOCATION: 1..732
US-09-166-094-12

Query Match 76.7%; Score 13.8; DB 3; Length 744;

Best Local Similarity 88.2%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17
DB 358 CGCTACCGGAGTAGAG 342

RESULT 48
US-09-443-213-12/c
Sequence 12, Application US/09443213
Patent No. 6515110
GENERAL INFORMATION:
APPLICANT: Whitlow, Marc
APPLICANT: Wood, James F.
APPLICANT: Hardman, Karl
APPLICANT: Bird, Robert
APPLICANT: Filpula, David
APPLICANT: Rollence, Michelle
TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, NW
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09443,213
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/166,094
FILING DATE: 05-OCT-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/392,338
FILING DATE: 22-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/989,846
FILING DATE: 20-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,936
FILING DATE: 25-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.003000E
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 744 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
FEATURE:
NAME/KEY: CDS
LOCATION: 1..732
US-09-443-213-12

Query Match 76.7%; Score 13.8; DB 4; Length 744;
Best Local Similarity 88.2%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17
DB 358 CGCTACCGGAGTAGAG 342

Db 358 CGCTACCGGAGTAGAG 342

RESULT 49

US-09-069-821-1/c
; Sequence 1, Application US/09069821
; Patent No. 6323322
; GENERAL INFORMATION:
; APPLICANT: FILPULA, DAVID
; APPLICANT: WANG, MAOLIANG
; APPLICANT: SHORR, ROBERT
; APPLICANT: WHITLOW, MARC
; APPLICANT: LEE, LIHSYNG S.
; TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
; CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/069,821
FILING DATE: 30-APR-1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/067,341
FILING DATE: 02-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/063,074
FILING DATE: 27-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/050,472
FILING DATE: 23-JUN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/044,449
FILING DATE: 30-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0977.2280003
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 758 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..747

US-09-069-821-1

Query Match 76.7%; Score 13.8; DB 3; Length 758;
Best Local Similarity 88.2%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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; Patent No. 6743896
; GENERAL INFORMATION:
; APPLICANT: FILPULA, DAVID
; APPLICANT: WANG, MAOLIANG
; APPLICANT: SHORR, ROBERT
; APPLICANT: WHITLOW, MARC
; APPLICANT: LEE, LIHSYNG S.
; TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
; CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/956,086
FILING DATE: 20-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
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FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/063,074
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: US 60/050,472
FILING DATE: 23-JUN-1997
APPLICATION NUMBER: US 60/044,449
FILING DATE: 30-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0977.2280003
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 758 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..747

US-09-956-086-1

Query Match 76.7%; Score 13.8; DB 4; Length 758;
Best Local Similarity 88.2%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGCCACCGGAGTAGAG 17

Db 358 CGCTACCGGAGTAGAG 342

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 25, 2005, 11:41:26 ; Search time 208.286 Seconds
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Title: US-10-688-489-64

Perfect score: 18

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Maximum Match 100%

Listing first 500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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c 127	13.8	76.7	271	10	US-09-923-876-5993	Sequence 5993, Ap	c 200	13.8	76.7	824	17	US-10-371-218A-12	Sequence 12, Appl
c 128	13.8	76.7	279	18	US-10-425-115-108956	Sequence 108956, A	c 201	13.8	76.7	824	17	US-10-456-573-12	Sequence 12, Appl
c 129	13.8	76.7	294	18	US-10-437-963-49607	Sequence 49607, A	c 202	13.8	76.7	824	18	US-10-785-116-12	Sequence 12, Appl
c 130	13.8	76.7	318	18	US-10-437-963-5115	Sequence 5115, Ap	c 203	13.8	76.7	830	18	US-10-425-115-26868	Sequence 26868, A
c 131	13.8	76.7	328	18	US-10-425-115-160530	Sequence 160530,	c 204	13.8	76.7	834	15	US-10-156-761-3300	Sequence 3300, Ap
c 132	13.8	76.7	339	17	US-10-335-977-3847	Sequence 3847, Ap	c 205	13.8	76.7	835	18	US-10-437-963-55487	Sequence 55487, A
c 133	13.8	76.7	344	17	US-10-242-535A-43458	Sequence 43458, A	c 206	13.8	76.7	855	17	US-10-425-114-4342	Sequence 4342, Ap
c 134	13.8	76.7	354	17	US-10-085-783A-43458	Sequence 43458, A	c 207	13.8	76.7	882	18	US-10-437-963-48660	Sequence 48660, A
c 135	13.8	76.7	355	18	US-10-425-115-5212	Sequence 5212, Ap	c 208	13.8	76.7	912	18	US-10-425-115-183238	Sequence 183238, A
c 136	13.8	76.7	401	17	US-10-424-599-113936	Sequence 113936,	c 209	13.8	76.7	973	17	US-10-425-114-12904	Sequence 12904, A
c 137	13.8	76.7	406	11	US-09-987-899-203	Sequence 203, App	c 210	13.8	76.7	978	14	US-10-227-884-51	Sequence 51, Appl
c 138	13.8	76.7	412	18	US-10-425-115-103241	Sequence 103241,	c 211	13.8	76.7	978	14	US-10-230-163-51	Sequence 51, Appl
c 139	13.8	76.7	420	18	US-10-437-963-39913	Sequence 39913, A	c 212	13.8	76.7	978	14	US-10-230-163-51	Sequence 51, Appl
c 140	13.8	76.7	433	18	US-10-425-115-14254	Sequence 14254, A	c 213	13.8	76.7	978	14	US-10-230-163-51	Sequence 51, Appl
c 141	13.8	76.7	466	10	US-09-918-995-21738	Sequence 21738, A	c 214	13.8	76.7	978	14	US-10-218-631-51	Sequence 51, Appl
c 142	13.8	76.7	483	18	US-10-425-115-56918	Sequence 56918, A	c 215	13.8	76.7	978	14	US-10-232-224-51	Sequence 51, Appl
c 143	13.8	76.7	484	18	US-10-767-701-29695	Sequence 29695, A	c 216	13.8	76.7	978	14	US-10-232-224-51	Sequence 51, Appl
c 144	13.8	76.7	512	18	US-10-425-115-107490	Sequence 107490,	c 217	13.8	76.7	978	14	US-10-216-159A-51	Sequence 51, Appl
c 145	13.8	76.7	524	18	US-10-767-701-26211	Sequence 26211, A	c 218	13.8	76.7	978	14	US-10-218-849-51	Sequence 51, Appl
c 146	13.8	76.7	529	17	US-10-437-963-46153	Sequence 46153, A	c 219	13.8	76.7	978	14	US-10-227-873-51	Sequence 51, Appl
c 147	13.8	76.7	531	17	US-10-425-114-20853	Sequence 20853, A	c 220	13.8	76.7	978	14	US-10-227-883-51	Sequence 51, Appl
c 148	13.8	76.7	531	18	US-10-425-115-160906	Sequence 160906,	c 221	13.8	76.7	978	14	US-10-219-076-51	Sequence 51, Appl
c 149	13.8	76.7	554	17	US-10-425-114-1869	Sequence 869, App	c 222	13.8	76.7	978	14	US-10-230-434-51	Sequence 51, Appl
c 150	13.8	76.7	560	17	US-10-424-599-130833	Sequence 130833,	c 223	13.8	76.7	978	14	US-10-219-003-51	Sequence 51, Appl
c 151	13.8	76.7	560	18	US-10-767-701-19354	Sequence 19354, A	c 224	13.8	76.7	978	14	US-10-219-075-51	Sequence 51, Appl
c 152	13.8	76.7	583	18	US-10-425-115-66546	Sequence 66546, A	c 225	13.8	76.7	978	14	US-10-219-464-51	Sequence 51, Appl
c 153	13.8	76.7	590	18	US-10-425-115-11524	Sequence 111524,	c 226	13.8	76.7	978	14	US-10-219-466-51	Sequence 51, Appl
c 154	13.8	76.7	591	18	US-10-437-963-99191	Sequence 99191, A	c 227	13.8	76.7	978	14	US-10-219-479-51	Sequence 51, Appl
c 155	13.8	76.7	593	13	US-10-027-632-84285	Sequence 84285, A	c 228	13.8	76.7	978	14	US-10-219-481-51	Sequence 51, Appl
c 156	13.8	76.7	593	13	US-10-027-632-84285	Sequence 84285, A	c 229	13.8	76.7	978	14	US-10-230-260-51	Sequence 51, Appl
c 157	13.8	76.7	704	13	US-10-027-632-277475	Sequence 277475,	c 230	13.8	76.7	978	14	US-10-232-231-51	Sequence 51, Appl

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C 232	13.8	76.7	978	14	US-10-216-165-51	Sequence 51, Appl	C 305	13.8	76.7	978	16	US-10-219-532-51	Sequence 51, Appl
C 233	13.8	76.7	978	14	US-10-218-956-51	Sequence 51, Appl	C 306	13.8	76.7	978	16	US-10-219-533-51	Sequence 51, Appl
C 234	13.8	76.7	978	14	US-10-219-468-51	Sequence 51, Appl	C 307	13.8	76.7	978	16	US-10-230-437-51	Sequence 51, Appl
C 235	13.8	76.7	978	14	US-10-219-478-51	Sequence 51, Appl	C 308	13.8	76.7	978	16	US-10-232-228-51	Sequence 51, Appl
C 236	13.8	76.7	978	14	US-10-219-536-51	Sequence 51, Appl	C 309	13.8	76.7	978	17	US-10-232-226-51	Sequence 51, Appl
C 237	13.8	76.7	978	14	US-10-233-205-51	Sequence 51, Appl	C 310	13.8	76.7	978	17	US-10-230-130-51	Sequence 51, Appl
C 238	13.8	76.7	978	14	US-10-219-072-51	Sequence 51, Appl	C 311	13.8	76.7	978	17	US-10-219-535-51	Sequence 51, Appl
C 239	13.8	76.7	978	14	US-10-219-470-51	Sequence 51, Appl	C 312	13.8	76.7	978	17	US-10-232-230-51	Sequence 51, Appl
C 240	13.8	76.7	978	14	US-10-219-474-51	Sequence 51, Appl	C 313	13.8	76.7	978	17	US-10-119-480-51	Sequence 51, Appl
C 241	13.8	76.7	978	14	US-10-219-524-51	Sequence 51, Appl	C 314	13.8	76.7	978	18	US-10-219-477-51	Sequence 51, Appl
C 242	13.8	76.7	978	14	US-10-219-528-51	Sequence 51, Appl	C 315	13.8	76.7	1040	18	US-10-767-701-7401	Sequence 7401, Ap
C 243	13.8	76.7	978	14	US-10-227-880-51	Sequence 51, Appl	C 316	13.8	76.7	1056	18	US-10-333-235A-8	Sequence 8, Appl
C 244	13.8	76.7	978	14	US-10-227-881-51	Sequence 51, Appl	C 317	13.8	76.7	1099	17	US-10-424-599-14392	Sequence 14392, A
C 245	13.8	76.7	978	14	US-10-227-882-51	Sequence 51, Appl	C 318	13.8	76.7	1102	17	US-10-424-599-57442	Sequence 57442, A
C 246	13.8	76.7	978	14	US-10-230-436-51	Sequence 51, Appl	C 319	13.8	76.7	1108	17	US-10-424-599-65473	Sequence 65473, A
C 247	13.8	76.7	978	14	US-10-232-223-51	Sequence 51, Appl	C 320	13.8	76.7	1155	17	US-10-424-599-10249	Sequence 10249, A
C 248	13.8	76.7	978	14	US-10-232-225-51	Sequence 51, Appl	C 321	13.8	76.7	1250	17	US-10-425-114-26729	Sequence 26729, A
C 249	13.8	76.7	978	14	US-10-232-227-51	Sequence 51, Appl	C 322	13.8	76.7	1253	17	US-10-425-114-30259	Sequence 30259, A
C 250	13.8	76.7	978	14	US-10-232-229-51	Sequence 51, Appl	C 323	13.8	76.7	1281	17	US-10-369-493-23719	Sequence 23719, A
C 251	13.8	76.7	978	14	US-10-232-234-51	Sequence 51, Appl	C 324	13.8	76.7	1326	17	US-10-425-114-8828	Sequence 8828, Ap
C 252	13.8	76.7	978	15	US-10-219-060-51	Sequence 51, Appl	C 325	13.8	76.7	1374	17	US-10-425-114-34379	Sequence 34379, A
C 253	13.8	76.7	978	15	US-10-216-160-51	Sequence 51, Appl	C 326	13.8	76.7	1386	18	US-10-437-963-62155	Sequence 62155, A
C 254	13.8	76.7	978	15	US-10-216-162-51	Sequence 51, Appl	C 327	13.8	76.7	1391	17	US-10-425-114-1026	Sequence 1026, Ap
C 255	13.8	76.7	978	15	US-10-216-164-51	Sequence 51, Appl	C 328	13.8	76.7	1391	17	US-10-425-114-20914	Sequence 20914, A
C 256	13.8	76.7	978	15	US-10-216-167-51	Sequence 51, Appl	C 329	13.8	76.7	1411	18	US-10-333-235A-10	Sequence 10, Appl
C 257	13.8	76.7	978	15	US-10-216-168-51	Sequence 51, Appl	C 330	13.8	76.7	1457	18	US-10-425-115-67882	Sequence 67882, A
C 258	13.8	76.7	978	15	US-10-219-065-51	Sequence 51, Appl	C 331	13.8	76.7	1472	17	US-10-424-599-10250	Sequence 10250, A
C 259	13.8	76.7	978	15	US-10-219-071-51	Sequence 51, Appl	C 332	13.8	76.7	1485	18	US-10-425-115-184438	Sequence 184438, A
C 260	13.8	76.7	978	15	US-10-219-074-51	Sequence 51, Appl	C 333	13.8	76.7	1500	17	US-10-424-599-65086	Sequence 65086, A
C 261	13.8	76.7	978	15	US-10-219-077-51	Sequence 51, Appl	C 334	13.8	76.7	1500	17	US-10-425-114-6300	Sequence 6300, Ap
C 262	13.8	76.7	978	15	US-10-219-465-51	Sequence 51, Appl	C 335	13.8	76.7	1552	17	US-10-424-599-47702	Sequence 47702, A
C 263	13.8	76.7	978	15	US-10-219-467-51	Sequence 51, Appl	C 336	13.8	76.7	1603	17	US-10-425-114-30639	Sequence 30639, A
C 264	13.8	76.7	978	15	US-10-219-469-51	Sequence 51, Appl	C 337	13.8	76.7	1617	17	US-10-260-238-1236	Sequence 1236, Ap
C 265	13.8	76.7	978	15	US-10-227-878-51	Sequence 51, Appl	C 338	13.8	76.7	1641	17	US-10-424-599-84251	Sequence 84251, A
C 266	13.8	76.7	978	15	US-10-229-974-51	Sequence 51, Appl	C 339	13.8	76.7	1641	18	US-10-437-963-88974	Sequence 88974, A
C 267	13.8	76.7	978	15	US-10-219-476-51	Sequence 51, Appl	C 340	13.8	76.7	1641	18	US-10-437-963-88978	Sequence 88978, A
C 268	13.8	76.7	978	15	US-10-219-482-51	Sequence 51, Appl	C 341	13.8	76.7	1652	18	US-10-425-115-26873	Sequence 26873, A
C 269	13.8	76.7	978	15	US-10-227-874-51	Sequence 51, Appl	C 342	13.8	76.7	1674	18	US-10-425-115-78655	Sequence 78655, A
C 270	13.8	76.7	978	15	US-10-230-183-51	Sequence 51, Appl	C 343	13.8	76.7	1693	18	US-10-739-930-4348	Sequence 4348, Ap
C 271	13.8	76.7	978	15	US-10-227-876-51	Sequence 51, Appl	C 344	13.8	76.7	1702	18	US-10-333-235A-11	Sequence 11, Appl
C 272	13.8	76.7	978	15	US-10-227-878-51	Sequence 51, Appl	C 345	13.8	76.7	1742	18	US-10-483-858-1	Sequence 1, Appl
C 273	13.8	76.7	978	15	US-10-229-974-51	Sequence 51, Appl	C 346	13.8	76.7	1796	18	US-10-425-115-182942	Sequence 182942, A
C 274	13.8	76.7	978	15	US-10-230-024-51	Sequence 51, Appl	C 347	13.8	76.7	1873	17	US-10-424-599-1155990	Sequence 1155990
C 275	13.8	76.7	978	15	US-10-230-113-51	Sequence 51, Appl	C 348	13.8	76.7	1907	18	US-10-437-963-19259	Sequence 19259, A
C 276	13.8	76.7	978	15	US-10-230-183-51	Sequence 51, Appl	C 349	13.8	76.7	2061	17	US-10-369-493-25516	Sequence 25516, A
C 277	13.8	76.7	978	15	US-10-230-234-51	Sequence 51, Appl	C 350	13.8	76.7	2146	18	US-10-425-115-184441	Sequence 184441, A
C 278	13.8	76.7	978	15	US-10-230-306-51	Sequence 51, Appl	C 351	13.8	76.7	2170	18	US-10-425-115-103901	Sequence 103901, A
C 279	13.8	76.7	978	15	US-10-230-426-51	Sequence 51, Appl	C 352	13.8	76.7	2175	18	US-10-425-114-34486	Sequence 34486, A
C 280	13.8	76.7	978	15	US-10-230-427-51	Sequence 51, Appl	C 353	13.8	76.7	2201	17	US-10-425-114-17054	Sequence 17054, A
C 281	13.8	76.7	978	15	US-10-230-435-51	Sequence 51, Appl	C 354	13.8	76.7	2205	18	US-10-425-115-78651	Sequence 78651, A
C 282	13.8	76.7	978	15	US-10-230-438-51	Sequence 51, Appl	C 355	13.8	76.7	2291	17	US-10-094-749-379	Sequence 379, App
C 283	13.8	76.7	978	15	US-10-232-222-51	Sequence 51, Appl	C 356	13.8	76.7	2298	17	US-10-369-493-36489	Sequence 36489, A
C 284	13.8	76.7	978	15	US-10-219-070-51	Sequence 51, Appl	C 357	13.8	76.7	2304	17	US-10-369-493-26433	Sequence 26433, A
C 285	13.8	76.7	978	15	US-10-219-472-51	Sequence 51, Appl	C 358	13.8	76.7	2317	18	US-10-425-115-71657	Sequence 71657, A
C 286	13.8	76.7	978	15	US-10-219-527-51	Sequence 51, Appl	C 359	13.8	76.7	2396	9	US-09-776-874A-43	Sequence 43, Appl
C 287	13.8	76.7	978	15	US-10-227-877-51	Sequence 51, Appl	C 360	13.8	76.7	2396	9	US-09-776-874A-45	Sequence 45, Appl
C 288	13.8	76.7	978	15	US-10-216-166-51	Sequence 51, Appl	C 361	13.8	76.7	2396	9	US-09-988-113-43	Sequence 43, Appl
C 289	13.8	76.7	978	15	US-10-218-612-51	Sequence 51, Appl	C 362	13.8	76.7	2396	9	US-09-988-113-45	Sequence 45, Appl
C 290	13.8	76.7	978	15	US-10-216-163-51	Sequence 51, Appl	C 363	13.8	76.7	2396	16	US-10-341-582-43	Sequence 43, Appl
C 291	13.8	76.7	978	16	US-10-218-765-51	Sequence 51, Appl	C 364	13.8	76.7	2396	16	US-10-341-582-45	Sequence 45, Appl
C 292	13.8	76.7	978	16	US-10-219-063-51	Sequence 51, Appl	C 365	13.8	76.7	2396	16	US-10-384-451-43	Sequence 43, Appl
C 293	13.8	76.7	978	16	US-10-219-066-51	Sequence 51, Appl	C 366	13.8	76.7	2396	16	US-10-384-451-45	Sequence 45, Appl
C 294	13.8	76.7	978	16	US-10-219-067-51	Sequence 51, Appl	C 367	13.8	76.7	2396	16	US-10-384-450-43	Sequence 43, Appl
C 295	13.8	76.7	978	16	US-10-219-068-51	Sequence 51, Appl	C 368	13.8	76.7	2396	16	US-10-384-450-45	Sequence 45, Appl
C 296	13.8	76.7	978	16	US-10-219-069-51	Sequence 51, Appl	C 369	13.8	76.7	2396	17	US-10-371-218A-43	Sequence 43, Appl
C 297	13.8	76.7	978	16	US-10-219-073-51	Sequence 51, Appl	C 370	13.8	76.7	2396	17	US-10-371-218A-45	Sequence 45, Appl
C 298	13.8	76.7	978	16	US-10-219-475-51	Sequence 51, Appl	C 371	13.8	76.7	2396	17	US-10-456-573-43	Sequence 43, Appl
C 299	13.8	76.7	978	16	US-10-219-480-51	Sequence 51, Appl	C 372	13.8	76.7	2396	17	US-10-456-573-45	Sequence 45, Appl
C 300	13.8	76.7	978	16	US-10-219-483-51	Sequence 51, Appl	C 373	13.8	76.7	2396	18	US-10-785-116-43	Sequence 43, Appl
C 301	13.8	76.7	978	16	US-10-219-525-51	Sequence 51, Appl	C 374	13.8	76.7	2396	18	US-10-785-116-45	Sequence 45, Appl
C 302	13.8	76.7	978	16	US-10-219-526-51	Sequence 51, Appl	C 375	13.8	76.7	2468	18	US-10-425-115-50904	Sequence 50904, A
C 303	13.8	76.7	978	16	US-10-219-530-51	Sequence 51, Appl	C 376	13.8	76.7	2472	17	US-10-425-114-24839	Sequence 24839, A

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c 378 13.8 76.7 2598 18 US-10-425-115-66550 Sequence 66550, A
c 379 13.8 76.7 2616 18 US-10-437-963-62681 Sequence 62681, A
c 380 13.8 76.7 2715 10 US-09-950-041-5 Sequence 5, Appl
c 381 13.8 76.7 2973 17 US-10-094-749-882 Sequence 882, App
c 382 13.8 76.7 3027 15 US-10-128-714-2156 Sequence 2156, App
c 383 13.8 76.7 3029 16 US-10-265-072-1 Sequence 1, Appl
c 384 13.8 76.7 3052 18 US-10-437-963-75712 Sequence 75712, A
c 385 13.8 76.7 3057 17 US-10-407-952-21 Sequence 21, Appl
c 386 13.8 76.7 3057 18 US-10-732-563-5 Sequence 5, Appl
c 387 13.8 76.7 3057 18 US-10-732-796A-5 Sequence 5, Appl
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c 389 13.8 76.7 3176 18 US-10-437-963-79138 Sequence 79138, A
c 390 13.8 76.7 3198 15 US-10-128-714-7156 Sequence 7156, App
c 391 13.8 76.7 3210 17 US-10-398-221-3803 Sequence 3803, App
c 392 13.8 76.7 3309 17 US-10-369-493-26915 Sequence 26915, A
c 393 13.8 76.7 3311 15 US-10-128-714-6156 Sequence 6156, App
c 394 13.8 76.7 3486 18 US-10-437-963-88912 Sequence 88912, A
c 395 13.8 76.7 3584 13 US-10-044-090-341 Sequence 341, App
c 396 13.8 76.7 4232 9 US-09-070-927A-71 Sequence 71, Appl
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c 398 13.8 76.7 4701 18 US-10-755-889-477 Sequence 477, App
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c 401 13.8 76.7 4892 17 US-10-117-722-492 Sequence 492, App
c 402 13.8 76.7 4964 15 US-10-037-270-491 Sequence 491, App
c 403 13.8 76.7 4964 17 US-10-117-722-491 Sequence 491, App
c 404 13.8 76.7 5081 15 US-10-128-714-156 Sequence 156, App
c 405 13.8 76.7 5311 15 US-10-161-927-35 Sequence 35, Appl
c 406 13.8 76.7 5650 17 US-10-161-927-35 Sequence 35, Appl
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c 408 13.8 76.7 27499 18 US-10-367-094-111 Sequence 111, App
c 409 13.8 76.7 34185 15 US-10-199-520-3 Sequence 3, Appl
c 410 13.8 76.7 34185 18 US-10-874-827-30 Sequence 3, Appl
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c 412 13.8 76.7 38734 11 US-09-989-687-30 Sequence 30, Appl
c 413 13.8 76.7 51259 17 US-10-374-077-209 Sequence 209, App
c 414 13.8 76.7 58645 13 US-10-087-192-1975 Sequence 1975, App
c 415 13.8 76.7 58645 17 US-10-293-864-11 Sequence 11, Appl
c 416 13.8 76.7 73900 17 US-10-085-117-295 Sequence 295, App
c 417 13.8 76.7 81098 13 US-10-087-192-2032 Sequence 2032, App
c 418 13.8 76.7 88853 13 US-10-087-192-85 Sequence 85, Appl
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c 430 13.4 74.4 25 15 US-10-098-263B-27588 Sequence 27588, A
c 431 13.4 74.4 25 19 US-10-719-900-228204 Sequence 228204, A
c 432 13.4 74.4 134 9 US-09-864-761-18378 Sequence 18378, A
c 433 13.4 74.4 151 9 US-09-923-876-3661 Sequence 3661, App
c 434 13.4 74.4 151 18 US-09-923-876-3661 Sequence 3661, App
c 435 13.4 74.4 156 18 US-10-425-115-58997 Sequence 58997, A
c 436 13.4 74.4 163 18 US-10-767-701-20717 Sequence 20717, A
c 437 13.4 74.4 169 18 US-10-437-963-68430 Sequence 68430, A
c 438 13.4 74.4 201 19 US-10-741-600-33956 Sequence 33956, A
c 439 13.4 74.4 208 9 US-09-783-590-3543 Sequence 3543, App
c 440 13.4 74.4 242 18 US-10-674-124A-25099 Sequence 25099, A
c 441 13.4 74.4 266 18 US-10-425-115-113717 Sequence 113717, A
c 442 13.4 74.4 275 9 US-09-923-876-5388 Sequence 5388, App
c 443 13.4 74.4 275 18 US-09-923-876-5388 Sequence 5388, App
c 444 13.4 74.4 276 18 US-10-425-115-104247 Sequence 104247, A
c 445 13.4 74.4 291 18 US-10-425-115-76494 Sequence 76494, A
c 446 13.4 74.4 302 17 US-10-425-115-137315 Sequence 137315, A
c 447 13.4 74.4 322 17 US-10-369-493-30456 Sequence 30456, A
c 448 13.4 74.4 324 18 US-10-425-115-59116 Sequence 59116, A
c 449 13.4 74.4 334 18 US-10-062-727-104 Sequence 104, App
c 450 13.4 74.4 377 9 US-09-867-701-1723 Sequence 1723, App

c 450 13.4 74.4 383 18 US-10-425-115-39728 Sequence 39728, A
c 451 13.4 74.4 395 13 US-10-027-632-305290 Sequence 305290, A
c 452 13.4 74.4 395 17 US-10-027-632-305290 Sequence 305290, A
c 453 13.4 74.4 414 17 US-10-378-029-17 Sequence 17, Appl
c 454 13.4 74.4 422 18 US-10-425-115-137972 Sequence 137972, A
c 455 13.4 74.4 423 18 US-10-437-963-30125 Sequence 30125, A
c 456 13.4 74.4 423 18 US-10-437-963-49282 Sequence 49282, A
c 457 13.4 74.4 425 18 US-10-425-115-46417 Sequence 46417, A
c 458 13.4 74.4 435 9 US-09-960-352-181 Sequence 181, App
c 459 13.4 74.4 438 18 US-10-437-963-48137 Sequence 48137, A
c 460 13.4 74.4 443 17 US-10-424-599-134081 Sequence 134081, A
c 461 13.4 74.4 454 14 US-10-062-727-32 Sequence 32, Appl
c 462 13.4 74.4 458 17 US-10-260-238-3714 Sequence 3714, App
c 463 13.4 74.4 459 16 US-10-029-386-19407 Sequence 19407, A
c 464 13.4 74.4 463 17 US-09-918-995-15839 Sequence 15839, A
c 465 13.4 74.4 471 17 US-10-260-238-4189 App Sequence 4189, App
c 466 13.4 74.4 472 13 US-10-027-632-60097 Sequence 60097, A
c 467 13.4 74.4 472 13 US-10-027-632-60595 Sequence 60595, A
c 468 13.4 74.4 472 13 US-10-027-632-61695 Sequence 61695, A
c 469 13.4 74.4 472 13 US-10-027-632-62185 Sequence 62185, A
c 470 13.4 74.4 472 13 US-10-027-632-63326 Sequence 63326, A
c 471 13.4 74.4 472 13 US-10-027-632-64085 Sequence 64085, A
c 472 13.4 74.4 472 17 US-10-027-632-60097 Sequence 60097, A
c 473 13.4 74.4 472 17 US-10-027-632-60595 Sequence 60595, A
c 474 13.4 74.4 472 17 US-10-027-632-61695 Sequence 61695, A
c 475 13.4 74.4 472 17 US-10-027-632-62185 Sequence 62185, A
c 476 13.4 74.4 472 17 US-10-027-632-63326 Sequence 63326, A
c 477 13.4 74.4 472 17 US-10-027-632-64085 Sequence 64085, A
c 478 13.4 74.4 475 17 US-10-424-599-49094 Sequence 49094, A
c 479 13.4 74.4 484 9 US-09-864-761-1620 Sequence 1620, App
c 480 13.4 74.4 485 18 US-10-767-701-19790 Sequence 19790, A
c 481 13.4 74.4 500 17 US-10-260-238-3742 Sequence 3742, App
c 482 13.4 74.4 501 9 US-09-783-590-11241 Sequence 11241, A
c 483 13.4 74.4 502 17 US-10-260-238-4242 Sequence 4242, App
c 484 13.4 74.4 507 17 US-10-260-238-3759 Sequence 3759, App
c 485 13.4 74.4 512 17 US-10-425-114-2771 Sequence 2771, App
c 486 13.4 74.4 516 17 US-10-260-238-4261 Sequence 4261, App
c 487 13.4 74.4 518 17 US-10-260-238-3752 Sequence 3752, App
c 488 13.4 74.4 529 18 US-10-468-488-292 Sequence 292, App
c 489 13.4 74.4 532 9 US-09-734-017A-39 Sequence 39, Appl
c 490 13.4 74.4 532 17 US-10-425-114-24747 Sequence 24747, A
c 491 13.4 74.4 535 9 US-09-770-152-774 Sequence 774, App
c 492 13.4 74.4 536 9 US-09-864-761-16465 Sequence 16465, A
c 493 13.4 74.4 536 17 US-10-260-238-3743 Sequence 3743, App
c 494 13.4 74.4 541 17 US-10-425-114-27467 Sequence 27467, A
c 495 13.4 74.4 542 17 US-10-260-238-4273 Sequence 4273, App
c 496 13.4 74.4 543 17 US-10-260-238-3748 Sequence 3748, App
c 497 13.4 74.4 543 17 US-10-425-114-23288 Sequence 23288, A
c 498 13.4 74.4 543 17 US-10-425-114-27397 Sequence 27397, A
c 499 13.4 74.4 544 17 US-10-260-238-3753 Sequence 3753, App
c 500 13.4 74.4 545 9 US-09-864-761-9887 Sequence 9887, App

ALIGNMENTS

RESULT 1
US-10-688-489-64
; Sequence 64, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Paul M.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: West Nile Virus
; FILE REFERENCE: GPI40-04 UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; PRIORITY FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16

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; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 64
; LENGTH: 18
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-64

Query Match      100.0%; Score 18; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGTTGAGT 18
Db 1 CGCCACCGGAGTTGAGT 18

RESULT 2
US-10-688-489-66
; Sequence 66, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GPI40-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 66
; LENGTH: 19
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-66
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Query Match      100.0%; Score 18; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGTTGAGT 18
Db 1 CGCCACCGGAGTTGAGT 18
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RESULT 3
US-10-688-489-62
; Sequence 62, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GPI40-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
```

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; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 62
; LENGTH: 20
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-62
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Query Match      100.0%; Score 18; DB 18; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGTTGAGT 18
Db 3 CGCCACCGGAGTTGAGT 20
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RESULT 4
US-10-688-489-63
; Sequence 63, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GPI40-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 21
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-63
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Query Match      100.0%; Score 18; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGTTGAGT 18
Db 3 CGCCACCGGAGTTGAGT 20
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RESULT 5
US-10-688-489-59
; Sequence 59, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
```

```
; TITLE OF INVENTION: West Nile Virus
; FILE REFERENCE: GPI40-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; SOFTWARE: FastSeq for Windows Version 3.0
; NUMBER OF SEQ ID NOS: 196
; SEQ ID NO 59
; LENGTH: 31
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-59

Query Match      100.0%; Score 18; DB 18; Length 31;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18
   |||||
Db 3 CGCCACCGGAAGTTGAGT 20

RESULT 6
US-10-361-002-5
; Sequence 5, Application US/10361002
; Publication No. US20040170954A1
; GENERAL INFORMATION:
; APPLICANT: Clearant, Inc.
; APPLICANT: McKenney, Keith
; APPLICANT: Gillmeister, Lidja
; APPLICANT: Marlowe, Kristina
; APPLICANT: Armistead, David
; TITLE OF INVENTION: Pathogen Inactivation Assay
; FILE REFERENCE: CI-0043
; CURRENT APPLICATION NUMBER: US/10/361,002
; CURRENT FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 10945
; TYPE: DNA
; ORGANISM: West Nile virus
US-10-361-002-5

Query Match      100.0%; Score 18; DB 18; Length 10945;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18
   |||||
Db 10482 CGCCACCGGAAGTTGAGT 10499

RESULT 7
US-10-361-004-5
; Sequence 5, Application US/10361004
; Publication No. US20040170981A1
; GENERAL INFORMATION:
; APPLICANT: Clearant, Inc.
; APPLICANT: McKenney, Keith
; APPLICANT: Gillmeister, Lidja
; APPLICANT: Marlowe, Kristina
; APPLICANT: Armistead, David
; TITLE OF INVENTION: Real-time Polymerase Chain Reaction Using Large Target Amplicons
; FILE REFERENCE: CI-0042
; CURRENT APPLICATION NUMBER: US/10/361,004
; CURRENT FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 99
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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 10945
; TYPE: DNA
; ORGANISM: West Nile virus
US-10-361-004-5

Query Match      100.0%; Score 18; DB 18; Length 10945;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18
   |||||
Db 10482 CGCCACCGGAAGTTGAGT 10499

RESULT 8
US-10-699-550-1
; Sequence 1, Application US/10699550
; Publication No. US20040197769A1
; GENERAL INFORMATION:
; APPLICANT: WONG, SUSAN J.
; APPLICANT: SHI, PEI-YONG
; TITLE OF INVENTION: DIAGNOSTIC TEST FOR WEST NILE VIRUS
; FILE REFERENCE: 454311-2232.1
; CURRENT APPLICATION NUMBER: US/10/699,550
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: 60/476,513
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/422,755
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: PCT/US02/09036
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: 60/402,860
; PRIOR FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/281,947
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/275,025
; PRIOR FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 1
; LENGTH: 10975
; TYPE: DNA
; ORGANISM: West Nile virus
US-10-699-550-1

Query Match      100.0%; Score 18; DB 18; Length 10975;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18
   |||||
Db 10506 CGCCACCGGAAGTTGAGT 10523

RESULT 9
US-10-699-550-2
; Sequence 2, Application US/10699550
; Publication No. US20040197769A1
; GENERAL INFORMATION:
; APPLICANT: WONG, SUSAN J.
; APPLICANT: SHI, PEI-YONG
; TITLE OF INVENTION: DIAGNOSTIC TEST FOR WEST NILE VIRUS
; FILE REFERENCE: 454311-2232.1
; CURRENT APPLICATION NUMBER: US/10/699,550
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: 60/476,513
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/422,755
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: PCT/US02/09036
; PRIOR FILING DATE: 2002-03-11
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; PRIOR APPLICATION NUMBER: 60/402,860
; PRIOR FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/281,947
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/275,025
; PRIOR FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 11029
; TYPE: DNA
; ORGANISM: West Nile virus
US-10-699-550-2

Query Match 100.0%; Score 18; DB 18; Length 11029;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18
|||
DB 10524 CGCCACCGGAAGTTGAGT 10541

RESULT 10
US-10-679-520A-66
; Sequence 66, Application US/10679520A
; Publication No. US20050031641A1
; GENERAL INFORMATION:
; APPLICANT: LOOSMORE, SHEENA MAY
; APPLICANT: AUDONNET, JEAN-CHRISTOPHE FRANCIS
; APPLICANT: MINKS, JULES MAARTEN
; TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST WEST NILE VIRUS
; FILE REFERENCE: 574313-3161.4
; CURRENT APPLICATION NUMBER: US/10/679,520A
; CURRENT FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: 10/374,953
; PRIOR FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: 10/116,298
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/281,923
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: PCT/FR02/01200
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: FR 01/04737
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 66
; LENGTH: 11029
; TYPE: DNA
; ORGANISM: West Nile virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (97)..(10395)
US-10-679-520A-66

Query Match 100.0%; Score 18; DB 19; Length 11029;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18
|||
DB 10524 CGCCACCGGAAGTTGAGT 10541

RESULT 11
US-10-706-892-1
; Sequence 1, Application US/10706892
; Publication No. US20050058987A1
; GENERAL INFORMATION:
; APPLICANT: SHI, PEI-YONG
; TITLE OF INVENTION: SCREENING FOR WEST NILE VIRUS ANTIVIRAL THERAPY
; FILE REFERENCE: 454311-2231.1

; CURRENT APPLICATION NUMBER: US/10/706,892
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/427,117
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 11029
; TYPE: DNA
; ORGANISM: West Nile virus
US-10-706-892-1

Query Match 100.0%; Score 18; DB 19; Length 11029;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18
|||
DB 10524 CGCCACCGGAAGTTGAGT 10541

RESULT 12
US-10-706-892-2
; Sequence 2, Application US/10706892
; Publication No. US20050058987A1
; GENERAL INFORMATION:
; APPLICANT: SHI, PEI-YONG
; TITLE OF INVENTION: SCREENING FOR WEST NILE VIRUS ANTIVIRAL THERAPY
; FILE REFERENCE: 454311-2231.1
; CURRENT APPLICATION NUMBER: US/10/706,892
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/427,117
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 11029
; TYPE: DNA
; ORGANISM: West Nile virus
US-10-706-892-2

Query Match 100.0%; Score 18; DB 19; Length 11029;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18
|||
DB 10524 CGCCACCGGAAGTTGAGT 10541

RESULT 13
US-10-688-489-65
; Sequence 65, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: LINNEN, JEFFREY M.
; APPLICANT: POLLNER, REINHOLD B.
; APPLICANT: WU, WEN
; APPLICANT: DENNIS, GEOFFREY G.
; APPLICANT: DARBY, PAUL M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0

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; SEQ ID NO 65
; LENGTH: 18
; TYPE: DNA
; ORGANISM: West Nile Virus
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1)...(1)
; OTHER INFORMATION: I
US-10-688-489-65

Query Match          94.4%; Score 17; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCACCGGAAGTTGAGT 18
   |||||
Db 2 GCCACCGGAAGTTGAGT 18

RESULT 14
US-10-688-489-60
; Sequence 60, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; TITLE OF INVENTION: West Nile Virus
; FILE REFERENCE: GP140-04.U7
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 60
; LENGTH: 19
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-60

Query Match          94.4%; Score 17; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 17
   |||||
Db 3 CGCCACCGGAAGTTGAGT 19

RESULT 15
US-10-688-489-61
; Sequence 61, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; TITLE OF INVENTION: West Nile Virus
; FILE REFERENCE: GP140-04.U7
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 60
; LENGTH: 19
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-60

Query Match          94.4%; Score 17; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 17
   |||||
Db 3 CGCCACCGGAAGTTGAGT 19

RESULT 16
US-10-719-900-668130/c
; Sequence 668130, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 668130
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-668130

Query Match          91.1%; Score 16.4; DB 19; Length 25;
Best Local Similarity 94.4%; Pred. No. 57;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18
   |||||
Db 20 CGCCACCGGAAGTTGAGT 3

RESULT 17
US-10-481-265-136/c
; Sequence 136, Application US/10481265
; Publication No. US20040254349A1
; GENERAL INFORMATION:
; APPLICANT: James, Brian William
; APPLICANT: Bacon, Joanna
; APPLICANT: Marsh, Philip
; TITLE OF INVENTION: Mycobacterial Antigens Expressed Under Low Oxygen Tension
; FILE REFERENCE: 1581.1020000
; CURRENT APPLICATION NUMBER: US/10/481,265
; CURRENT FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: GB 0115365.9
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: GB 0121780.1
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: PCT/GB02/02845
; PRIOR FILING DATE: 2002-06-21
```


; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 136
; LENGTH: 1323
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; US-10-481-263-136

Query Match 88.9%; Score 16; DB 18; Length 1323;

Best Local Similarity 100.0%; Pred. No. 96;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCACCGGAAGTTGAG 17
|||||
DB 1037 GCCACCGGAAGTTGAG 1022

RESULT 18

US-09-712-363-49/c
; Sequence 49, Application US/09712363
; Patent No. US20020164588A1

; GENERAL INFORMATION:

; APPLICANT: Eisenberg, David

; APPLICANT: Rotstein, Sergio H.

; APPLICANT: Marcotte, Edward M.

; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND

; INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS

; FILE REFERENCE: 07419-032001

; CURRENT APPLICATION NUMBER: US/09/712,363

; CURRENT FILING DATE: 2000-11-13

; PRIOR APPLICATION NUMBER: PCT/US00/02246

; PRIOR FILING DATE: 2000-01-28

; PRIOR APPLICATION NUMBER: 60/179,531

; PRIOR FILING DATE: 2000-02-01

; PRIOR APPLICATION NUMBER: 60/117,844

; PRIOR FILING DATE: 1999-01-29

; PRIOR APPLICATION NUMBER: 60/118,206,

; PRIOR FILING DATE: 1999-02-01

; PRIOR APPLICATION NUMBER: 60/126,593

; PRIOR FILING DATE: 1999-03-26

; PRIOR APPLICATION NUMBER: 60/134,093

; PRIOR FILING DATE: 1999-05-14

; PRIOR APPLICATION NUMBER: 60/134,092

; PRIOR FILING DATE: 1999-05-14

; PRIOR APPLICATION NUMBER: 60/165,124

; PRIOR FILING DATE: 1999-11-12

; PRIOR APPLICATION NUMBER: 60/165,086

; PRIOR FILING DATE: 1999-11-12

; NUMBER OF SEQ ID NOS: 292

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 49

; LENGTH: 1326

; TYPE: DNA

; ORGANISM: Mycobacterium tuberculosis

; US-09-712-363-49

Query Match 88.9%; Score 16; DB 9; Length 1326;

Best Local Similarity 100.0%; Pred. No. 96;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCACCGGAAGTTGAG 17
|||||
DB 1037 GCCACCGGAAGTTGAG 1022

RESULT 19

US-10-027-632-299210/c

; Sequence 299210, Application US/10027632

; Publication No. US20020198371A1

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; Polymorphisms in the Human Genome

; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 299210
; LENGTH: 631
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-299210

Query Match 85.6%; Score 15.4; DB 13; Length 631;

Best Local Similarity 94.1%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCCACCGGAAGTTGAGT 18
|||||
DB 520 GCCACCGGAAGTTGAGT 504

RESULT 20

US-10-027-632-299210/c

; Sequence 299210, Application US/10027632

; Publication No. US20030204075A9

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; Polymorphisms in the Human Genome

; FILE REFERENCE: 108827.129

; CURRENT APPLICATION NUMBER: US/10/027,632

; CURRENT FILING DATE: 2002-04-30

; PRIOR APPLICATION NUMBER: US 60/218,006

; PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/198,676

; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 60/193,483

; PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: US 60/185,218

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 60/146,002

; PRIOR FILING DATE: 1999-08-09

; NUMBER OF SEQ ID NOS: 325720

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 299210

; LENGTH: 631

; TYPE: DNA

; ORGANISM: Human

; US-10-027-632-299210

Query Match 85.6%; Score 15.4; DB 17; Length 631;

Best Local Similarity 94.1%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCCACCGGAAGTTGAGT 18
|||||

Db 520 GCCAACGGAAGTTGAGT 504

RESULT 21

US-10-027-632-44859/c
; Sequence 44859, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/195,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44859
; LENGTH: 669
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-44859

Query Match 85.6%; Score 15.4; DB 13; Length 669;
Best Local Similarity 94.1%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCCACCGGAAGTTGAGT 18
|||||
Db 504 GCCAACGGAAGTTGAGT 488

RESULT 22

US-10-027-632-44859/c
; Sequence 44859, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44859

; LENGTH: 669
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-44859

Query Match 85.6%; Score 15.4; DB 17; Length 669;
Best Local Similarity 94.1%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCCACCGGAAGTTGAGT 18
|||||
Db 504 GCCAACGGAAGTTGAGT 488

RESULT 23

US-10-767-701-11247/c
; Sequence 11247, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 11247
; LENGTH: 793
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS19479_1
US-10-767-701-11247

Query Match 85.6%; Score 15.4; DB 18; Length 793;
Best Local Similarity 94.1%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17
|||||
Db 326 CGCCCGCGGAAGTTGAG 310

RESULT 24

US-10-425-115-119320/c
; Sequence 119320, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 119320
; LENGTH: 1989
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_40302C.1
US-10-425-115-119320

Query Match 85.6%; Score 15.4; DB 18; Length 1989;
Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAG 17

```

Db      1470 CGCCCCCGGAAGTTGAGT 1454
||||| ||||| ||||| ||||| |||||

RESULT 25
US-10-425-115-119315/c
; Sequence 119315, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 119315
; LENGTH: 2358
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_40299C.1
US-10-425-115-119315

Query Match      85.6%; Score 15.4; DB 18; Length 2358;
Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGCCACCGGAAGTTGAGT 17
||||| ||||| ||||| ||||| |||||

Db      1874 CGCCCCCGGAAGTTGAGT 1858

RESULT 26
US-10-600-230-69
; Sequence 69, Application US/10600230
; Publication No. US2004092020A1
; GENERAL INFORMATION:
; APPLICANT: Wilkinson, Jack
; APPLICANT: McBride, Kevin
; APPLICANT: Bertain, Sean
; TITLE OF INVENTION: GENETIC CONSTRUCTS HAVING HETEROLOGOUS
; TITLE OF INVENTION: 3' POLYADENYLATION SIGNAL SEQUENCE MOTIFS THAT FUNCTION IN
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 0325.210
; CURRENT APPLICATION NUMBER: US/10/600,230
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: 60/390,529
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 69
; LENGTH: 2878
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-10-600-230-69

Query Match      85.6%; Score 15.4; DB 17; Length 2878;
Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGCCACCGGAAGTTGAGT 17
||||| ||||| ||||| ||||| |||||

Db      727 CGCCACCGGAAGTCGAG 743

RESULT 27
US-10-719-993-7004/c
; Sequence 7004, Application US/10719993
; Publication No. US20040265849A1

```

```
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 263852
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3814)..(4319)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6552)..(6571)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (17206)..(17225)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (19680)..(19699)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (24320)..(24339)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (26572)..(26591)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (32986)..(33005)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (56103)..(56724)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (59672)..(59691)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (61525)..(61544)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (71035)..(71054)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (79771)..(79807)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (91343)..(91801)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (141749)..(141768)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (144739)..(144758)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (164171)..(164340)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature-
```

```
; LOCATION: (173689)..(173708)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (175051)..(175070)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (192924)..(192993)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (202010)..(202029)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (247837)..(247856)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (251852)..(252421)
; OTHER INFORMATION: n is a, c, g, or t
US-10-812-232-6
```

Query Match 85.6%; Score 15.4; DB 18; Length 263852;
Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCCACCGGAAGTTGAGT 18
|||||

Db 208679 GCCACCTGAAGTTGAGT 208695
|||||

RESULT 30

```
US-10-719-993-6822
; Sequence 6822, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 5342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6822
; LENGTH: 786452
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(786452)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-719-993-6822
```

Query Match 85.6%; Score 15.4; DB 18; Length 786452;
Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCCACCGGAAGTTGAGT 18
|||||

Db 503852 GCCACCTGAAGTTGAGT 503868
|||||

RESULT 31

```
US-10-098-263B-27587
; Sequence 27587, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
```

; CURRENT APPLICATION NUMBER: US/10/098,263B
 ; CURRENT FILING DATE: 2003-01-08
 ; PRIOR APPLICATION NUMBER: 60/276,759
 ; PRIOR FILING DATE: 2001-03-16
 ; NUMBER OF SEQ ID NOS: 131066
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 27587
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-10-098-263B-27587

Query Match 83.3%; Score 15; DB 15; Length 25;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CACCGGAAGTTGAGT 18
 |||||
 Db 2 CACCGGAAGTTGAGT 16

RESULT 32
 US-10-425-115-139988/c
 ; Sequence 139988, Application US/10425115
 ; Publication No. US20040214272A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53222)B
 ; CURRENT APPLICATION NUMBER: US/10/425,115
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 369326
 ; SEQ ID NO 139988
 ; LENGTH: 351
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: MRT4577_59153C.1
 US-10-425-115-139988

Query Match 83.3%; Score 15; DB 18; Length 351;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CACCGGAAGTTGAG 17
 |||||
 Db 268 CACCGGAAGTTGAG 254

RESULT 33
 US-10-767-701-25132/c
 ; Sequence 25132, Application US/10767701
 ; Publication No. US20040172684A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53535)B
 ; CURRENT APPLICATION NUMBER: US/10/767,701
 ; CURRENT FILING DATE: 2004-01-29
 ; NUMBER OF SEQ ID NOS: 63128
 ; SEQ ID NO 25132
 ; LENGTH: 685
 ; TYPE: DNA
 ; ORGANISM: Sorghum bicolor
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: 30947447

US-10-767-701-25132

Query Match 83.3%; Score 15; DB 18; Length 685;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCACCGGAAGTTGAG 17
 |||||
 Db 250 CCACCGGAAGTTGAG 236

RESULT 34
 US-09-738-626-437/c
 ; Sequence 437, Application US/09738626
 ; Publication No. US20020197605A1
 ; GENERAL INFORMATION:
 ; APPLICANT: NAKAGAWA, SATOSHI
 ; APPLICANT: MIZOGUCHI, HIROSHI
 ; APPLICANT: ANDO, SEIKO
 ; APPLICANT: HAYASHI, MIKIRO
 ; APPLICANT: OCHIAI, KEIKO
 ; APPLICANT: YOKOI, HARUHIKO
 ; APPLICANT: TATEISHI, NAKO
 ; APPLICANT: SENOH, AKIHIRO
 ; APPLICANT: IKEDA, MASATO
 ; APPLICANT: OZAKI, AKIO
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ; FILE REFERENCE: 249-125
 ; CURRENT APPLICATION NUMBER: US/09/738,626
 ; CURRENT FILING DATE: 2000-12-18
 ; PRIOR APPLICATION NUMBER: JP 99/377484
 ; PRIOR FILING DATE: 1999-12-16
 ; PRIOR APPLICATION NUMBER: JP 00/159162
 ; PRIOR FILING DATE: 2000-04-07
 ; PRIOR APPLICATION NUMBER: JP 00/280988
 ; PRIOR FILING DATE: 2000-08-03
 ; NUMBER OF SEQ ID NOS: 7059
 ; SOFTWARE: PatentIn ver. 3.0
 ; SEQ ID NO 437
 ; LENGTH: 1863
 ; TYPE: DNA
 ; ORGANISM: Corynebacterium glutamicum
 US-09-738-626-437

Query Match 83.3%; Score 15; DB 9; Length 1863;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCACCGGAAGTTGAG 17
 |||||
 Db 734 CCACCGGAAGTTGAG 720

RESULT 35
 US-10-494-672-341/c
 ; Sequence 341, Application US/10494672
 ; Publication No. US20050003494A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Zelder, Oskar
 ; APPLICANT: Pompejus, Markus
 ; APPLICANT: Schroder, Hartwig
 ; APPLICANT: Kroger, Burkhard
 ; APPLICANT: Klepprogge, Corinna
 ; APPLICANT: Haberhauser, Gregor
 ; TITLE OF INVENTION: Genes coding for novel proteins
 ; FILE REFERENCE: BGI-169US
 ; CURRENT APPLICATION NUMBER: US/10/494,672
 ; CURRENT FILING DATE: 2004-05-04
 ; PRIOR APPLICATION NUMBER: PCT/EP02/12134
 ; PRIOR FILING DATE: 2002-10-31
 ; PRIOR APPLICATION NUMBER: DE 10154177
 ; PRIOR FILING DATE: 2001-11-05
 ; NUMBER OF SEQ ID NOS: 434

```
; SEQ ID NO 341
; LENGTH: 1969
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(1939)
; OTHER INFORMATION: RXA02825
US-10-494-672-341

Query Match      83.3%; Score 15; DB 18; Length 1969;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 CCACCGGAAGTTGAG 17
Db      810 CCACCGGAAGTTGAG 796

RESULT 36
US-10-425-114-35701/c
; Sequence 35701, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 35701
; LENGTH: 2066
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMROB73080G04_FLI
US-10-425-114-35701

Query Match      83.3%; Score 15; DB 17; Length 2066;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 CCACCGGAAGTTGAG 17
Db      1689 CCACCGGAAGTTGAG 1675

RESULT 37
US-09-738-626-1/c
; Sequence 1, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
```

```
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1
; LENGTH: 3309400
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1

Query Match      83.3%; Score 15; DB 9; Length 3309400;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 CCACCGGAAGTTGAG 17
Db      411416 CCACCGGAAGTTGAG 411402

RESULT 38
US-10-719-900-668131/c
; Sequence 668131, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 668131
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-668131

Query Match      82.2%; Score 14.8; DB 19; Length 25;
Best Local Similarity 88.9%; Pred. No. 4.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CGCCACCGGAAGTTGAGT 18
Db      20 CGCCACCGGAAGTTGAGT 3

RESULT 39
US-10-437-963-69977/c
; Sequence 69977, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 69977
; LENGTH: 447
; TYPE: DNA
```

```
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_70594C.1
US-10-437-963-69977

Query Match      82.2%; Score 14.8; DB 18; Length 447;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18
    |||||
Db 258 CGCCGCCCGAAGTTGAGT 241

RESULT 40
US-10-767-701-4048/c
; Sequence 4048, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 4048
; LENGTH: 590
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS7084_1
US-10-767-701-4048

Query Match      82.2%; Score 14.8; DB 18; Length 590;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18
    |||||
Db 146 CGCCACCGGTAGTGAGT 129

RESULT 41
US-10-357-930-23087/c
; Sequence 23087, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28954
; LENGTH: 872
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1, 2, 3, 866, 867, 868, 869, 870, 871, 872
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-28954

Query Match      82.2%; Score 14.8; DB 18; Length 872;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18
    |||||
Db 236 CGCCACCGGAAGTTGAGT 219

RESULT 42
US-10-357-930-28954/c
; Sequence 28954, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28954
; LENGTH: 872
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1, 2, 3, 866, 867, 868, 869, 870, 871, 872
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-28954

Query Match      82.2%; Score 14.8; DB 18; Length 872;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18
    |||||
Db 236 CGCCACCGGAAGTTGAGT 219

RESULT 43
US-09-938-842A-1526/c
; Sequence 1526, Application US/09938842A
```

```
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23087
; LENGTH: 872
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1, 2, 3, 866, 867, 868, 869, 870, 871, 872
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-23087

Query Match      82.2%; Score 14.8; DB 18; Length 872;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18
    |||||
Db 236 CGCCACCGGAAGTTGAGT 219

RESULT 42
US-10-357-930-28954/c
; Sequence 28954, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28954
; LENGTH: 872
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1, 2, 3, 866, 867, 868, 869, 870, 871, 872
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-28954

Query Match      82.2%; Score 14.8; DB 18; Length 872;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAAGTTGAGT 18
    |||||
Db 236 CGCCACCGGAAGTTGAGT 219

RESULT 43
US-09-938-842A-1526/c
; Sequence 1526, Application US/09938842A
```

```
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRI1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1526
; LENGTH: 945
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-09-938-842A-1526
```

```
Query Match 82.2%; Score 14.8; DB 9; Length 945;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 CGCCACCGGAAGTTGAGT 18
Db 770 CGCCACCGTGAGTTGAGT 753
|||||
```

RESULT 44

```
US-09-938-842A-1526/c
; Sequence 1526, Application US/09939842A
; Publication No. US20040009476A9
```

```
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRI1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1526
; LENGTH: 945
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-09-938-842A-1526
```

```
Query Match 82.2%; Score 14.8; DB 11; Length 945;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 CGCCACCGGAAGTTGAGT 18
Db 770 CGCCACCGTGAGTTGAGT 753
|||||
```

RESULT 45

```
US-09-956-004-27/c
; Sequence 27, Application US/09956004
; Patent No. US20020072595A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Patrick J. Dillon et al.
; TITLE OF INVENTION: Nucleotide Sequences of Escherichia coli Pathogenicity Islands
; FILE REFERENCE: PB324D1
; CURRENT APPLICATION NUMBER: US/09/956,004
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 08/976,259
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/061,953
; PRIOR FILING DATE: 1997-10-14
; PRIOR APPLICATION NUMBER: 60/031,626
; PRIOR FILING DATE: 1996-11-22
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 1118
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (142)..(142)
; OTHER INFORMATION: n equals a, t, g, or c
; NAME/KEY: misc_feature
; LOCATION: (228)..(228)
; OTHER INFORMATION: n equals a, t, g, or c
; NAME/KEY: misc_feature
; LOCATION: (261)..(261)
; OTHER INFORMATION: n equals a, t, g, or c
; NAME/KEY: misc_feature
; LOCATION: (693)..(693)
; OTHER INFORMATION: n equals a, t, g, or c
; US-09-956-004-27
```

```
Query Match 82.2%; Score 14.8; DB 9; Length 1118;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 CGCCACCGGAAGTTGAGT 18
Db 1054 CGCCACAGGAGGTGAGT 1037
|||||
```

RESULT 46

```
US-10-808-570-27/c
; Sequence 27, Application US/10808570
; Publication No. US20040192903A1
; GENERAL INFORMATION:
; APPLICANT: Patrick J. Dillon et al.
; TITLE OF INVENTION: Nucleotide Sequences of Escherichia coli Pathogenicity Islands
; FILE REFERENCE: PB324D1
; CURRENT APPLICATION NUMBER: US/10/808,570
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/956,004
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 08/976,259
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/061,953
; PRIOR FILING DATE: 1997-10-14
; PRIOR APPLICATION NUMBER: 60/031,626
; PRIOR FILING DATE: 1996-11-22
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 1118
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (142)..(142)
; OTHER INFORMATION: n equals a, t, g, or c
; NAME/KEY: misc_feature
; LOCATION: (228)..(228)
```


OTHER INFORMATION: n equals a, t, g, or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (261)..(261)
OTHER INFORMATION: n equals a, t, g, or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (693)..(693)
OTHER INFORMATION: n equals a, t, g, or c
US-10-808-570-27

Query Match 82.2%; Score 14.8; DB 18; Length 1118;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGTTGAGT 18
DB 1054 CGCCACGAGGTTGAGT 1037

RESULT 47

US-09-738-626-3346/c
Sequence 3346, Application US/09738626
Publication No. US20020197605A1

GENERAL INFORMATION:

APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125

CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 3346

LENGTH: 1125
TYPE: DNA

ORGANISM: Corynebacterium glutamicum
US-09-738-626-3346

Query Match 82.2%; Score 14.8; DB 9; Length 1125;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGTTGAGT 18
DB 838 CGCCACCGGAGTTGGT 821

RESULT 48

US-10-282-122A-6914/c

Sequence 6914, Application US/10282122A
Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith

APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6914

LENGTH: 1149
TYPE: DNA
ORGANISM: Escherichia coli
US-10-282-122A-6914

Query Match 82.2%; Score 14.8; DB 17; Length 1149;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCCACCGGAGTTGAGT 18
DB 1107 CGCCACCGGAGTGCAGT 1090

RESULT 49

US-10-282-122A-7527

Sequence 7527, Application US/10282122A
Publication No. US20040029129A1

GENERAL INFORMATION:

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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/230,335
 ; PRIOR FILING DATE: 2000-09-06
 ; PRIOR APPLICATION NUMBER: 60/230,347
 ; PRIOR FILING DATE: 2000-09-09
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/267,636
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 78614
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 7527
 ; LENGTH: 1479
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 US-10-282-122A-7527

Query Match 82.2%; Score 14.8; DB 9; Length 1479;
 Best Local Similarity 88.9%; Pred. No. 4.4e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 DB 1184 CGCCACCGGAGCGGAGT 1201

RESULT 50

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 ; Sequence 2696, Application US/09738626
 ; Publication No. US20020197605A1
 ; GENERAL INFORMATION:
 ; APPLICANT: NAKAGAWA, SATOSHI
 ; APPLICANT: MIZOGUCHI, HIROSHI
 ; APPLICANT: ANDO, SEIKO
 ; APPLICANT: HAYASHI, MIKIRO
 ; APPLICANT: OCHIAI, KEIKO
 ; APPLICANT: YOKOI, HARUHIKO
 ; APPLICANT: TATEISHI, NAKO
 ; APPLICANT: SENOH, AKIHIRO
 ; APPLICANT: IKEDA, MASATO
 ; APPLICANT: OZAKI, AKIO
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ; FILE REFERENCE: 249-125
 ; CURRENT APPLICATION NUMBER: US/09/738,626
 ; CURRENT FILING DATE: 2000-12-18
 ; PRIOR APPLICATION NUMBER: JP 99/377484
 ; PRIOR FILING DATE: 1999-12-16
 ; PRIOR APPLICATION NUMBER: JP 00/159162
 ; PRIOR FILING DATE: 2000-04-07
 ; PRIOR APPLICATION NUMBER: JP 00/280988
 ; PRIOR FILING DATE: 2000-08-03
 ; NUMBER OF SEQ ID NOS: 7059
 ; SOFTWARE: PatentIn ver. 3.0
 ; SEQ ID NO 2696
 ; LENGTH: 2103
 ; TYPE: DNA
 ; ORGANISM: Corynebacterium glutamicum
 US-09-738-626-2696

Query Match 82.2%; Score 14.8; DB 9; Length 2103;
 Best Local Similarity 88.9%; Pred. No. 4.4e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 640 CGCCACCGGAGTTGAGT 623

Search completed: March 25, 2005, 14:02:52
 Job time : 259.286 secs

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OM nucleic - nucleic search, using sw model

Run on: March 25, 2005, 07:23:09 ; Search time 945.418 Seconds
(without alignments)
2460.130 Million cell updates/sec

Title: US-10-688-489-73

Perfect score: 48
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Scoring table: OLIGO NUC
Gapop_60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

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Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 3	48	100.0	463	14	AF458355 West Nile
C 4	48	100.0	542	14	AF297854 Kunjin vi
C 5	48	100.0	587	14	KUNNS5GAA
C 6	48	100.0	587	14	KUNNS5GAB
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C 8	48	100.0	607	14	AF297841 Kunjin vi
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C 14	48	100.0	633	14	AF297858 Kunjin vi
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C 30	41	85.4	593	14	AF297847 Kunjin vi
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C 95	24	50.0	395	14	AF458358	AF458358 West Nile	C 168	22	45.8	10978	14	AY184212	Japanese
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C 97	24	50.0	481	14	AF458359	AF458359 West Nile	C 170	20	41.7	225005	2	AC102985	Rattus no
C 98	24	50.0	481	14	AF458357	AF458357 West Nile	C 171	20	41.7	239694	2	AC128965	Rattus no
C 99	24	50.0	483	14	AF458354	AF458354 West Nile	C 172	19	39.6	459	14	JEVNS5GAB	Japanese en
C 100	24	50.0	483	14	AF458357	AF458357 West Nile	C 173	19	39.6	562	14	FVNS5GAH	Japanese en
C 101	24	50.0	484	14	AF196533	AF196533 West Nile	C 174	18	37.5	99592	9	AF263284	Mouse sapi
C 102	24	50.0	591	14	AF196534	AF196534 West Nile	C 175	18	37.5	129841	2	AC140102	Fella cat
C 103	24	50.0	593	14	WVNS5GAA	WVNS5GAA West Nile v	C 176	18	37.5	173053	10	AL844145	Mouse sapi
C 104	24	50.0	607	14	KUNNS5	L49311 Kunjin viru	C 177	18	37.5	187204	9	AC084082	Mouse sapi
C 105	24	50.0	674	14	AF196535	AF196535 West Nile	C 178	17	35.4	2774	5	BC076107	Danio rer
C 106	24	50.0	687	14	AF196539	AF196539 West Nile	C 179	17	35.4	70203	2	AC091058	Homo sapi
C 107	24	50.0	917	14	AF208017	AF208017 West Nile	C 180	17	35.4	91436	8	NCB14A6	Neurospor
C 108	24	50.0	10962	14	WNEFCG	M12294 West Nile v	C 181	17	35.4	131140	2	AC027474	Homo sapi
C 109	24	50.0	11057	14	AF688948	AF688948 West Nile	C 182	17	35.4	151032	9	AC105201	Homo sapi
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C 111	22	45.8	424	14	AF092550	AF092550 Japanese	C 184	17	35.4	162508	2	AC025870	Homo sapi
C 112	22	45.8	424	14	AF092552	AF092552 Japanese	C 185	17	35.4	171729	2	BX323824	Danio rer
C 113	22	45.8	424	14	AF092553	AF092553 Japanese	C 186	17	35.4	174200	2	AC022797	Homo sapi
C 114	22	45.8	424	14	JEVNSGAC	L54067 Japanese en	C 187	17	35.4	177675	10	AC123034	AC123034 Mus muscu
C 115	22	45.8	424	14	JEVNSGAD	L54068 Japanese en	C 188	17	35.4	180360	9	AC011139	Homo sapi
C 116	22	45.8	424	14	JEVNSGAE	L54069 Japanese en	C 189	17	35.4	182448	2	AC090323	Homo sapi
C 117	22	45.8	424	14	JEVNSGAF	L54070 Japanese en	C 190	17	35.4	184683	2	AP001640	Homo sapi
C 118	22	45.8	424	14	JEVNSGAG	L54071 Japanese en	C 191	17	35.4	186773	10	AC135356	Homo sapi
C 119	22	45.8	424	14	JEVNSGAH	L54072 Japanese en	C 192	17	35.4	188893	10	AL147108	Mus muscu
C 120	22	45.8	424	14	JEVNSGAI	L54122 Japanese en	C 193	17	35.4	189104	10	AL806522	Mouse DNA
C 121	22	45.8	424	14	JEVNSGAJ	L54123 Japanese en	C 194	17	35.4	189115	2	AC107680	Mus muscu
C 122	22	45.8	463	14	AF458343	AF458343 West Nile	C 195	17	35.4	220458	9	AC010320	Homo sapi
C 123	22	45.8	463	14	AF278556	AF278556 Japanese	C 196	17	35.4	255755	2	AC115792	Mus muscu
C 124	22	45.8	533	14	JEVNSGAA	L48967 Japanese en	C 197	16	33.3	576	14	AF306515	Japanese
C 125	22	45.8	536	14	AF148900	AF148900 Japanese	C 198	16	33.3	576	14	AF306516	Japanese
C 126	22	45.8	566	14	VPNG6544P2	AF139531 Japanese	C 199	16	33.3	681	9	HS330526	Homo sapi
C 127	22	45.8	572	14	AF306514	AF306514 Japanese	C 200	16	33.3	1336	8	BT003419	Arabidops
C 128	22	45.8	582	14	AF218068	AF218068 Japanese	C 201	16	33.3	1389	8	AK062201	Arabidops
C 129	22	45.8	583	14	AF251616	AF251616 Japanese	C 202	16	33.3	1516	8	BT006103	Oryza sat
C 130	22	45.8	598	14	AF289816	AF289816 Japanese	C 203	16	33.3	1585	8	ATU79159	Arabidops
C 131	22	45.8	625	14	AF318291	AF318291 Japanese	C 204	16	33.3	1583	8	ATU79159	Arabidops
C 132	22	45.8	972	14	AF3111748	AF3111748 Japanese	C 205	16	33.3	1599	8	ATU79159	Arabidops
C 133	22	45.8	10951	14	JEVLINGCG	L78128 Japanese en	C 206	16	33.3	1744	8	ATU79159	Arabidops
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C 136	22	45.8	10965	14	AB051292	AB051292 Japanese	C 209	16	33.3	2886	8	AY491400	Setaria i
C 137	22	45.8	10968	14	AY585242	AY585242 Japanese	C 210	16	33.3	3307	8	AF271995	Echinochl
C 138	22	45.8	10968	14	AY585243	AY585243 Japanese	C 211	16	33.3	3310	8	AK065029	Oryza sat
C 139	22	45.8	10969	14	JEU15763	U15763 Japanese en	C 212	16	33.3	3319	8	AK065029	Oryza sat
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C 240	16	33.3	132353	9	AC134393	AC134393	Homo sapi	313	16	33.3	232657	9	AC108234	AC108234	Rattus no
C 241	16	33.3	144429	2	AC032017	AC032017	Homo sapi	314	16	33.3	234771	9	AC133536	AC133536	Homo sapi
C 242	16	33.3	145416	5	AC147826	AC147826	Xenopus t	315	16	33.3	237258	2	AC124867	AC124867	Rattus no
C 243	16	33.3	149143	2	AC092974	AC092974	Homo sapi	316	16	33.3	241179	10	AC111141	AC111141	Mus muscu
C 244	16	33.3	150887	2	AC018580	AC018580	Homo sapi	317	16	33.3	241792	2	AC134640	AC134640	Rattus no
C 245	16	33.3	153997	9	AC073348	AC073348	Homo sapi	C 318	16	33.3	246941	2	AC145215	AC145215	Homo sapi
C 246	16	33.3	154485	2	AC116894	AC116894	Mus muscu	C 319	16	33.3	249232	2	AC102120	AC102120	Mus muscu
C 247	16	33.3	154758	9	AC112491	AC112491	Homo sapi	C 320	16	33.3	250666	2	AC103019	AC103019	Rattus no
C 248	16	33.3	162041	2	AC137797	AC137797	Homo sapi	C 321	16	33.3	256754	2	AC109139	AC109139	Mus muscu
C 249	16	33.3	162902	8	AC137609	AC137609	Oryza sat	C 322	16	33.3	258387	2	AC125990	AC125990	Rattus no
C 250	16	33.3	163357	2	AC023276	AC023276	Homo sapi	C 323	16	33.3	259921	2	AC114206	AC114206	Rattus no
C 251	16	33.3	165653	2	AC117818	AC117818	Mus muscu	C 324	16	33.3	260145	2	AC099658	AC099658	Rattus no
C 252	16	33.3	168421	10	AC113328	AC113328	Mus muscu	C 325	16	33.3	276742	2	AC096514	AC096514	Rattus no
C 253	16	33.3	168991	2	AC090411	AC090411	Homo sapi	C 326	16	33.3	340000	9	AP001731	AP001731	Homo sapi
C 254	16	33.3	169866	9	AC133561	AC133561	Homo sapi	C 327	15	31.2	422	6	BD058596	BD058596	Secreted
C 255	16	33.3	171987	9	AC100757	AC100757	Homo sapi	C 328	15	31.2	459	8	BT014827	BT014827	Arabidops
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C 257	16	33.3	172659	2	AC024320	AC024320	Homo sapi	C 330	15	31.2	489	5	AF202806	AF202806	Empidonax
C 258	16	33.3	172755	9	CNS01RGL	AL158111	Homo chr	C 331	15	31.2	495	14	MVEN5SGAD	L48972 Murray Vall	
C 259	16	33.3	173913	2	AC139181	AC139181	Pan trogl	C 332	15	31.2	525	14	MVEN5SGAA	L48972 Murray Vall	
C 260	16	33.3	174423	2	AC141189	AC141189	Rattus no	C 333	15	31.2	525	14	MVEN5SGAB	M35172 Murray Vall	
C 261	16	33.3	174477	9	AC136616	AC136616	Homo sapi	C 334	15	31.2	558	14	MVEAAA	G87185 S208P6541RH	
C 262	16	33.3	174844	8	AC137003	AC137003	Oryza sat	C 335	15	31.2	571	11	G87185	Q0717980 Sequence	
C 263	16	33.3	174930	9	AC145889	AC145889	Pan trogl	C 336	15	31.2	645	6	Q0717980	AL685780 Penicilli	
C 264	16	33.3	175050	2	AC136439	AC136439	Homo sapi	C 337	15	31.2	652	11	PM4A4B	AX508057 Sequence	
C 265	16	33.3	175691	9	AC136440	AC136440	Homo sapi	C 338	15	31.2	721	6	AX508057	AX508057 Sequence	
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C 267	16	33.3	176399	9	CNS05TE1	AL359398	Human chr	C 340	15	31.2	860	5	AX488254	AX488254 Sericorni	
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C 269	16	33.3	177574	9	AC142086	AC142086	Homo sapi	C 342	15	31.2	918	1	UBZ93994	Z93994 Unidentifie	
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C 271	16	33.3	182559	9	AC073476	AC073476	Homo sapi	C 344	15	31.2	990	5	GGU51737	U51737 Gallus gall	
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C 295	16	33.3	205191	2	AC145314	AC145314	Homo sapi	C 368	15	31.2	2099	5	AF360282	AF360282 Danio rer	
C 296	16	33.3	206056	2	AC141453	AC141453	Homo sapi	C 369	15	31.2	2161	8	AY062544	AY062544 Arabidops	
C 297	16	33.3	206476	2	AC112776	AC112776	Homo sapi	C 370	15	31.2	2193	8	BT000695	BT000695 Arabidops	
C 298	16	33.3	206536	2	AC145310	AC145310	Homo sapi	C 371	15	31.2	2260	5	BC054716	BC054716 Danio rer	
C 299	16	33.3	207477	2	AC141262	AC141262	Homo sapi	C 372	15	31.2	2274	1	AF321091	AF321091 Pseudomon	
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391	15	31.2	5319	6	AX336321	Sequence	C 464	15	31.2	115768	2	AP000712	Homo sapi
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393	15	31.2	5329	10	AK122205	AK122205 Mus muscu	C 466	15	31.2	118705	8	AC126009	Medicago
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399	15	31.2	9086	5	AB092649	AB092649 Oryza sat	C 472	15	31.2	122324	10	EX004791	Mouse DNA
400	15	31.2	11014	14	AF161266	AF161266 Murray Va	C 473	15	31.2	125041	2	AC068693	Homo sapi
401	15	31.2	11231	1	AE012315	AE012315 Xanthomon	C 474	15	31.2	126682	8	AC150229	Carollia
402	15	31.2	11627	1	AE004582	AE004582 Pseudomon	C 475	15	31.2	127053	2	AC136220	Oryza sat
403	15	31.2	12277	1	AE010598	AE010598 Fusbacte	C 476	15	31.2	127945	9	AC074033	Homo sapi
404	15	31.2	15015	1	AE000774	AE000774 Aquifex a	C 477	15	31.2	128091	2	AC139626	Takifugu
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414	15	31.2	44725	9	AF036405	AF036405 Homo sapi	C 487	15	31.2	139255	2	AC141580	Rattus no
415	15	31.2	44799	5	BS539322	BS539322 Zebrafish	C 488	15	31.2	139267	2	AC135174	Homo sapi
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438	15	31.2	95310	8	ATAC011437	ATAC011437 Arabidops							
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ALIGNMENTS

RESULT 1
AF458344/c

LOCUS
DEFINITION

AF458344
West Nile virus strain 68856 nonstructural protein 5 gene, partial cds.

AF458344.1
GI:21636467

ACCESSION
VERSION

KEYWORDS
SOURCE

ORGANISM
West Nile virus (WNV)

West Nile virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.

REFERENCE
1 (bases 1 to 463)

AUTHORS
Beasley, D.W., Li, L., Suderman, M.T. and Barrett, A.D.

TITLE
Mouse neuroinvasive phenotype of West Nile virus strains varies depending upon virus genotype

JOURNAL
Virology 296 (1), 17-23 (2002)

PUBMED
12036314

REFERENCE
2 (bases 1 to 463)

AUTHORS
Beasley, D.W.C., Li, L., Suderman, M.T. and Barrett, A.D.T.

TITLE
Direct Submission

JOURNAL
Submitted (14-DEC-2001) Department of Pathology and WHO
Collaborating Center for Tropical Diseases, The University of Texas
Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA

TITLE The relationships between West Nile and Kunjin viruses
 JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)
 MEDLINE 21469816
 PUBMED 11585535
 REFERENCE 2 (bases 1 to 542)
 AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
 TITLE Definitive studies of the relationships between West Nile and
 Kunjin viruses
 JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 542)
 AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
 TITLE Direct Submission
 JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University
 of Queensland, St Lucia, QLD 4072, Australia
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 Db 469 TCCGAGACGGTCTCAGGGCTTACATGCATCCTCGCAGCTTTGTTTC 422
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 DEFINITION Kunjin virus nonstructural protein (NS5) gene, 3' end of cds.
 ACCESSION L48978
 VERSION NS5 gene; nonstructural protein.
 KEYWORDS Kunjin virus
 SOURCE Kunjin virus
 ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 Flavivirus; Japanese encephalitis virus group.
 REFERENCE 1 (bases 1 to 587)
 AUTHORS Poidinger,M., Hall,R.A. and Mackenzie,J.S.
 TITLE Molecular characterization of the Japanese encephalitis serocomplex
 of the flavivirus genus
 JOURNAL Virology 218 (2), 417-421 (1996)
 MEDLINE 96193756
 PUBMED 8610471
 COMMENT Original source text: Kunjin virus (strain MRM61C) cDNA to genomic
 RNA.
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 Best Local Similarity 100.0%; Pred. No. 2.8e-19;
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 Db 469 TCCGAGACGGTCTCAGGGCTTACATGCATCCTCGCAGCTTTGTTTC 422
 RESULT 5
 KUNNS5GAA/c
 LOCUS Kunjin virus nonstructural protein (NS5) gene, 3' end of cds. linear VRL 07-JUN-1996
 DEFINITION Kunjin virus nonstructural protein (NS5) gene, 3' end of cds.
 ACCESSION L48978
 VERSION NS5 gene; nonstructural protein.
 KEYWORDS Kunjin virus
 SOURCE Kunjin virus
 ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 Flavivirus; Japanese encephalitis virus group.
 REFERENCE 1 (bases 1 to 587)
 AUTHORS Poidinger,M., Hall,R.A. and Mackenzie,J.S.
 TITLE Molecular characterization of the Japanese encephalitis serocomplex
 of the flavivirus genus
 JOURNAL Virology 218 (2), 417-421 (1996)
 MEDLINE 96193756
 PUBMED 8610471
 COMMENT Original source text: Kunjin virus (strain MRM61C) cDNA to genomic
 RNA.
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 source Location/Qualifiers
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 Best Local Similarity 100.0%; Pred. No. 2.8e-19;
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCCGAGACGGTCTCAGGGCTTACATGCATCCTCGCAGCTTTGTTTC 48
 Db 461 TCCGAGACGGTCTCAGGGCTTACATGCATCCTCGCAGCTTTGTTTC 414
 RESULT 6
 KUNNS5GAB/c
 LOCUS Kunjin virus nonstructural protein (NS5) gene, 3' end of cds. linear VRL 07-JUN-1996
 DEFINITION Kunjin virus nonstructural protein (NS5) gene, 3' end of cds.
 ACCESSION L48979
 VERSION NS5 gene; nonstructural protein.
 KEYWORDS Kunjin virus
 SOURCE Kunjin virus
 ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 Flavivirus; Japanese encephalitis virus group.
 REFERENCE 1 (bases 1 to 587)
 AUTHORS Poidinger,M., Hall,R.A. and Mackenzie,J.S.
 TITLE Molecular characterization of the Japanese encephalitis serocomplex
 of the flavivirus genus
 JOURNAL Virology 218 (2), 417-421 (1996)
 MEDLINE 96193756
 PUBMED 8610471
 COMMENT Original source text: Kunjin virus (strain MRM16) cDNA to genomic
 RNA.
 FEATURES
 source Location/Qualifiers
 1..587
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 /mol_type="genomic RNA"
 /strain="MRM16"
 /db_xref="taxon:11077"
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 /codon_start=1
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 /protein_id="AA02078.1"
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 /translation="WMEDKTPVEKWSVPYSGKREDIWCGSLIGTRARATWAENIQVA
 INQVRSIIIGDEKYDYMSWKRYEDTTLVEDTVL"
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 Query Match 100.0%; Score 48; DB 14; Length 587;
 Best Local Similarity 100.0%; Pred. No. 2.8e-19;
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCCGAGACGGTCTCAGGGCTTACATGCATCCTCGCAGCTTTGTTTC 48
 Db 461 TCCGAGACGGTCTCAGGGCTTACATGCATCCTCGCAGCTTTGTTTC 414
 RESULT 7
 AF297844/c
 LOCUS Kunjin virus isolate CH16549E nonstructural protein 5 gene, partial
 cds.
 DEFINITION Kunjin virus isolate CH16549E nonstructural protein 5 gene, partial
 cds.
 ACCESSION AF297844
 VERSION AF297844
 KEYWORDS Kunjin virus
 SOURCE Kunjin virus
 ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;


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Kunjin viruses
Unpublished
REFERENCE 3 (bases 1 to 623)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE Direct Submission
JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University
of Queensland, St Lucia, QLD 4072, Australia
FEATURES
source
1..623
/organism="Kunjin virus"
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/isolates="CHI6532C"
/db_xref="taxon:11077"
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/notes="NS5"
/codon_start=1
/product="nonstructural protein 5"
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/db_xref="GI:11991977"
/translation="EYEMEDTTPVEKNDVPYSGKREDIWCGSLIGTRARATWAEADI
QVAINQVRSIIIGDEKYVDYMSSLKRYEDTTLVEDTVL"
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Query Match 100.0%; Score 48; DB 14; Length 623;
Best Local Similarity 100.0%; Pred. No. 2.8e-19;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCGAGACGGTCTGAGGGCTTACATGGATCACTTCGACGCTTTGTC 48
Db 472 TCCGAGACGGTCTGAGGGCTTACATGGATCACTTCGACGCTTTGTC 425
RESULT 13
KUNNONCODEB/c
LOCUS KUNNONCODEB 627 bp ss-RNA linear VRL 09-AUG-1994
DEFINITION Kunjin virus 3' UTR.
ACCESSION L24512
VERSION L24512.1 GI:403464
KEYWORDS
SOURCE Kunjin virus
ORGANISM Kunjin virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 627)
AUTHORS Coia,G., Parker,M.D., Speight,G., Byrne,M.B. and Westaway,E.G.
TITLE Nucleotide and complete amino acid sequences of Kunjin virus:
definitive gene order and characteristics of the virus-specified
proteins
J. Gen. Virol. 69 (Pt 1), 1-21 (1988)
JOURNAL 2826659
MEDLINE 88089524
PUBMED 2826659
REFERENCE 2 (bases 1 to 627)
AUTHORS Khromykh,A.A. and Westaway,E.G.
TITLE Completion of Kunjin virus RNA sequence and recovery of an
infectious RNA transcribed from stably cloned full-length cDNA
J. Virol. 68 (7), 4580-4588 (1994)
JOURNAL 94267921
MEDLINE 94267921
PUBMED 8207832
COMMENT Original source text: Kunjin virus (strain MRM 61C) mature RNA.
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/organism="Kunjin virus"
/mol_type="genomic RNA"
/strain="MRM 61C"
/db_xref="taxon:11077"
/dev_stage="mature"
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/notes="putative"
/citation=[2]
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Query Match 100.0%; Score 48; DB 14; Length 627;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
3' UTR
/notes=[2]
ORIGIN
Kunjin virus isolate OR205 nonstructural protein 5 gene, partial
AF297858 633 bp RNA linear VRL 05-MAR-2002
LOCUS Kunjin virus isolate OR205 nonstructural protein 5 gene, partial
DEFINITION cds.
ACCESSION AF297858
VERSION AF297858.1 GI:11992006
KEYWORDS
SOURCE Kunjin virus
ORGANISM Kunjin virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 633)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE The relationships between West Nile and Kunjin viruses
Emerging Infect. Dis. 7 (4), 697-705 (2001)
JOURNAL 21459816
MEDLINE 21459816
PUBMED 11585535
REFERENCE 2 (bases 1 to 633)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE Definitive studies of the relationships between West Nile and
Kunjin viruses
Unpublished
REFERENCE 3 (bases 1 to 633)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE Direct Submission
JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University
of Queensland, St Lucia, QLD 4072, Australia
FEATURES
source
1..633
/organism="Kunjin virus"
/mol_type="genomic RNA"
/isolates="OR205"
/db_xref="taxon:11077"
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/notes="NS5"
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/product="nonstructural protein 5"
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/db_xref="GI:11992007"
/translation="TCKYKNGYGRYKTPVEKNSDVPYSGKREDIWCGSLIGTRARAT
WAENIQVAINQVRSIIIGDEKYVDYMSSLKRYEDTTLVEDTVL"
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Best Local Similarity 100.0%; Pred. No. 2.8e-19;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCGAGACGGTCTGAGGGCTTACATGGATCACTTCGACGCTTTGTC 48
Db 487 TCCGAGACGGTCTGAGGGCTTACATGGATCACTTCGACGCTTTGTC 440
RESULT 15
AF297848/c
LOCUS Kunjin virus isolate K1738 nonstructural protein 5 gene, partial
DEFINITION cds
ACCESSION AF297848
VERSION AF297848.1 GI:11991986
KEYWORDS
SOURCE Kunjin virus
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ORGANISM Kunjin virus
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 Flavivirus; Japanese encephalitis virus group.
 1 (bases 1 to 644)
 Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
 Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
 The relationships between West Nile and Kunjin viruses
 Emerging Infect. Dis. 7 (4), 697-705 (2001)
 MEDLINE 21469816
 PUBMED 11585535
 2 (bases 1 to 644)
 Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
 and Hall,R.A.
 Definitive studies of the relationships between West Nile and
 Kunjin viruses
 Unpublished
 3 (bases 1 to 644)
 Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
 and Hall,R.A.
 Direct Submission
 Submitted (22-AUG-2000) Microbiology and Parasitology, University
 of Queensland, St Lucia, QLD 4072, Australia
 Location/Qualifiers
 1. .644
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 /mol_type="genomic RNA"
 /isolate="K1738"
 /db_xref="taxon:11077"
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 /codon_start=2
 /product="nonstructural protein 5"
 /protein_id="AAG42386.1"
 /db_xref="GI:11991987"
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 AENIQVAIQVRSIIIGDEKIVDMSSLKRYEDMTLVEDTVL"
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 Query Match 100.0%; Score 48; DB 14; Length 644;
 Best Local Similarity 100.0%; Pred. No. 2.8e-19;
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 485 TCCGACGCGTCTGAGGCTTACATGATCATTCCGACGCTTGTC 438
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 RESULT 16
 AF297855/c
 LOCUS AF297855.1 GI:11992000
 DEFINITION Kunjin virus isolate OR354 nonstructural protein 5 gene, partial cds.
 ACCESSION AF297855
 VERSION AF297855.1
 KEYWORDS
 SOURCE Kunjin virus
 ORGANISM Kunjin virus
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 Flavivirus; Japanese encephalitis virus group.
 1 (bases 1 to 652)
 Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
 Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
 The relationships between West Nile and Kunjin viruses
 Emerging Infect. Dis. 7 (4), 697-705 (2001)
 MEDLINE 21469816
 PUBMED 11585535
 2 (bases 1 to 652)
 Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
 and Hall,R.A.
 Definitive studies of the relationships between West Nile and
 Kunjin viruses
 Unpublished
 3 (bases 1 to 652)

AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
 and Hall,R.A.
 TITLE Direct Submission
 JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University
 of Queensland, St Lucia, QLD 4072, Australia
 FEATURES
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 /protein_id="AAG42393.1"
 /db_xref="GI:11992001"
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 Best Local Similarity 100.0%; Pred. No. 2.8e-19;
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 Db 491 TCCGACGCGTCTGAGGCTTACATGATCATTCCGACGCTTGTC 444
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 RESULT 17
 AF297849/c
 LOCUS AF297849.1 GI:11991988
 DEFINITION Kunjin virus isolate K5374 nonstructural protein 5 gene, partial cds.
 ACCESSION AF297849
 VERSION AF297849.1
 KEYWORDS
 SOURCE Kunjin virus
 ORGANISM Kunjin virus
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 Flavivirus; Japanese encephalitis virus group.
 1 (bases 1 to 657)
 Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
 Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
 The relationships between West Nile and Kunjin viruses
 Emerging Infect. Dis. 7 (4), 697-705 (2001)
 MEDLINE 21469816
 PUBMED 11585535
 2 (bases 1 to 657)
 Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
 and Hall,R.A.
 Definitive studies of the relationships between West Nile and
 Kunjin viruses
 Unpublished
 3 (bases 1 to 657)
 Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
 and Hall,R.A.
 Direct Submission
 Submitted (22-AUG-2000) Microbiology and Parasitology, University
 of Queensland, St Lucia, QLD 4072, Australia
 Location/Qualifiers
 1. .657
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 /mol_type="genomic RNA"
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 /db_xref="taxon:11077"
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 /note="NS5"
 /codon_start=1
 /product="nonstructural protein 5"
 /protein_id="AAG42387.1"
 /db_xref="GI:11991989"
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 Query Match 100.0%; Score 48; DB 14; Length 657;
 Best Local Similarity 100.0%; Pred. No. 2.8e-19;
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 |||||
 Db 491 TCCGACGCGTCTGAGGCTTACATGATCATTCCGACGCTTGTC 444
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ATWAENIQAINQVRSIIIGDEKYVDYMSSLKRYEDMTLVEDTVL"

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Query Match 100.0%; Score 48; DB 14; Length 657;
Best Local Similarity 100.0%; Pred. No. 2.8e-19;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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|||||
DB 493 TCCGAGACGGTCTGAGGGCTTACATGGATCACTTCGACGCTTTGTTTC 446

RESULT 18
AF017254/c
LOCUS
DEFINITION West Nile virus nonstructural protein NS5 (NS5) gene, partial cds.
ACCESSION AF017254
VERSION AF017254.2 GI:11497617
KEYWORDS
SOURCE West Nile virus
ORGANISM West Nile virus
Viruses: ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
AUTHORS Yamahchikov, V.F., Wengler, G., Brinton, M.A. and Compans, R.W.
TITLE A stable infectious clone of West Nile flavivirus
JOURNAL Unpublished
REFERENCE
AUTHORS Yamahchikov, V.F. and Brinton, M.A.
TITLE Direct Submission
JOURNAL Submitted (04-AUG-1997) OVRD/DVP, FDA, 29 Lincoln Drive, Bethesda, MD 20892, USA
REFERENCE
AUTHORS Yamahchikov, V.F. and Brinton, M.A.
TITLE Direct Submission
JOURNAL Submitted (01-DEC-2000) OVRD/DVP, FDA, 29 Lincoln Drive, Bethesda, MD 20892, USA
REMARK
COMMENT Sequence update by submitter
FEATURES
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1..1524
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/mol_type="genomic RNA"
/strain="Eg101"
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/note="viral replicase; polyprotein; putative"
/product="nonstructural protein NS5"
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LMAALCAVAVNVPVPTGRTTSHAGSEWNTDMLVWNRVWIEENWMDKTPVE
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EDTLVEDTVL"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 2.6e-19;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCGAGACGGTCTGAGGGCTTACATGGATCACTTCGACGCTTTGTTTC 48
|||||
DB 1095 TCCGAGACGGTCTGAGGGCTTACATGGATCACTTCGACGCTTTGTTTC 1048

RESULT 19

KUNCG/c
LOCUS
DEFINITION Kunjin virus gene for polyprotein (C, prM, E, NS1, NS2A, NS2B, NS3, NS4A, NS4B, NS5), complete cds.
ACCESSION D00246
VERSION D00246.1 GI:221966
KEYWORDS M (membrane protein); prM (precursor of M); NS5; NS4B; NS4A; NS3; NS2B; NS2A; NS1; E (envelope protein); C (core protein);
SOURCE Kunjin virus
ORGANISM Kunjin virus
Viruses: ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
AUTHORS Coia, G., Parker, M.D., Speight, G., Byrne, M.E. and Westaway, E.G.
TITLE Nucleotide and complete amino acid sequences of Kunjin virus: definitive gene order and characteristics of the virus-specified proteins
JOURNAL J. Gen. Virol. 69 (Pt 1), 1-21 (1988)
MEDLINE 88089524
PUBMED 2826659
COMMENT A kunjin (KUN) virus cDNA sequence of 10664 nucleotides which encoded a single open reading frame for 3433 amino acids was obtained and compared with the complete amino acid sequences of yellow fever and West Nile viruses. Partial N-terminal amino acid analyses of KUN virus-specified proteins identified the polyprotein cleavage sites and the definitive gene order. Three stop codons in the correct reading frame occur within the first 25 nucleotides beyond the 3' end of the coding sequence.
Location/Qualifiers
1..10664
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/mol_type="genomic RNA"
/strain="MRM61C"
/db_xref="taxon:11077"
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76..10377
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/product="polyprotein"
/protein_id="BAA00176.1"
/db_xref="GI:221967"

CDS

/translation="MSKRPGLGPGKSRVAVNMLKRGMPRVLSLTGLKRAMLSLIDRGRT
RFVLLALAFRPTALAPTRAVLDNRVSNKQAMKHLISFKKELGTLTSAINRSSKQ
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AMDVGMCDTITVECPVLSAGNDPEDICWCTKLAVYVGRCTKTHRSRSRSLT
VQTGESLTKKAGWMDSTKATRYLVKTESWILNPGVALVAIVGMIGMNTMORV
VFAVLLLVPAFSPNCLGMSNRDPLEGSGATVDVLLEGDSCTVIMSKDPTDVK
MMNMEANLAEVRSYCYLATVSELSTKACPTMGHNDKADPSPFCVQGVDRGW
NGCGLFGKSIDTCAKFCATKRTILKENIKYEVAIFVHGPTTVSHGNYFTQT
AAQGRFSITPAAPSYTLKGEYGVTVDCPRSGIDTSAYVYMTVGTFTLVHREWF
MDLNLPMSSASNVRNRETLMEFEHPHATKQSVIALGSEGALHQAAGAIPIVERSS
NTVLTSGHLKCRVMEKQLKGTITVVCSCAFRIFGTPADTGHGTVVLLEQYTDG
PKDIPSSVSLNDLTPVRLVTVNPFVSVANAKVLIELEPPGDSYIVVGRGQ
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RSLFGCMGWIQGLIGALLMGINARDSIALTFLAVGVLLFLSVNVNADTCAID
ISRELRCGSGVFIHNDVEAWIDRYKYPETPGQAKIIQAKHKGVCGLRSVSLRH
QMEAWKDELATLLKENGVDLSIYVEKQEGYKSAPRLTATTEKLEIGWKAGKSL
FAPELANNTVIDGTECPCTQNRANWNEVEFDGFLTSTFMELVRESNTEGDS
KIIGTAVKXNLAIHSDLSYIESRFDNRFDKLERAVLGEVKSCTPTETHLWDGCVLES
DLIIPTTLAGPRSNHRRPGYKTSQGWDEGRVIDFCPTGTTVLSGCHRGPA
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DMIDPFOLGLLVFLATQVLRKWTAKISMPAILIALLVFGGITYTDVLRVYTLV
GNAFAESNSGGDVHLMATFKIOPVMAFSLKARTNQENILMLAAAFQWAVY
DARQILMEFEDVLNSAVAMMILRAITFTTTSNVVPLLLATLTPGLRCNLNDVRIIL
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TEWTAAGMFIAVGLAEIDISNAIPMTIAGLMFAAFVISEKSTDMWERTADISW
EGDAEITGSSERVDRLDDGDFOLMDPGAPKIWMRLMACLAISATYPMWAILPSV
GFWITLOVTKRGVLDTPSKYKRGDTTTCGYVTRIMRGLLGSYQAGAGVWVGVFH
TLWHTTKAALMSGREDLPYSGVSKRDTTCGYVTRIMRGLLGSYQAGAGVWVGVFH
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AIVQGRMDEPVPAGFPEMLRKKQITVLDLHPGAGKTRILPQIIKEAINRHLTAV
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 SAQRKDDFTVTDISEMGANFKASRVIDSRKSVKPTIITEGGEVILGEPSSAVTAA
 PEREKVYTDMDGEYRLRGEERKNFLELLRTADLPVLAIVKVAAGVYHRRWCFQDGY
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 LKGMPEHFMGTWEALDYMVVAATEKGGRAHMALEELPDALQTTALIALSVMTMG
 VFLLMQRKIGIKIGGGVILGAATFCWNAEVPCKIAGMLLSLLMLVILPEPEK
 QRSQTDNOLAVFLICVLTVLGAANEMGLDKTSDISGLFGRLTETKENSIGEFEL
 LDRPATAMSLYAVTAVTLPPLKHLITSDYITSTLSINVQASALFTLARGPFVDV
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 TLDGIIVATDPELERTPIIMOKKVGOMLILVSLTWTLVNMEKPKGLKAGKGRULGE
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 VKERLNQMTKEEFIRYKEAITVEDRSAAKARKERNITGHPVSRGTAKRLWLVER
 RFLPEPKVIDLDCGGGCGYMATQKQVQEVYTKGGPHEEPOLVOSYGNWIVTM
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 CPMYKVIEMQELLQRRYGGGLVRNPLSNSTHEMYWVSRAAGNVVHSVNMSTQVLLG
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 PYRTWNYHGSYEVKPTGSSSLVNGVVRLLSKPMDTITNTVTMTAMDTTTPGQORVEK
 EKVDTKAPPEGVKYVLNETTNMLWAFIAREKPRMCSREFFIRKYNSSNAALGAMPE
 EQNWSAREAVEDPKFEMWDEERAHLRGECITCIYNNMGREKKPGEFGKAGSR
 AIFWMIGARFLEALGFELNEDHMLGRKNSGGVGLGLQKGLYILREVGRPGGR
 YADDTAGWDTIRTRADLENAEKVLELDGHEHRLARAIITLYRHKVVMRPAADGR
 TMDVLSRGDQSGOVVYALNTFTNLAVQLVRMMEGEGVIGPDDVEKLVKKGPKVY
 RTWLSNGBERLSMAVSGDDCVKPLDDRFATSLHFLNAMSKVROIOEWKPSGMY
 DMQVPPFCNSHFTLIMKDGRTLVTPCRGQDELVGRIARISPGAGNVRDTCIAKSYA
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 415. .945
 /product="prM (precursor of M)"
 721. .945
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 946. .2448
 /product="E (envelope protein)"
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 6895. .7659
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 DEFINITION Kunjin virus clone FLSDX polyprotein mRNA, complete cds.
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 VERSION AY274504.1 GI:32306849
 KEYWORDS Kunjin virus
 SOURCE Kunjin virus
 ORGANISM Kunjin virus
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 Flavivirus; Japanese encephalitis virus group.

REFERENCE 1 (bases 1 to 11022)
 AUTHORS Liu, W.J., Chen, H.B. and Khromykh, A.A.
 TITLE Molecular and Functional Analyses of Kunjin Virus Infectious cDNA Clones Demonstrate the Essential Roles for NS2A in Virus Assembly and for a Nonconservative Residue in NS3 in RNA Replication
 J. Virol. 77 (14), 7804-7813 (2003)
 MEDLINE 22713678
 PUBMED 12829820
 REFERENCE 2 (bases 1 to 11022)
 AUTHORS Khromykh, A.A., Liu, W.J. and Chen, H.B.
 TITLE Direct Submission
 JOURNAL Submitted (11-APR-2003) Clinical Medical Virology Centre,
 University of Queensland/Sir Albert Sakzewski Virus Research
 Centre, Royal Children's Hospital, Herston Rd., Herston, Brisbane,
 QLD 4029, Australia

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Best Local Similarity 100.0%; Pred. No. 2.2e-19;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 10622 TCCGAGACGGTCTGAGGCGTACATGATCCTTCGAGCTTGTTC 10575
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ACCESSION AY274505
VERSION AY274505.1 GI:32306851
KEYWORDS Kunjin virus
SOURCE Kunjin virus
ORGANISM Kunjin virus
Flaviviridae; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 11022)
AUTHORS Liu W.J., Chen, H.B. and Khromykh, A.A.
TITLE Molecular and Functional Analyses of Kunjin Virus Infectious cDNA
Clones Demonstrate the Essential Roles for NS2A in Virus Assembly
and for a Nonconservative Residue in NS3 in RNA Replication
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J. Virol. 77 (14), 7804-7813 (2003)
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2 (bases 1 to 11022)
Khromykh, A.A., Liu, W.J. and Chen, H.B.
Direct Submission
Submitted (11-APR-2003) Clinical Medical Virology Centre,
University of Queensland/Sir Albert Sakzewski Virus Research
Centre, Royal Children's Hospital, Herston Rd., Herston, Brisbane,
QLD 4029, Australia
FEATURES
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Best Local Similarity 100.0%; Pred. No. 2.2e-19;

Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTTCTGAGGCGCTTACATGGATCCTTCGACGCTTTGTC 48

Db 10622 TCCGAGACGGTTCTGAGGCGCTTACATGGATCCTTCGACGCTTTGTC 10575

RESULT 22

AY490240/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AY490240 West Nile virus strain Chin-01, complete genome. VRL 08-APR-2004

AY490240 West Nile virus strain Chin-01, complete genome.

AY490240.2 GI:46277828

West Nile virus (WNV)

West Nile virus

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

Flavivirus; Japanese encephalitis virus group.

1 (bases 1 to 11028)

Jiang, T., Qin, E. and Deng, Y.

Sequence determination and analysis of West Nile Virus Chin strain

Unpublished

2 (bases 1 to 11028)

Jiang, T., Qin, E. and Deng, Y.

Direct Submission

Submitted (28-NOV-2003) Virology, Institute of Microbiology and

Epidemiology, Fengtai Dongda Street, Beijing 100071, China

REFERENCE 3 (bases 1 to 11028)

AUTHORS

TITLE

JOURNAL

REMARK

COMMENT

FEATURES

source

Jiang, T., Qin, E. and Deng, Y.

Direct Submission

Submitted (08-APR-2004) Virology, Institute of Microbiology and

Epidemiology, Fengtai Dongda Street, Beijing 100071, China

Sequence update by submitter

On Apr 8, 2004 this sequence version replaced gi:40362614.

Location/Qualifiers

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AIWFMWLGARLEFEALGFLNEDHMLGRKNKSGVGEGLGLOK

YADDTAGWTRITRADLENEAKVLELLEDGHRRLARALIELY

RHKVVKVMPADGR

TMDVIRSDEQSGGVVYALNTFTNLAVQLVRWMEGEGVIG

DDVEKLTGKGGPKV

RTWLPENGEBLSRMAVSGDDCVVPLDDRRFATSLHFLNAMSKVRRKDIQEWKPGSTGY
DQWQVFCNSHFTLIMKDRGLTAVPCQDELVRGARSIPGAMNVRVITACLAQSYA
QWMLLYFHRDLRLMANAICSAVPVNVPTGRTTWSIHAGGEMWTEGLVNRVW
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ORIGIN

Query Match 100.0%; Score 48; DB 14; Length 11028;
Best Local Similarity 100.0%; Pred. No. 2.2e-19;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTCTGAGCGCTTACATGATCACTTCGACGCTTGTTC 48
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Db 10629 TCCGAGACGGTCTGAGCGCTTACATGATCACTTCGACGCTTGTTC 10582

RESULT 23

AF260968/c

LOCUS

West Nile virus strain Egi101, complete genome. VRL 27-AUG-2000

DEFINITION

ACCESSION

AF260968

VERSION

AF260968.1

KEYWORDS

SOURCE

ORGANISM

West Nile virus

West Nile virus

Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;

Flavivirus; Japanese encephalitis virus group.

Bowen, M., Meyer, R.F., McKinney, N., Morrill, W. and Lanciotti, R.

1 (bases 1 to 11029)

Complete genomic sequence of West Nile virus strain Egi101

Unpublished

2 (bases 1 to 11029)

Bowen, M., Meyer, R.F., McKinney, N., Morrill, W. and Lanciotti, R.

Direct Submission

Submitted (27-APR-2000) Arbovirus Diseases Branch, Centers for

Disease Control & Prevention, Rampart Road, Fort Collins, CO 80521,

USA

FEATURES

source

1. .11029

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/db_xref="taxon:11082"

97. .10398

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EQONVSAREAVEDPKFWMDDEEAHLREKCHTCIYNMGKREKPGCEFGKAGSR
AIFWMLGARFLFEALGFLNEDHNLGRKNSGGVGGLOKGLYTLREVGTTPGKI
YADDTAGDTRITRADLENAKVLLELGEHRLRLARAILIYLRHYKVRMRAADGR
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RTWLPENGEBLSRMAVSGDDCVVPLDDRRFATSLHFLNAMSKVRRKDIQEWKPGSTGY
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QWMLLYFHRDLRLMANAICSAVPVNVPTGRTTWSIHAGGEMWTEGLVNRVW
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ORIGIN

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Best Local Similarity

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Qy 1 TCCGAGACGGTCTGAGCGCTTACATGATCACTTCGACGCTTGTTC 48

|||||

Db 10629 TCCGAGACGGTCTGAGCGCTTACATGATCACTTCGACGCTTGTTC 10582

|||||

RESULT 24

AF458351/c

LOCUS

Kunjin virus strain MRM16 nonstructural protein 5 gene, partial

DEFINITION

456 bp RNA linear

VRL 18-JUN-2003

cde.

AF458351
 AF458351.1 GI:21636481
 Kunjin virus
 Kunjin virus
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 Flavivirus; Japanese encephalitis virus group.
 1 (bases 1 to 456)
 Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
 Mouse neuroinvasive phenotype of West Nile virus strains varies
 depending upon virus genotype
 Virology 296 (1), 17-23 (2002)
 22033887
 PUBMED
 12036314
 2 (bases 1 to 456)
 Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
 Direct Submission
 Submitted (14-DEC-2001) Department of Pathology and WHO
 Collaborating Center for Tropical Diseases, The University of Texas
 Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
 Location/Qualifiers
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 175..>456
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 Query Match 97.9%; Score 47; DB 14; Length 456;
 Best Local Similarity 100.0%; Pred. No. 1.2e-18;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CCGAGACGGTCTGAGGGCTTACATGATCCTTCGACCTTGTTC 48
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 Db 397 CCGAGACGGTCTGAGGGCTTACATGATCCTTCGACCTTGTTC 351
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 RESULT 25
 AF297856/c
 LOCUS
 Kunjin virus isolate P1553 nonstructural protein 5 gene, partial
 DEFINITION
 Cds.
 AF297856
 VERSION
 AF297856.1 GI:11992002
 KEYWORDS
 SOURCE
 Kunjin virus
 ORGANISM
 Kunjin virus
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 Flavivirus; Japanese encephalitis virus group.
 1 (bases 1 to 609)
 Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
 Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
 The relationships between West Nile and Kunjin viruses
 Emerging Infect. Dis. 7 (4), 697-705 (2001)
 21469816
 PUBMED
 11585535
 2 (bases 1 to 609)
 Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
 and Hall,R.A.
 DEFINITIVE studies of the relationships between West Nile and
 Kunjin viruses
 Unpublished
 3 (bases 1 to 609)
 REFERENCE

AUTHORS
 Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
 and Hall,R.A.
 TITLE
 Direct Submission
 JOURNAL
 Submitted (22-AUG-2000) Microbiology and Parasitology, University
 of Queensland, St Lucia, QLD 4072, Australia
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 Best Local Similarity 100.0%; Pred. No. 2.3e-17;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCCGAGACGGTCTGAGGGCTTACATGATCCTTCGACCTTTC 45
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 Db 490 TCCGAGACGGTCTGAGGGCTTACATGATCCTTCGACCTTTC 446
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 RESULT 26
 AF458356/c
 LOCUS
 Kunjin virus strain K6453 nonstructural protein 5 gene, partial
 DEFINITION
 Cds.
 AF458356
 VERSION
 AF458356.1 GI:21636491
 KEYWORDS
 SOURCE
 Kunjin virus
 ORGANISM
 Kunjin virus
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 Flavivirus; Japanese encephalitis virus group.
 1 (bases 1 to 458)
 Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
 Mouse neuroinvasive phenotype of West Nile virus strains varies
 depending upon virus genotype
 Virology 296 (1), 17-23 (2002)
 22033887
 PUBMED
 12036314
 2 (bases 1 to 458)
 Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
 Direct Submission
 Submitted (14-DEC-2001) Department of Pathology and WHO
 Collaborating Center for Tropical Diseases, The University of Texas
 Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
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 ORIGIN

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Best Local Similarity 100.0%; Pred. No. 8.5e-15;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGGTTCTGAGGCGTTACATGGATCACTTCGCGAGCTTTGTC 48
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Db 393 CGGTTCTGAGGCGTTACATGGATCACTTCGCGAGCTTTGTC 353

RESULT 27
AF297851/c
LOCUS AF297851
DEFINITION Kunjin virus isolate M1465 nonstructural protein 5 gene, partial cds.
ACCESSION AF297851
VERSION AF297851.1 GI:11991992
SOURCE Kunjin virus
ORGANISM Kunjin virus
REFERENCE 1 (bases 1 to 524)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V., Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE The relationships between West Nile and Kunjin viruses
JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE 21469816
PUBMED 11585535
REFERENCE 2 (bases 1 to 524)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.
TITLE Definitive studies of the relationships between West Nile and Kunjin viruses
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 524)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.
TITLE Direct Submission
JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University of Queensland, St Lucia, QLD 4072, Australia
FEATURES
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            1..524
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Best Local Similarity 100.0%; Pred. No. 8.4e-15;
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QY 8 CGGTTCTGAGGCGTTACATGGATCACTTCGCGAGCTTTGTC 48
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Db 425 CGGTTCTGAGGCGTTACATGGATCACTTCGCGAGCTTTGTC 385

RESULT 28
AF297850/c
LOCUS AF297850
DEFINITION Kunjin virus isolate K6590 nonstructural protein 5 gene, partial cds.
ACCESSION AF297850
VERSION AF297850.1 GI:11991990
SOURCE Kunjin virus
ORGANISM Kunjin virus
REFERENCE 1 (bases 1 to 524)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V., Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE The relationships between West Nile and Kunjin viruses
JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE 21469816
PUBMED 11585535
REFERENCE 2 (bases 1 to 585)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.
TITLE Definitive studies of the relationships between West Nile and Kunjin viruses
JOURNAL Unpublished

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SOURCE
ORGANISM Kunjin virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 545)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V., Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE The relationships between West Nile and Kunjin viruses
JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE 21469816
PUBMED 11585535
REFERENCE 2 (bases 1 to 545)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.
TITLE Definitive studies of the relationships between West Nile and Kunjin viruses
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 545)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.
TITLE Direct Submission
JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University of Queensland, St Lucia, QLD 4072, Australia
FEATURES
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Best Local Similarity 100.0%; Pred. No. 8.3e-15;
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QY 8 CGGTTCTGAGGCGTTACATGGATCACTTCGCGAGCTTTGTC 48
    |||||
Db 424 CGGTTCTGAGGCGTTACATGGATCACTTCGCGAGCTTTGTC 384

RESULT 29
AF297840/c
LOCUS AF297840
DEFINITION Kunjin virus isolate Boort nonstructural protein 5 gene, partial cds.
ACCESSION AF297840
VERSION AF297840.1 GI:11991970
SOURCE Kunjin virus
ORGANISM Kunjin virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 585)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V., Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE The relationships between West Nile and Kunjin viruses
JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE 21469816
PUBMED 11585535
REFERENCE 2 (bases 1 to 585)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.
TITLE Definitive studies of the relationships between West Nile and Kunjin viruses
JOURNAL Unpublished

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REFERENCE 3 (bases 1 to 585)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE Direct Submission
JOURNAL Microbiology and Parasitology, University
of Queensland, St Lucia, QLD 4072, Australia
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Best Local Similarity 100.0%; Pred. No. 8.3e-15;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 446 CGGTTCTGAGGCTTACATGATCCTTCGCGAGCTTTGTC 406
|||||

ORIGIN

RESULT 30
LOCUS AF297847/c
DEFINITION Kunjin virus isolate Hu6774 nonstructural protein 5 gene, partial
cds.
ACCESSION AF297847
VERSION AF297847.1 GI:11991984
KEYWORDS
SOURCE Kunjin virus
ORGANISM Kunjin virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
1 (bases 1 to 593)
Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
The relationships between West Nile and Kunjin viruses
Emerging Infect. Dis. 7 (4), 697-705 (2001)
21469816
PUBMED 11585535

REFERENCE 2 (bases 1 to 593)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE Definitive studies of the relationships between West Nile and
Kunjin viruses
Unpublished
3 (bases 1 to 593)
Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
Direct Submission
JOURNAL Microbiology and Parasitology, University
of Queensland, St Lucia, QLD 4072, Australia
FEATURES
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Best Local Similarity 100.0%; Pred. No. 8.3e-15;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 CGGTTCTGAGGCTTACATGATCCTTCGCGAGCTTTGTC 48
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Db 463 CGGTTCTGAGGCTTACATGATCCTTCGCGAGCTTTGTC 423
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Best Local Similarity 100.0%; Pred. No. 8.3e-15;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 CGGTTCTGAGGCTTACATGATCCTTCGCGAGCTTTGTC 48
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Db 466 CGGTTCTGAGGCTTACATGATCCTTCGCGAGCTTTGTC 426
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RESULT 31

LOCUS AF297852/c
DEFINITION Kunjin virus isolate M695 nonstructural protein 5 gene, partial
cds.

ACCESSION AF297852

VERSION AF297852.1 GI:11991994

KEYWORDS

ORGANISM

Kunjin virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
1 (bases 1 to 593)
Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
The relationships between West Nile and Kunjin viruses
Emerging Infect. Dis. 7 (4), 697-705 (2001)
21469816
PUBMED 11585535

REFERENCE

AUTHORS

1 (bases 1 to 593)
Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE Definitive studies of the relationships between West Nile and
Kunjin viruses
Unpublished
3 (bases 1 to 593)
Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
Direct Submission
JOURNAL Microbiology and Parasitology, University
of Queensland, St Lucia, QLD 4072, Australia
FEATURES
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/protein_id="AAG42390.1"
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REFERENCE

AUTHORS

1 (bases 1 to 593)
Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE Definitive studies of the relationships between West Nile and
Kunjin viruses
Unpublished
3 (bases 1 to 593)
Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
Direct Submission
JOURNAL Microbiology and Parasitology, University
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REFERENCE

AUTHORS

1 (bases 1 to 593)
Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE Definitive studies of the relationships between West Nile and
Kunjin viruses
Unpublished
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Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
Direct Submission
JOURNAL Microbiology and Parasitology, University
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AUTHORS

1 (bases 1 to 593)
Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE Definitive studies of the relationships between West Nile and
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Unpublished
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Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
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1 (bases 1 to 593)
Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE Definitive studies of the relationships between West Nile and
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3 (bases 1 to 593)
Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
Direct Submission
JOURNAL Microbiology and Parasitology, University
of Queensland, St Lucia, QLD 4072, Australia
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/product="nonstructural protein 5"
/protein_id="AAG42385.1"

REFERENCE

AUTHORS

1 (bases 1 to 593)
Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE Definitive studies of the relationships between West Nile and
Kunjin viruses
Unpublished
3 (bases 1 to 593)
Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
Direct Submission
JOURNAL Microbiology and Parasitology, University
of Queensland, St Lucia, QLD 4072, Australia
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Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE Definitive studies of the relationships between West Nile and
Kunjin viruses
Unpublished
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Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
Direct Submission
JOURNAL Microbiology and Parasitology, University
of Queensland, St Lucia, QLD 4072, Australia
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/mol_type="genomic RNA"
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/codon_start=2
/product="nonstructural protein 5"
/protein_id="AAG42385.1"

DEFINITION Kunjin virus isolate SH183 nonstructural protein 5 gene, partial cds.

ACCESSION AF297853

VERSION AF297853.1 GI:11991996

KEYWORDS Kunjin virus

SOURCE Kunjin virus

ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group.

REFERENCE 1 (bases 1 to 594)

AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V., Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.

TITLE The relationships between West Nile and Kunjin viruses

JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)

MEDLINE 21469816

PUBMED 11585535

REFERENCE 2 (bases 1 to 594)

AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.

TITLE Definitive studies of the relationships between West Nile and Kunjin viruses

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 594)

AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.

TITLE Direct Submission

JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University of Queensland, St Lucia, QLD 4072, Australia

FEATURES

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Best Local Similarity 100.0%; Pred. No. 8.3e-15; Length 594;

Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGGTTCTGAGGCTTACATGGATCACTTCGCAGCTTTGTC 48

Db 462 CGGTTCTGAGGCTTACATGGATCACTTCGCAGCTTTGTC 422

RESULT 33

AF297846/c

LOCUS Kunjin virus isolate FC15 nonstructural protein 5 gene, partial cds

DEFINITION Kunjin virus isolate FC15 nonstructural protein 5 gene, partial cds

ACCESSION AF297846

VERSION AF297846.1 GI:11991982

KEYWORDS Kunjin virus

SOURCE Kunjin virus

ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group.

REFERENCE 1 (bases 1 to 600)

AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V., Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.

TITLE The relationships between West Nile and Kunjin viruses

JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)

MEDLINE 21469816

PUBMED 11585535

REFERENCE 2 (bases 1 to 600)

AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.

TITLE Definitive studies of the relationships between West Nile and Kunjin viruses

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 600)

AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.

TITLE Direct Submission

JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University of Queensland, St Lucia, QLD 4072, Australia

FEATURES

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Best Local Similarity 100.0%; Pred. No. 8.3e-15; Length 600;

Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGGTTCTGAGGCTTACATGGATCACTTCGCAGCTTTGTC 48

Db 455 CGGTTCTGAGGCTTACATGGATCACTTCGCAGCTTTGTC 415

RESULT 34

AF458350/c

LOCUS West Nile virus strain And-27875 nonstructural protein 5 gene, partial cds.

DEFINITION West Nile virus

ACCESSION AF458350

VERSION AF458350.1 GI:21636479

KEYWORDS West Nile virus (WNV)

SOURCE West Nile virus

ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group.

REFERENCE 1 (bases 1 to 462)

AUTHORS Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.

TITLE Mouse neuroinvasive phenotype of West Nile virus strains varies depending upon virus genotype

JOURNAL Virology 296 (1), 17-23 (2002)

MEDLINE 22033887

PUBMED 12036314

REFERENCE 2 (bases 1 to 462)

AUTHORS Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.

TITLE Direct Submission

JOURNAL Submitted (14-DEC-2001) Department of Pathology and WHO Collaborating Center for Tropical Diseases, The University of Texas Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA

FEATURES

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Dd	405	TCCGAGACGGTTCGAGGGCTTACATGCATCACTTCGC 368
RESULT 38		
AY590190/c		
LOCUS	AY590190 464 bp RNA linear VRL 30-MAY-2004	
DEFINITION	West Nile virus strain 03002094 3' UTR, partial sequence.	
ACCESSION	AY590190	
VERSION	AY590190.1 GI:47121677	
KEYWORDS		
SOURCE	West Nile virus (WNV)	
ORGANISM	West Nile virus	
REFERENCE	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;	
AUTHORS	Flavivirus; Japanese encephalitis virus group.	
TITLE	1 (bases 1 to 464)	
JOURNAL	Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and	
REFERENCE	Kramer,L.D.	
AUTHORS	Genetic and phenotypic variation of West Nile virus in New York,	
TITLE	2000-2003	
JOURNAL	Am. J. Trop. Med. Hyg. (2004) In press	
REFERENCE	2 (bases 1 to 464)	
AUTHORS	Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and	
TITLE	Kramer,L.D.	
JOURNAL	Direct Submission	
FEATURES	Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth	
source	Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA	
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Dd	106	TCCGAGACGGTTCGAGGGCTTACATGCATCACTTCGC 69
RESULT 39		
AY590191/c		
LOCUS	AY590191 464 bp RNA linear VRL 30-MAY-2004	
DEFINITION	West Nile virus strain 03000360 3' UTR, partial sequence.	

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Query Match      79.2%; Score 38; DB 14; Length 464;
Best Local Similarity 100.0%; Pred. No. 7e-13;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 106 TCGAGACGGTTCTGAGGGTTACATGATCACTTCGC 69

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RESULT	41
AY590193/c	
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DEFINITION	West Nile virus strain 03001426 3' UTR, partial sequence.
ACCESSION	AY590193
VERSION	AY590193.1 GI:47121680
	linear RNA 464 bp
	VRL 30-MAY-2004

KEYWORDS	West Nile virus (WNV)
SOURCE	West Nile virus
ORGANISM	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group.
REFERENCE	1 (bases 1 to 464)
AUTHORS	Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and Kramer,L.D.
TITLE	Genetic and phenotypic variation of West Nile virus in New York,

2000-2003
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES

Am. J. Trop. Med. Hyg. (2004) In press
(bases 1 to 464)
Ebel,G.D.; Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kraemer,L.D.
Direct Submission
Submitted (05/APR-2004) The Arbovirus Laboratories, Wadsworth
Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
Location/Qualifiers
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LOCUS
DEFINITION
ACCESSION
VERSION
AY590194
West Nile virus strain 03001516 3' UTR, partial sequence.
AY590194
AY590194.1 GI:47121681
464 bp RNA linear VRL 30-MAY-2004

KEYWORDS	West Nile virus (WNV)
SOURCE	West Nile virus
ORGANISM	Flavivirus; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Viruses; Japanese encephalitis virus group.
REFERENCE	1 (bases 1 to 464)
AUTHORS	Ebel,G.D., Carriacaburu,J.E., Young,D.S., Bernard,K.A. and Kramer,G.D.
TITLE	Genetic and phenotypic variation of West Nile virus in New York, 2000-2003
JOURNAL	Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE	2 (bases 1.to 464)

AUTHORS

AUTHORS Ebel, G.D., Carricaburu, J.E., Young, D.S., Bernard, K.A. and Kramer, L.D.
TITLE Direct Submission
JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
FEATURES Location/Qualifiers

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S.T. 12404

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Db
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LOCUS	AY590195	464 bp	RNA	linear	VRL 30-MAY-2004
DEFINITION	West Nile virus strain 03001543	3' UTR,			
ACCESSION	AY590195				
VERSION	AY590195.1	GI:47121682			
KEYWORDS	.				
SOURCE	West Nile virus (WNV)				
AY590195/c					

SOURCE
ORGANISM

ORGANISM
West Nile virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.

REFERENCE

AUTHORS
Ebel, G.D., Carricaburu, J.E., Young, D.S., Bernard, K.A. and Kramer, L.D.

TITLE
Genetic and phenotypic variation of West Nile virus in New York, 2000-2003

JOURNAL

REFERENCE
AUTHORS

TITLE

JOURNAL
Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
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Location/Qualifiers

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106 TCCGAGACGGTTC TAGGGGCTTACATGGATCACTTCGC

RESULT 44

AY590196/c	AY590196/c	AY590196	464 bp	RNA	linear	VRT, 30-MAY-2004
AY590196/c	AY590196/c	AY590196	464 bp	RNA	linear	VRT, 30-MAY-2004


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ACCESSION AY590196
VERSION AY590196.1 GI:47121683
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ORGANISM West Nile virus
REFERENCE Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
AUTHORS Flavivirus; Japanese encephalitis virus group.
1 (bases 1 to 464)
Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
TITLE Genetic and phenotypic variation of West Nile virus in New York,
2000-2003
JOURNAL Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE 2 (bases 1 to 464)
AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
TITLE Direct Submission
JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
Center, 5668 State Farm Rd., Slingerlands, NY 12159, USA
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Db 106 TCCGAGACGGTCTCGAGGCTTACATGGATCACTTCGC 69
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LOCUS West Nile virus strain 03001700 3' UTR, partial sequence.
DEFINITION West Nile virus strain 03001700 3' UTR, partial sequence.
ACCESSION AY590197
VERSION AY590197.1 GI:47121684
KEYWORDS
SOURCE West Nile virus (WNV)
ORGANISM West Nile virus
REFERENCE Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
AUTHORS Flavivirus; Japanese encephalitis virus group.
1 (bases 1 to 464)
Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
TITLE Genetic and phenotypic variation of West Nile virus in New York,
2000-2003
JOURNAL Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE 2 (bases 1 to 464)
AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
TITLE Direct Submission
JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
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Db 106 TCCGAGACGGTCTCGAGGCTTACATGGATCACTTCGC 69
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DEFINITION West Nile virus strain 03001721 3' UTR, partial sequence.
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VERSION AY590198.1 GI:47121685
KEYWORDS
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ORGANISM West Nile virus
REFERENCE Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
AUTHORS Flavivirus; Japanese encephalitis virus group.
1 (bases 1 to 464)
Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
TITLE Genetic and phenotypic variation of West Nile virus in New York,
2000-2003
JOURNAL Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE 2 (bases 1 to 464)
AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
TITLE Direct Submission
JOURNAL Submitted (05-APR-2004) The Arbovirus Laboratories, Wadsworth
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DEFINITION West Nile virus strain 03001734 3' UTR, partial sequence.
ACCESSION AY590199
VERSION AY590199.1 GI:47121686
KEYWORDS
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ORGANISM West Nile virus
REFERENCE Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
AUTHORS Flavivirus; Japanese encephalitis virus group.
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Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
Kramer,L.D.
TITLE Genetic and phenotypic variation of West Nile virus in New York,
2000-2003
JOURNAL Am. J. Trop. Med. Hyg. (2004) In press
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ORGANISM West Nile virus
REFERENCE Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
AUTHORS Flavivirus; Japanese encephalitis virus group.
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Kramer,L.D.
TITLE Genetic and phenotypic variation of West Nile virus in New York,
2000-2003
JOURNAL Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE 2 (bases 1 to 464)
AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
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Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
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2000-2003
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REFERENCE 2 (bases 1 to 464)
AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
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REFERENCE 1 (bases 1 to 464)
AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
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TITLE Genetic and phenotypic variation of West Nile virus in New York,
        2000-2003
JOURNAL Am. J. Trop. Med. Hyg. (2004) In press
REFERENCE 2 (bases 1 to 464)
AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
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REFERENCE 1 (bases 1 to 464)
AUTHORS Ebel,G.D., Carricaburu,J.E., Young,D.S., Bernard,K.A. and
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TITLE Genetic and phenotypic variation of West Nile virus in New York,
        2000-2003
JOURNAL Am. J. Trop. Med. Hyg. (2004) In press
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TITLE Genetic and phenotypic variation of West Nile virus in New York,
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JOURNAL Am. J. Trop. Med. Hyg. (2004) In press
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TITLE Genetic and phenotypic variation of West Nile virus in New York,
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JOURNAL Am. J. Trop. Med. Hyg. (2004) In press
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TITLE Genetic and phenotypic variation of West Nile virus in New York,
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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9	33	68.8	87	ADN36779	Adn36779 West Nile
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c 99	15	31.2	1080	4	AAK69934	Aak69934 Human imm	172	15	31.2	5407	10	ADP81470	Adp81470 Leukaemia
c 100	15	31.2	1117	4	AAK69935	Aak69935 Human imm	173	15	31.2	5434	10	ADE98336	Ade98336 Cancer-li
c 101	15	31.2	1521	11	ABD07891	Abd07891 Pseudomon	174	15	31.2	5436	10	ADE98331	Ade98331 Cancer-li
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c 107	15	31.2	1929	8	ADA68221	Ada68221 Arabidops	c 179	14	29.2	42881	5	ACN04658	Acn04658 Human neu
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c 109	15	31.2	3961	12	AD116314	Adi16314 Human nuc	c 181	14	29.2	17	6	ACN14215	Acn14215 WNV minus
c 110	15	31.2	4021	8	ACC42350	Acc42350 Human MAP	c 182	14	29.2	110	3	ACN01378	Acn01378 WNV Hamme
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c 112	15	31.2	4607	10	ADE98371	Ade98371 Cancer-li	c 184	14	29.2	110	3	AAI13420	Aai13420 Human sec
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c 140	15	31.2	5069	10	ADE98330	Ade98330 Cancer-li	c 212	14	29.2	624	11	ACH95180	Ach95180 Kiebsiell
c 141	15	31.2	5073	10	ADE98315	Ade98315 Cancer-li	c 213	14	29.2	633	13	ADQ53771	Adq53771 Novel can
c 142	15	31.2	5076	10	ADE98341	Ade98341 Cancer-li	c 214	14	29.2	697	6	ABL61138	Ab161138 Murine al
c 143	15	31.2	5078	10	ADE98374	Ade98374 Cancer-li	c 215	14	29.2	704	4	AAH04805	Aah04805 Human cDN
c 144	15	31.2	5083	10	ADE98380	Ade98380 Cancer-li	c 216	14	29.2	723	6	ABK54536	Abk54536 Human col
c 145	15	31.2	5088	10	ADE98348	Ade98348 Cancer-li	c 217	14	29.2	745	6	ABL61122	Ab161122 Murine al
c 146	15	31.2	5094	10	ADE98309	Ade98309 Cancer-li	c 218	14	29.2	804	8	ADA68235	Ada68235 Arabidops
c 147	15	31.2	5137	10	ADE98339	Ade98339 Cancer-li	c 219	14	29.2	818	3	AAA95781	Aaa95781 Human imm
c 148	15	31.2	5146	10	ADE98307	Ade98307 Cancer-li	c 220	14	29.2	831	9	ADB09972	Adb09972 Allicooc
c 149	15	31.2	5164	10	ADE98377	Ade98377 Cancer-li	c 221	14	29.2	831	11	ABD000450	Abd000450 Kiebsiell
c 150	15	31.2	5169	10	ADE98352	Ade98352 Cancer-li	c 222	14	29.2	873	6	ABO91480	Abg91480 M. capaul
c 151	15	31.2	5175	10	ADE98373	Ade98373 Cancer-li	c 223	14	29.2	909	11	ACH97522	Ach97522 Kiebsiell
c 152	15	31.2	5183	10	ADE98385	Ade98385 Cancer-li	c 224	14	29.2	936	4	ABA77122	AbA77122 Prolifera
c 153	15	31.2	5185	10	ADE98347	Ade98347 Cancer-li	c 225	14	29.2	948	4	AAS52100	Aas52100 Staphyloc
c 154	15	31.2	5190	10	ADE98335	Ade98335 Cancer-li	c 226	14	29.2	978	8	ACF73711	Acf73711 Staphyloc
c 155	15	31.2	5232	10	ADE98337	Ade98337 Cancer-li	c 227	14	29.2	981	8	ACA20302	AcA20302 Prokaryot
c 156	15	31.2	5243	10	ADE98306	Ade98306 Cancer-li	c 228	14	29.2	1049	8	ACA48612	AcA48612 Prokaryot
c 157	15	31.2	5264	10	ADE98382	Ade98382 Cancer-li	c 229	14	29.2	1209	8	ACA40155	AcA40155 Prokaryot
c 158	15	31.2	5271	10	ADE98329	Ade98329 Cancer-li	c 230	14	29.2	1242	4	AAS56263	Aas56263 Salmonell
c 159	15	31.2	5280	10	ADE98384	Ade98384 Cancer-li	c 231	14	29.2	1242	8	ACA51807	AcA51807 Prokaryot
c 160	15	31.2	5285	10	ADE98379	Ade98379 Cancer-li	c 232	14	29.2	1276	10	ADK60153	Adk60153 Plant DNA
c 161	15	31.2	5287	10	ADE98334	Ade98334 Cancer-li	c 233	14	29.2	1384	8	ADA89845	Ada89845 Staphyloc
c 162	15	31.2	5319	6	ABL68493	Ab168493 Kidney ca	c 234	14	29.2	1404	3	AAC54576	Aac54576 Arabidops
c 163	15	31.2	5339	8	ACC42351	Acc42351 Human MAP	c 235	14	29.2	1458	2	ABX72217	Abx72217 Human NOV
c 164	15	31.2	5359	8	ACC42351	Acc42351 Human MAP	c 236	14	29.2	1492	2	AAZ00814	Aaz00814 Human sec
c 165	15	31.2	5361	10	ADE98381	Ade98381 Cancer-li	c 237	14	29.2	1492	8	ADA39903	Ada39903 Human sec
c 166	15	31.2	5366	10	ADE98351	Ade98351 Cancer-li	c 238	14	29.2	1492	8	ACC50492	Acc50492 Human sec
c 167	15	31.2	5366	10	ADE98351	Ade98351 Cancer-li	c 239	14	29.2	1492	8	ABZ71274	Abz71274 Human sec

C 240	14	29.2	1492	9	ADB91180	Adb91180 Human sec	C 313	14	29.2	5765	12	ADO20387	Ado20387 Human PRO
C 241	14	29.2	1492	10	ADC73557	Adc73557 Human sec	314	14	29.2	5771	12	ADK60290	Adk60290 Angiogene
C 242	14	29.2	1492	10	ADC73614	Adc73614 Human sec	315	14	29.2	5771	12	ADK60591	Adk60591 Angiogene
C 243	14	29.2	1492	10	ADA56093	Ada56093 Gene enco	316	14	29.2	5771	12	ADP73214	Adp73214 Angiogene
C 244	14	29.2	1508	11	ADM02282	Adm02282 Human cDN	317	14	29.2	5843	10	ADP73214	Adp73214 Angiogene
C 245	14	29.2	1584	10	ACC60774	Acc60774 Gene sequ	C 318	14	29.2	5955	5	ABA20275	Abas20275 Human PRO
C 246	14	29.2	1584	10	ADK61973	Adk61973 Disease t	C 319	14	29.2	5987	11	ACN89038	Acn89038 Breast ca
C 247	14	29.2	1584	13	ADT47333	Adt47333 Bacterial	C 320	14	29.2	5987	5	ABA20274	Abas20274 Human ner
C 248	14	29.2	1619	6	ABL61992	AbL61992 Colon ade	321	14	29.2	6871	13	ADL84323	Adl84323 Aspergill
C 249	14	29.2	1635	11	ABD00187	Abd00187 Klebsiell	322	14	29.2	7120	4	ABL04480	AbL04480 Drosophil
C 250	14	29.2	1662	8	ACA35379	AcA35379 Prokaryot	323	14	29.2	7376	4	ABL29946	AbL29946 Drosophil
C 251	14	29.2	1731	10	ADA7838	Ada7838 Human gen	324	14	29.2	7751	4	ABL16582	AbL16582 Drosophil
C 252	14	29.2	1736	10	ADB63042	AdB63042 Human cDN	325	14	29.2	8296	12	ADO10003	Ado10003 Human SIM
C 253	14	29.2	1778	4	AAK84200	Aak84200 Human imm	326	14	29.2	9096	2	AAT88015	Aat88015 Human int
C 254	14	29.2	1824	6	ABN90694	Abn90694 Staphyloc	C 327	14	29.2	9404	6	AAD25318	Aad25318 Human HSD
C 255	14	29.2	1824	13	ADS03917	AdS03917 Staphyloc	C 328	14	29.2	9404	6	AAD25261	Aad25261 Human HSD
C 256	14	29.2	1968	9	ADB09644	AdB09644 Alloccoc	C 329	14	29.2	9500	4	AAH57414	Aah57414 Human ova
C 257	14	29.2	1968	9	ADB09642	AdB09642 Alloccoc	330	14	29.2	17310	2	AAV74334	Aav74334 Staphyloc
C 258	14	29.2	1968	12	ADJ27112	AdJ27112 Alloccoc	331	14	29.2	20001	13	ACN37237	Acn37237 Human per
C 259	14	29.2	2000	6	ABZ17521	Abz17521 Arabidops	C 332	14	29.2	21045	4	AAS26721	Aas26721 Human gen
C 260	14	29.2	2024	10	ADI21894	Adi21894 Novel hum	C 333	14	29.2	21045	8	ABX74070	Abx74070 Human nov
C 261	14	29.2	2066	4	AAK52372	Aak52372 Human pol	334	14	29.2	23307	4	AAI02958	Aai02958 Human rep
C 262	14	29.2	2123	4	AAK53356	Aak53356 Human pol	C 335	14	29.2	23307	4	AAI02842	Aai02842 Human rep
C 263	14	29.2	2166	6	ABL55863	AbL55863 Human oxi	336	14	29.2	23307	8	ADA41565	Ada41565 Human sec
C 264	14	29.2	2232	8	ADA69632	Ada69632 Rice gene	C 337	14	29.2	23307	10	ADC74654	Adc74654 Human sec
C 265	14	29.2	2533	4	ABL25714	AbL25714 Drosophil	338	14	29.2	23307	10	ADD38122	Add38122 cDNA clon
C 266	14	29.2	2623	4	AAH15617	Aah15617 Human cDN	339	14	29.2	23307	10	ADA57698	Ada57698 BAC fragm
C 267	14	29.2	2623	6	ABK09777	AbK09777 Human ova	C 340	14	29.2	23333	4	ABL14260	AbL14260 Drosophil
C 268	14	29.2	2638	13	ADS48658	AdS48658 Bacterial	341	14	29.2	23694	11	ACN45138	Acn45138 Human gen
C 269	14	29.2	2709	4	AAK82737	Aak82737 Human imm	342	14	29.2	32502	4	AAAS9542	Aaas9542 Propionib
C 270	14	29.2	2757	2	AAK06821	Aak06821 Chlamydia	343	14	29.2	32502	8	ACF64471	Acf64471 Propionib
C 271	14	29.2	2823	12	ADO10008	Ado10008 Human SIM	344	14	29.2	35048	4	ABL06102	AbL06102 Drosophil
C 272	14	29.2	2859	6	AAD30523	Aad30523 Human sin	345	14	29.2	36976	13	ABD32930	Abd32930 Human can
C 273	14	29.2	2913	4	AAH14490	Aah14490 Human cDN	C 346	14	29.2	37004	13	ABD33353	Abd33353 Human can
C 274	14	29.2	2957	3	AAZ61509	Aaz61509 DNA encod	C 347	14	29.2	44147	6	ABK84481	AbK84481 Human cDN
C 275	14	29.2	2960	8	AAQ47249	Aaq47249 Human sca	C 348	14	29.2	44147	10	ADD14691	Add14691 Human src
C 276	14	29.2	3048	2	AAQ75343	Aaq75343 Soybean p	349	14	29.2	47322	13	ABD33395	Abd33395 Murine ca
C 277	14	29.2	3129	13	ACN40913	Acn40913 Tumour-as	C 350	14	29.2	51256	10	ADB85543	AdB85543 Human sen
C 278	14	29.2	3130	6	ABL69700	AbL69700 Prostate	C 351	14	29.2	51256	10	ADK66161	AdK66161 Human pro
C 279	14	29.2	3130	8	ABL67710	AbL67710 Oesophagu	C 352	14	29.2	51719	6	AAD31365	Aad31365 52Kb gene
C 280	14	29.2	3210	6	ABL732158	AbL732158 Human neu	353	14	29.2	53458	13	ABD32806_6	Abd32806_6
C 281	14	29.2	3211	2	AAQ75344	Aaq75344 Soybean p	C 354	14	29.2	58822	9	ADA02540	Ada02540 Human TCO
C 282	14	29.2	3294	13	ACN40914	Acn40914 Tumour-as	C 355	14	29.2	58822	10	ADB72278	AdB72278 Human TCO
C 283	14	29.2	3295	12	ADQ87105	AdQ87105 Human tum	C 356	14	29.2	58822	10	ADE95788	AdE95788 Human TCO
C 284	14	29.2	3295	13	ADQ86058	AdQ86058 Human tum	C 357	14	29.2	59065	6	ABL42416	AbL42416 Human ser
C 285	14	29.2	3312	12	ADK67724	AdK67724 Human sim	C 358	14	29.2	59065	6	ABD41839	Abd41839 Human LIM
C 286	14	29.2	3334	4	AAK82796	Aak82796 Human imm	C 359	14	29.2	59065	10	ADG98727	AdG98727 Human kin
C 287	14	29.2	3405	12	ADI61914	Adi61914 Fiber exp	C 360	14	29.2	59065	13	ADR44808	AdR44808 Human kin
C 288	14	29.2	3405	12	AAI56402	Aai56402 Cotton fi	361	14	29.2	79329	12	ADQ97506	AdQ97506 Mouse can
C 289	14	29.2	3560	11	ADM02910	Adm02910 Human cDN	C 362	14	29.2	92139	6	AD31364	Ad31364 92Kb gene
C 290	14	29.2	3621	11	ACN89500	Acn89500 Breast ca	C 363	14	29.2	96587	9	ADA02984	Ada02984 Human MAP
C 291	14	29.2	3828	12	ADQ22517	AdQ22517 Human eof	C 364	14	29.2	96587	10	ADB72722	AdB72722 Human MAP
C 292	14	29.2	3885	6	ABK922169	AbK922169 Prostate	C 365	14	29.2	96587	10	ADC85464	AdC85464 Human Map
C 293	14	29.2	3885	12	ADO10007	Ado10007 Human SIM	C 366	14	29.2	96587	12	ADM74579	Adm74579 Human car
C 294	14	29.2	3920	6	AAAD30522	Aad30522 Human sin	C 367	14	29.2	99957	9	ADA03032	Ada03032 Human mCG
C 295	14	29.2	3936	12	ADK60411	AdK60411 Angiogene	C 368	14	29.2	99957	10	ADB72770	AdB72770 Human CA
C 296	14	29.2	3936	12	ADK60712	AdK60712 Angiogene	C 369	14	29.2	99957	10	ADC85512	AdC85512 Human gen
C 297	14	29.2	3936	12	ADP73335	Adp73335 Human RIN	C 370	14	29.2	99957	12	ADM74627	Adm74627 Human car
C 298	14	29.2	3937	4	AAH15767	Aah15767 Human cDN	371	14	29.2	101169	12	ADQ97584	AdQ97584 Mouse can
C 299	14	29.2	4236	4	ABL04910	AbL04910 Drosophil	C 372	14	29.2	105184	6	ABK24122	AbK24122 Bacterial
C 300	14	29.2	4481	4	ABL04908	AbL04908 Drosophil	C 373	14	29.2	110000	2	AAK91990_00	Aak91990_00 Nucleotid
C 301	14	29.2	4493	8	ACC44335	Acc44335 Full leng	C 374	14	29.2	110000	5	AAI61373_3	AAI61373_3
C 302	14	29.2	4679	13	ADP73067	AdP73067 Angiogene	C 375	14	29.2	110000	6	ABA03041_22	ABA03041_22
C 303	14	29.2	4954	13	ADN35280	Adn35280 Synthetic	C 376	14	29.2	110000	9	ADB12064_09	ADB12064_09
C 304	14	29.2	4091	2	AAT39809	Aat39809 Mouse H74	C 377	14	29.2	110000	9	ADB12064_10	ADB12064_10
C 305	14	29.2	4236	4	ABL04910	AbL04910 Drosophil	C 378	14	29.2	110000	10	ADG70447_3	ADG70447_3
C 306	14	29.2	4481	4	ABL04908	AbL04908 Drosophil	C 379	14	29.2	110000	10	ABZ79565_3	ABZ79565_3
C 307	14	29.2	4679	13	ADP73067	AdP73067 Angiogene	C 380	14	29.2	110000	12	ADN46845_14	ADN46845_14
C 308	14	29.2	4954	13	ADN08350	AdN08350 Full leng	C 381	14	29.2	110000	12	ADN47591_06	ADN47591_06
C 309	14	29.2	4978	10	ADF74208	AdF74208 Human nov	C 382	14	29.2	110000	12	ADN46123_14	ADN46123_14
C 310	14	29.2	5022	6	ABK84067	AbK84067 Human cDN	C 383	14	29.2	110000	12	ADN47209_06	ADN47209_06
C 311	14	29.2	5022	10	ADD14628	Add14628 Human src	384	14	29.2	110000	12	ADN46464_14	ADN46464_14
C 312	14	29.2	5022	10	ADH28889	Adh28889 Human chr	C 385	14	29.2	110000	12	ADN47960_06	ADN47960_06

386	14	29.2	118951	8	ABT17385	Abt17385 Human IG	13	27.1	288	12	ADL83774	Adl83774 DNA up-re
387	14	29.2	123920	11	ACN44816	Acn44816 Mouse gen	13	27.1	289	5	ABV60671	Abv60671 Human pro
388	14	29.2	128978	6	ABK83459	Abk83459 Human cDN	13	27.1	291	5	ABV60616	Abv60616 Human pro
389	14	29.2	128978	8	AAD54587	Aad54587 Human LIM	13	27.1	291	5	ABV60425	Abv60425 Human pro
390	14	29.2	128978	13	ADR52994	Adr52994 Drug ther	13	27.1	293	8	ACA14435	Aca14435 Prokaryot
391	14	29.2	130320	10	ADF11613	Adf11613 Human scl	13	27.1	293	8	ACA14435	Aca14435 Prokaryot
392	14	29.2	133893	9	AAD54538	Aad54538 Human pro	13	27.1	295	5	ABV60518	Abv60518 Human pro
393	14	29.2	134442	13	ABD32824	Abd32824 Mouse can	13	27.1	295	5	ABV60582	Abv60582 Human pro
394	14	29.2	135995	13	ABD33534	Abd33534 Murine ca	13	27.1	299	5	ABV60557	Abv60557 Human pro
395	14	29.2	185695	8	ABQ77405	Abq77405 Human THB	13	27.1	300	11	ACH94504	Ach94504 Klebsiell
396	14	29.2	185695	8	AAD55693	Aad55693 Human THB	13	27.1	301	5	ABV60513	Abv60513 Human pro
397	14	29.2	192427	10	ADL13825	Adl13825 Osteoarth	13	27.1	301	5	ABV60513	Abv60513 Human pro
398	14	29.2	200000	12	ADO47150	Ado47150 DNA seque	13	27.1	302	5	ABV60381	Abv60381 Human pro
399	14	29.2	210528	11	ACN44040	Acn44040 Mouse gen	13	27.1	303	5	ABV60615	Abv60615 Human pro
400	14	29.2	215221	11	ACN44754	Acn44754 Human gen	13	27.1	304	8	ACA15490	Aca15490 Prokaryot
401	14	29.2	228006	12	ADQ97143	Adq97143 Mouse can	13	27.1	304	10	ABX88536	Abx88536 Corn ear-
402	14	29.2	256157	11	ACN44650	Acn44650 Human gen	13	27.1	305	5	ABV60474	Abv60474 Human pro
403	14	29.2	256157	13	ABD33570	Abd33570 Human can	13	27.1	307	5	ABV60417	Abv60417 Human pro
404	14	29.2	256190	13	ABD33276	Abd33276 Human can	13	27.1	308	5	ABV60598	Abv60598 Human pro
405	14	29.2	302603	11	ADP75187	Adp75187 Human can	13	27.1	311	5	ABV60437	Abv60437 Human pro
406	14	29.2	337022	12	ADQ59416	Adq59416 Human can	13	27.1	311	5	ABV60437	Abv60437 Human pro
407	14	29.2	347001	12	ADP43517	Adp43517 Human MAD	13	27.1	315	3	AAC09617	Aac09617 Human sec
408	13	27.1	17	6	ACN03370	Acn03370 MNV Inozy	13	27.1	315	3	AAC09617	Aac09617 Human sec
409	13	27.1	17	6	ACN09611	Acn09611 MNV minus	13	27.1	320	5	ABV60633	Abv60633 Human pro
410	13	27.1	18	2	AAV08120	Aav08120 Primer Vb	13	27.1	320	5	ABV60633	Abv60633 Human pro
411	13	27.1	20	2	AAT15131	Aat15131 Hypermuta	13	27.1	321	8	ACA14847	Aca14847 Prokaryot
412	13	27.1	20	2	AAT15111	Aat15111 Hypermuta	13	27.1	321	8	ACA14282	Aca14282 Prokaryot
413	13	27.1	20	2	AAV21003	Aav21003 Microsate	13	27.1	321	13	ACN47162	Acn47162 Cotton pr
414	13	27.1	20	2	AAV21035	Aav21035 Microsate	13	27.1	324	5	ABV60585	Abv60585 Human pro
415	13	27.1	20	2	AAV36433	Aav36433 Primer IA	13	27.1	324	5	ABV60524	Abv60524 Human pro
416	13	27.1	20	2	AAZ21659	Aaz21659 Exemplary	13	27.1	327	8	ACA33375	Aca33375 Prokaryot
417	13	27.1	20	2	AAZ21691	Aaz21691 Exemplary	13	27.1	327	8	ACA33375	Aca33375 Prokaryot
418	13	27.1	20	2	AAH42021	Aah42021 Disease t	13	27.1	330	5	ADL36309	Adl36309 Human ova
419	13	27.1	25	9	ACK12719	Ack12719 Human mic	13	27.1	330	5	ADL36309	Adl36309 Human ova
420	13	27.1	31	2	AAQ72252	Aaq72252 Chloramph	13	27.1	332	6	ABK76318	Abk76318 Bacillus
421	13	27.1	32	2	AAQ31901	Aaq31901 PCR prime	13	27.1	341	8	ABX37643	Abx37643 Bovine ES
422	13	27.1	38	12	ADU63902	Adu63902 Plant lip	13	27.1	345	6	ABK78754	Abk78754 Bacillus
423	13	27.1	60	13	AD553324	Ad553324 Eucalyptu	13	27.1	345	8	ACA35241	Aca35241 Prokaryot
424	13	27.1	64	12	ADN02062	Adn02062 Primer ml	13	27.1	353	4	AA337145	Aa337145 Novel hum
425	13	27.1	65	6	ABN51566	Abn51566 Mouse spl	13	27.1	353	4	AA337145	Aa337145 Novel hum
426	13	27.1	81	12	ADF99890	Adf99890 Nicotiana	13	27.1	363	3	AAC08176	Aac08176 Human sec
427	13	27.1	100	8	ACD75393	AcD75393 E. coli K	13	27.1	363	3	AAC08176	Aac08176 Human sec
428	13	27.1	100	8	ACD75392	AcD75392 E. coli K	13	27.1	366	5	ABV60488	Abv60488 Human pro
429	13	27.1	186	9	ADA30667	Ada30667 DNA encod	13	27.1	375	8	ABX45584	Abx45584 Bovine ES
430	13	27.1	201	4	AAI25931	Aai25931 Probe #15	13	27.1	377	4	AAI23951	Aai23951 Probe #13
431	13	27.1	201	4	ABA72821	Aba72821 Human foe	13	27.1	377	4	ABA69070	AbA69070 Human foe
432	13	27.1	201	4	AAI53247	Aai53247 Probe #21	13	27.1				
433	13	27.1	201	4	ABA38439	Aba38439 Probe #16	13	27.1				
434	13	27.1	201	4	AAK47409	Aak47409 Human bon	13	27.1				
435	13	27.1	201	4	AAK21252	Aak21252 Human bra	13	27.1				
436	13	27.1	201	4	AB847150	Ab847150 Human liv	13	27.1				
437	13	27.1	201	6	AB821547	Ab821547 Human gen	13	27.1				
438	13	27.1	207	8	ABZ20336	Abz20336 Group III	13	27.1				
439	13	27.1	210	8	ACA15334	Aca15334 Prokaryot	13	27.1				
440	13	27.1	231	8	ACA15310	Aca15310 Prokaryot	13	27.1				
441	13	27.1	231	8	ACA15262	Aca15262 Prokaryot	13	27.1				
442	13	27.1	231	11	ACH98322	Ach98322 Klebsiell	13	27.1				
443	13	27.1	259	7	ADS65726	Ads65726 Corn seed	13	27.1				
444	13	27.1	261	8	ACA14491	Aca14491 Prokaryot	13	27.1				
445	13	27.1	266	5	ABV60668	Abv60668 Human pro	13	27.1				
446	13	27.1	267	8	ACA14036	Aca14036 Prokaryot	13	27.1				
447	13	27.1	270	5	ABV60479	Abv60479 Human pro	13	27.1				
448	13	27.1	270	6	ABK15986	Abk15986 Human lun	13	27.1				
449	13	27.1	270	10	ADB95249	Adb95249 Human lun	13	27.1				
450	13	27.1	272	5	ABV60436	Abv60436 Human pro	13	27.1				
451	13	27.1	276	5	ABV60618	Abv60618 Human pro	13	27.1				
452	13	27.1	277	5	ABV60395	Abv60395 Human pro	13	27.1				
453	13	27.1	278	5	ABV60480	Abv60480 Human pro	13	27.1				
454	13	27.1	281	5	ABV60566	Abv60566 Human pro	13	27.1				
455	13	27.1	282	3	AAA87497	Aaa87497 Rat hepat	13	27.1				
456	13	27.1	282	5	ABV60532	Abv60532 Human pro	13	27.1				
457	13	27.1	286	5	ABV60363	Abv60363 Human pro	13	27.1				
458	13	27.1	288	12	ADL83775	Adl83775 DNA up-re	13	27.1				

ALIGNMENTS

RESULT 1
ADN36751
ID ADN36751 standard; DNA; 48 BP.
AC ADN36751;
XX
XX
DT 15-JUL-2004 (first entry)
XX
DE West Nile virus detection-related oligonucleotide probe SeqID73.
XX
KW hybridisation assay probe; nucleic acid detection;
KW target-complementary sequence; flavivirus; West Nile virus; WNV;
KW RNA virus; infection; meningitis; encephalitis;
XX high throughput screening; probe; ss.
OS West Nile virus.
XX
FN WO2004036190-A2.
XX
PD 29-APR-2004.
XX
PF 10-OCT-2003; 2003WO-US033639.
XX
PR 16-OCT-2002; 2002US-041891P.
PR 25-NOV-2002; 2002US-0429006P.
PR 24-FEB-2003; 2003US-0449810P.

XX (GENP-) GEN-PROBE INC.
XX Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX WPI; 2004-389590/36.
XX New hybridization assay probe comprising target-complementary sequence of
XX bases, useful in detecting flavivirus, e.g. West Nile virus.
XX Claim 18; SEQ ID NO 73; 135pp; English.
XX This invention relates to a novel hybridisation assay probe, for
XX detecting a nucleic acid, which is a probe sequence that comprises a
XX target-complementary sequence of bases, and optionally one or more base
XX sequences that are not complementary to the nucleic acid that is to be
XX detected. The hybridisation assay probes and the kits are useful in
XX detecting and amplifying a target nucleic acid sequence, for example
XX flavivirus like West Nile virus, that may be present in a biological
XX sample. West Nile virus (WNV) is an RNA virus that primarily infects
XX birds and culex mosquitoes, with humans and horses serving as incidental
XX hosts. Infection of humans can lead to meningitis or encephalitis. The
XX invention may allow for accurate and efficient high throughput screening.
XX The present sequence is that of an oligonucleotide probe which is related
XX to the invention.
XX Sequence 48 BP; 8 A; 12 C; 13 G; 15 T; 0 U; 0 Other;
SQ Query Match 100.0%; Score 48; DB 12; Length 48;
Best Local Similarity 100.0%; Pred. No. 9.1e-17;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCGAGACGGTCTGAGGGCTTACATGGATCATTGCGAGCTTTGTTTC 48
DB 1 TCCGAGACGGTCTGAGGGCTTACATGGATCATTGCGAGCTTTGTTTC 48
RESULT 2
ADN36750
ID ADN36750 standard; DNA; 70 BP.
XX AC ADN36750;
XX 15-JUL-2004 (first entry)
XX West Nile virus detection-related oligonucleotide probe SeqID72.
XX hybridisation assay probe; nucleic acid detection;
XX target-complementary sequence; flavivirus; West Nile virus; WNV;
XX RNA virus; infection; meningitis; encephalitis;
XX high throughput screening; probe; ss.
XX West Nile virus.
XX WO2004036190-A2.
XX 29-APR-2004.
XX 10-OCT-2003; 2003WO-US033639.
XX 16-OCT-2002; 2002US-0418891P.
XX 25-NOV-2002; 2002US-0429006P.
XX 24-FEB-2003; 2003US-0449810P.
XX (GENP-) GEN-PROBE INC.
XX Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX WPI; 2004-389590/36.
XX New hybridization assay probe comprising target-complementary sequence of
XX bases, useful in detecting flavivirus, e.g. West Nile virus.
XX

PS Disclosure; SEQ ID NO 72; 135pp; English.
XX This invention relates to a novel hybridisation assay probe, for
XX detecting a nucleic acid, which is a probe sequence that comprises a
XX target-complementary sequence of bases, and optionally one or more base
XX sequences that are not complementary to the nucleic acid that is to be
XX detected. The hybridisation assay probes and the kits are useful in
XX detecting and amplifying a target nucleic acid sequence, for example
XX flavivirus like West Nile virus, that may be present in a biological
XX sample. West Nile virus (WNV) is an RNA virus that primarily infects
XX birds and culex mosquitoes, with humans and horses serving as incidental
XX hosts. Infection of humans can lead to meningitis or encephalitis. The
XX invention may allow for accurate and efficient high throughput screening.
XX The present sequence is that of an oligonucleotide probe which is related
XX to the invention.
XX Sequence 70 BP; 11 A; 19 C; 20 G; 20 T; 0 U; 0 Other;
SQ Query Match 100.0%; Score 48; DB 12; Length 70;
Best Local Similarity 100.0%; Pred. No. 8.9e-17;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCGAGACGGTCTGAGGGCTTACATGGATCATTGCGAGCTTTGTTTC 48
DB 1 TCCGAGACGGTCTGAGGGCTTACATGGATCATTGCGAGCTTTGTTTC 48
RESULT 3
ADR32078/c
ID ADR32078 standard; DNA; 10945 BP.
XX AC ADR32078;
XX 18-NOV-2004 (first entry)
XX Genomic DNA of a West Nile virus.
XX analysis; target; real time PCR; ds; genomic.
XX West Nile virus.
XX WO2004072230-A2.
XX 26-AUG-2004.
XX 10-FEB-2004; 2004WO-US002012.
XX 10-FEB-2003; 2003US-00361004.
XX (CLEA-) CLEARANT INC.
XX Mckenney K, Gillmeister L, Marlowe K, Armistead D;
XX WPI; 2004-625843/60.
XX Analyzing a target nucleic acid sequence in a biological material by real
XX time PCR using nucleic acid primers that are separated by at least 750
XX nucleic acid residues in the target sequence.
XX Disclosure; SEQ ID NO 5; 96pp; English.
XX The invention relates to a novel method for analysing a target nucleic
XX acid sequence in a biological material. The method comprises adding at
XX least two nucleic acid primers that hybridise under stringent conditions
XX to predetermined nucleic acid sequences of the target nucleic acid
XX sequence that are separated by at least 750 nucleic acid residues,
XX amplifying the target nucleic acid sequence by PCR, and detecting and
XX quantifying the target nucleic acid sequence. The methods and
XX compositions of the present invention are useful for analysing a target
XX nucleic acid sequence in a biological material by real time PCR using
XX nucleic acid primers that are separated by at least 750 nucleic acid
XX residues in the target sequence. This polynucleotide sequence represents
XX the genomic DNA of a West Nile virus used in the target analysis method

CC of the invention.
 XX Sequence 10945 BP; 2999 A; 2457 C; 3143 G; 2346 T; 0 U; 0 Other;
 SQ Query Match 79.2%; Score 38; DB 13; Length 10945;
 Best Local Similarity 100.0%; Pred. No. 2.7e-11;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTGAGGGCTTACATGCATCACTTCGC 38
 |||||
 Db 10587 TCCGAGACGGTTCTGAGGGCTTACATGCATCACTTCGC 10550

RESULT 4
 ADR67768/c
 ID ADR67768 standard; DNA; 10945 BP.
 XX ADR67768;
 AC ADR67768;
 XX 18-NOV-2004 (first entry)
 DT West Nile virus DNA detected by novel detection method.
 DE
 XX ds; detection; pathogen.
 XX West Nile virus.
 OS WO2004072231-A2.
 PN 26-AUG-2004.
 PD 10-FEB-2004; 2004WO-US002013.
 PF 10-FEB-2003; 2003US-00361002.
 PR (CLEA-) CLEARANT INC.
 XX Mckenney K, Gillmeister L, Marlowe K, Armistead D;
 XX WPI; 2004-625844/60.
 XX
 XX Determining level of potentially active biological pathogens in
 PT biological material, by adding nucleic acid primer pairs to biological
 PT material, amplifying target nucleic acid by PCR, detecting and
 PT quantifying target nucleic acid.
 XX Disclosure; SEQ ID NO 5; 11pp; English.

CC The invention relates to a method of determining (M1) level of
 CC potentially active biological pathogens in biological material, involves
 CC adding at least two nucleic acid primer pairs to biological material,
 CC amplifying target nucleic acid sequences by PCR, and detecting and
 CC quantifying target nucleic acid sequences, where quantity of the nucleic
 CC acid sequences is proportional to number of biological pathogens in
 CC biological material. (M1) is useful for determining level of potentially
 CC active biological pathogens in a biological material such as cells,
 CC tissues, blood or blood components, proteins, enzymes, immunoglobulins,
 CC botanicals, food, ligaments, tendons, nerves, bone, teeth, skin grafts,
 CC bone marrow, heart valves, cartilage, corneas, arteries, veins, organs,
 CC lipids, carbohydrates, collagen, chitin and its derivatives, forensic
 CC samples, mummified material, human or animal remains, stem cells, islet
 CC of Langerhans cells, cells for transplantation, red blood cells, white
 CC blood cells or platelets. The biological pathogen is chosen from
 CC bacteria, viruses, fungi and single cell parasites. The biological
 CC pathogen is chosen from Aspergillus, Candida, Histoplasma,
 CC Saccharomyces, Coccidioides, Cryptococcus, Escherichia, Bacillus,
 CC Campylobacter, Helicobacter, Listeria, Clostridium, Streptococcus,
 CC Enterococcus, Staphylococcus, Brucella, Haemophilus, Salmonella,
 CC Yersinia, Pseudomonas, Serratia, Enterobacter, Klebsiella, Proteus,
 CC Citrobacter, Corynebacterium, Propionibacterium and Coxiella. The
 CC biological pathogen is chosen from Adeno-associated virus (AAV), The
 CC California encephalitis virus, Coronavirus, Coxsackievirus-A,
 CC Coxsackievirus-B, Eastern equine encephalitis virus (EEEV), Echovirus,

CC Hantavirus, Hepatitis A virus (HAV), Hepatitis C virus (HCV), Hepatitis
 CC delta virus (HDV), Hepatitis E virus (HEV), Hepatitis G virus (HGV), HIV,
 CC Human T-lymphotropic virus (HTLV), Influenza virus (Flu virus), Measles
 CC virus (Rubella), Mumps virus, Norwalk virus, Parainfluenza virus, Polio
 CC virus, Rabies virus, Respiratory Syncytial virus, Rhinovirus, Rubella
 CC virus, Saint Louis encephalitis virus, Western equine encephalitis virus
 CC (WEEV), Yellow fever virus, Adenovirus, Cytomegalovirus (CMV), Epstein-
 CC Barr virus (EBV), Hepatitis B virus (HBV), Herpes simplex virus 1, Herpes
 CC simplex virus 2, Molluscum contagiosum, Papilloma virus (HPV), Smallpox
 CC virus (Variola), Vaccinia virus, Venezuelan equine encephalitis virus
 CC (VEEV), Ebola virus, West Nile virus, Human parvovirus B19 and Rotavirus.
 CC (M1) is useful for determining the effectiveness of a sterilization
 CC process applied to a biological material. (M1) is useful in determining
 CC whether the biological pathogen is inactive or active. (M1) enables
 CC determination of whether the particular biological pathogen is present in
 CC a biological material as shown by amplification of first target sequence
 CC and whether the biological pathogen is inactive or active. (M1) enables
 CC evaluation of the effectiveness of sterilization processes, and
 CC determination of both the original level and the residual level of
 CC potentially active biological pathogens. This sequence corresponds to a
 CC West Nile virus DNA detected by the method of the invention.
 XX
 SQ Sequence 10945 BP; 2999 A; 2457 C; 3143 G; 2346 T; 0 U; 0 Other;
 Query Match 79.2%; Score 38; DB 13; Length 10945;
 Best Local Similarity 100.0%; Pred. No. 2.7e-11;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTGAGGGCTTACATGCATCACTTCGC 38
 |||||
 Db 10587 TCCGAGACGGTTCTGAGGGCTTACATGCATCACTTCGC 10550

RESULT 5
 ADR98022/c
 ID ADR98022 standard; DNA; 10975 BP.
 XX ADR98022;
 AC ADR98022;
 XX 29-JUL-2004 (first entry)
 DT West Nile Virus isolate 2741 complete genome sequence.
 DE ds; West Nile Virus; envelope protein; glycoprotein E; flavivirus;
 XX Japanese encephalitis virus; Dengue virus; St Louis encephalitis virus.
 XX West Nile virus.
 OS WO2004040263-A2.
 PN 13-MAY-2004.
 PD 31-OCT-2003; 2003WO-US034823.
 PF 31-OCT-2002; 2002US-0422755P.
 PR 06-JUN-2003; 2003US-0476513P.
 XX (HEAL-) HEALTH RES INC.
 XX Wong SJ, Pei-Yong S;
 XX WPI; 2004-400223/37.
 XX GENBANK; AF206518.
 XX New diagnostic kit comprising West Nile Virus (WNV) envelope protein
 XX reactive with antibody against WNV and cross-reactive with antibody
 XX against a flavivirus, useful in diagnosing flavivirus infection caused by
 XX DENV, WNV, JEV or SLEV.
 XX Disclosure; Fig 37; 212pp; English.
 XX The invention relates to a diagnostic kit comprising at least one
 CC isolated and purified polypeptide comprising a West Nile Virus (WNV)

CC envelope (E) protein or its immunogenic fragment having a native
 CC conformation or non-denatured structure and that is reactive with
 CC antibodies against WNV and cross-reactive with antibodies against a
 CC flavivirus. The diagnostic kit is useful in diagnosing flavivirus
 CC infection caused by DENV, WNV, JEV or SLEV. This sequence corresponds to
 CC the complete nucleotide sequence of the WNV isolate 2741.

SQ Sequence 10975 BP; 3007 A; 2460 C; 3149 G; 2359 T; 0 U; 0 Other;
 Query Match 79.2%; Score 38; DB 12; Length 10975;
 Best Local Similarity 100.0%; Pred. No. 2.7e-11;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCCGAGACGGTTCTGAGGGCTTACATGATCACTTCGC 38
 |||||
 DB 10611 TCCGAGACGGTTCTGAGGGCTTACATGATCACTTCGC 10574

RESULT 6
 ABZ68481/c
 ID ABZ68481 standard; DNA; 11029 BP.

AC ABZ68481;

DT 22-APR-2003 (first entry)

DE Nucleotide sequence of the genome of West Nile virus IS-98-ST1.

KW WNV; IS-98-ST1; Flavivirus; infection; encephalitis; gene; ss.

OS West nile virus.

Key Location/Qualifiers
 CDS 97..10397
 FT /*tag= a
 FT /product= "polyprotein"

PN WO200281511-A1.

PD 17-OCT-2002.

PF 04-APR-2002; 2002WO-FR001168.

PR 04-APR-2001; 2001FR-00004599.

PR 06-SEP-2001; 2001PR-00011525.

PA (INSP) INST PASTEUR.

PA (KIMR-) KIMRON VETERINARY INST.

PI Despres P, Deubel V, Guenet J, Drouet M, Malkinson M, Banet C;

PI Freinkel M, Courageot M, Coulibaly F, Catteau A, Flamand M, Weber P;

PI Ceccaldi P;

XX WPI; 2003-058498/05.

DR P-PSDB; ABP70647.

XX New neurovirulent strain of West Nile virus, useful in diagnosis and

XX screening for antiviral agents, also related nucleic acids, proteins and

XX antibodies.

PS Claim 1; Page 34-49; 68pp; French.

XX The present sequence represents the genome of a strain of West Nile virus

XX (WNV), designated IS-98-ST1. This strain is a neuroinvasive and

XX neurovirulent strain of WNV. Polynucleotides and polypeptides derived

XX from the IS-98-ST1 genome are useful for diagnosis and prognosis of

XX Flavivirus infection, specifically WNV-mediated encephalitis. They are

SQ Sequence 11029 BP; 3019 A; 2471 C; 3167 G; 2372 T; 0 U; 0 Other;

Query Match 79.2%; Score 38; DB 8; Length 11029;

Best Local Similarity 100.0%; Pred. No. 2.7e-11;

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCCGAGACGGTTCTGAGGGCTTACATGATCACTTCGC 38

|||||

DB 10629 TCCGAGACGGTTCTGAGGGCTTACATGATCACTTCGC 10592

RESULT 7

ABV74821/c

ID ABV74821 standard; DNA; 11029 BP.

AC ABV74821;

DT 28-MAR-2003 (first entry)

DE West Nile virus strain NY99-flamingo 382-99 complete genome.

KW Virucide; hepatotropic; antiinflammatory; antiviral; OAS;

KW 2'-5'-oligoadenylate synthase; Flavivirus infection; gene; ss.

OS West Nile Virus.

Key Location/Qualifiers

CDS 97..10398

FT /*tag= a

FT /product= "West Nile Virus protein"

PN WO200281741-A2.

PD 17-OCT-2002.

PF 04-APR-2002; 2002WO-FR001169.

PR 04-APR-2001; 2001FR-00004598.

PR (INSP) INST PASTEUR.

PR (CNRS) CNRS CENT NAT RECH SCI.

PI Guenet J, Mashimo T, Simon-Chazottes D, Montagutelli X;

PI Freinkel M, Despres P, Deubel V, Bonhomme F, Lucas M;

XX WPI; 2003-058566/05.

DR P-PSDB; ABS98821.

XX Identifying stimulators of oligoadenylate synthase family genes, useful

XX as antiviral agents against Flavivirus, also mutated genes responsible

XX for sensitivity to virus.

PS Example 1; Page 52-67; 93pp; French.

XX The present invention relates to a method for identifying compounds (I)

XX that can stimulate a gene of the OAS (2'-5'-oligoadenylate synthase)

XX family. The method comprises: (a) inducing expression of the OAS gene in

XX a culture of cells from a non-human mammal (Flvr/Flvr or Flvr/Flva;

XX indicating resistance or sensitivity to Flavivirus infection); (b)

XX treating cells with test compound; and (c) measuring activity of OAS gene

XX relative to a control. (i) are potentially useful as antiviral agents for

XX treating infections by Flaviviruses (e.g. hepatitis C; dengue; yellow

XX fever and various forms of encephalitis). Genomic OAS DNA and derived

XX cDNA, also the encoded proteins, are useful: (a) for treating Flavivirus

XX infection; (b) in screening for anti-Flavivirus agents; and (c) for

XX evaluating sensitivity of subjects to Flavivirus infection and their

XX likely response to interferon treatment, e.g. to identify patients at

XX risk of developing severe forms of such infections. The present sequence

XX is West Nile Virus strain NY99-flamingo 382-99 (IS-98-ST1) complete

XX genome, which was used in an example from the invention. West Nile Virus

XX is one such Flavivirus

XX Sequence 11029 BP; 3019 A; 2471 C; 3167 G; 2372 T; 0 U; 0 Other;

Query Match 79.2%; Score 38; DB 10; Length 11029;
 Best Local Similarity 100.0%; Pred. No. 2.7e-11;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTGAGGCTTACATGGATCACTTCGC 38
 |||||

Db 10629 TCCGAGACGGTCTGAGGCTTACATGGATCACTTCGC 10592
 |||||

RESULT 8

ADN98023/c
 ID ADN98023 standard; DNA; 11029 BP.

XX AC ADN98023;

XX DT 29-JUL-2004 (first entry)

XX DE West Nile Virus isolate 3356 complete genome sequence.

XX KW ds; West Nile Virus; envelope protein; glycoprotein E; flavivirus;
 XX Japanese encephalitis virus; Dengue virus; St Louis encephalitis virus.

XX OS West Nile virus.

XX PN WO2004040263-A2.

XX PD 13-MAY-2004.

XX PF 31-OCT-2003; 2003WO-US034823.

XX PR 31-OCT-2002; 2002US-0422755P.

XX PR 06-JUN-2003; 2003US-0476513P.

XX PA (HEAL-) HEALTH RES INC.

XX PI Wong SJ, Pei-Yong S;

XX DR WPI: 2004-400223/37.

XX DR GENBANK; AF404756.

XX PT New diagnostic kit comprising West Nile Virus (WNV) envelope protein
 PT reactive with antibody against WNV and cross-reactive with antibody
 PT against a flavivirus, useful in diagnosing flavivirus infection caused by
 PT DENV, WNV, JEV or SLEV.

XX PS Disclosure; Fig 38; 212pp; English.

XX CC The invention relates to a diagnostic kit comprising at least one
 CC isolated and purified polypeptide comprising a West Nile Virus (WNV)
 CC envelope (E) protein or its immunogenic fragment having a native
 CC conformation or non-denatured structure and that is reactive with
 CC antibodies against WNV and cross-reactive with antibodies against a
 CC flavivirus. The diagnostic kit is useful in diagnosing flavivirus
 CC infection caused by DENV, WNV, JEV or SLEV. This sequence corresponds to
 CC the complete nucleotide sequence of the WNV isolate 3356.

XX SQ Sequence 11029 BP; 3017 A; 2466 C; 3172 G; 2374 T; 0 U; 0 Other;

Query Match 79.2%; Score 38; DB 12; Length 11029;
 Best Local Similarity 100.0%; Pred. No. 2.7e-11;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTGAGGCTTACATGGATCACTTCGC 38
 |||||

Db 10629 TCCGAGACGGTCTGAGGCTTACATGGATCACTTCGC 10592
 |||||

RESULT 9

ADN36779/c

ID ADN36779 standard; DNA; 87 BP.

XX AC ADN36779;

XX

DT 15-JUL-2004 (first entry)

XX DE West Nile virus detection-related oligonucleotide probe SeqID101.

XX KW hybridisation assay probe; nucleic acid detection;
 KW target-complementary sequence; flavivirus; West Nile virus; WNV;
 KW RNA virus; infection; meningitis; encephalitis;
 KW high throughput screening; probe; ss.

XX OS West Nile virus.

XX PN WO2004036190-A2.

XX PD 29-APR-2004.

XX PF 10-OCT-2003; 2003WO-US033639.

XX PR 16-OCT-2002; 2002US-0418891P.

XX PR 25-NOV-2002; 2002US-0429006P.

XX PR 24-FEB-2003; 2003US-0449810P.

XX PA (GENP-) GEN-PROBE INC.

XX PI Linmen JM, Pollner RB, Wu W, Dennis GG, Darby PM;

XX DR WPI: 2004-389590/36.

XX PT New hybridization assay probe comprising target-complementary sequence of
 PT bases, useful in detecting flavivirus, e.g. West Nile virus.

XX PS Claim 1; SEQ ID NO 101; 135pp; English.

XX CC This invention relates to a novel hybridisation assay probe, for
 CC detecting a nucleic acid, which is a probe sequence that comprises a
 CC target-complementary sequence of bases, and optionally one or more base
 CC sequences that are not complementary to the nucleic acid that is to be
 CC detected. The hybridisation assay probes and the kits are useful in
 CC detecting and amplifying a target nucleic acid sequence, for example
 CC flavivirus like West Nile virus, that may be present in a biological
 CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
 CC birds and culex mosquitoes, with humans and horses serving as incidental
 CC hosts. Infection of humans can lead to meningitis or encephalitis. The
 CC invention may allow for accurate and efficient high throughput screening.
 CC The present sequence is that of an oligonucleotide probe which is related
 CC to the invention.

XX SQ Sequence 87 BP; 23 A; 25 C; 26 G; 13 T; 0 U; 0 Other;

Query Match 68.8%; Score 33; DB 12; Length 87;
 Best Local Similarity 100.0%; Pred. No. 1.9e-08;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GACGGTCTGAGGCTTACATGGATCACTTCGC 38
 |||||

Db 87 GACGGTCTGAGGCTTACATGGATCACTTCGC 55
 |||||

RESULT 10

ADN36752

ID ADN36752 standard; DNA; 24 BP.

XX AC ADN36752;

XX DT 15-JUL-2004 (first entry)

XX DE West Nile virus detection-related oligonucleotide probe SeqID74.

XX KW hybridisation assay probe; nucleic acid detection;
 KW target-complementary sequence; flavivirus; West Nile virus; WNV;
 KW RNA virus; infection; meningitis; encephalitis;
 KW high throughput screening; probe; ss.

XX

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OS West Nile virus.
PN WO2004036190-A2.
XX
XX
PD 29-APR-2004.
XX
PF 10-OCT-2003; 2003WO-US033639.
XX
XX 16-OCT-2002; 2002US-0418891P.
PR 25-NOV-2002; 2002US-0429006P.
PR 24-FEB-2003; 2003US-0449810P.
XX
XX (GENP-) GEN-PROBE INC.
PA
XX Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX WPI; 2004-389590/36.
XX
XX New hybridization assay probe comprising target-complementary sequence of
PT bases, useful in detecting flavivirus, e.g. West Nile virus.
PT
XX Claim 27; SEQ ID NO 74; 135pp; English.
PS
XX This invention relates to a novel hybridisation assay probe, for
CC detecting a nucleic acid, which is a probe sequence that comprises a
CC target-complementary sequence of bases, and optionally one or more base
CC sequences that are not complementary to the nucleic acid that is to be
CC detected. The hybridisation assay probes and the kits are useful in
CC detecting and amplifying a target nucleic acid sequence, for example
CC flavivirus like West Nile virus, that may be present in a biological
CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC birds and culex mosquitoes, with humans and horses serving as incidental
CC hosts. Infection of humans can lead to meningitis or encephalitis. The
CC invention may allow for accurate and efficient high throughput screening.
CC The present sequence is that of an oligonucleotide probe which is related
CC to the invention.
XX
XX Sequence 24 BP; 4 A; 6 C; 8 G; 6 T; 0 U; 0 Other;
SQ
Query Match 50.0%; Score 24; DB 12; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTGAGGCTTAC 24
Db 1 TCCGAGACGGTCTGAGGCTTAC 24

RESULT 11
ADN36753
ID ADN36753 standard; DNA; 24 BP.
XX
XX ADN36753;
AC
XX 15-JUL-2004 (first entry)
XX
XX West Nile virus detection-related oligonucleotide probe SeqID75.
DE
XX hybridisation assay probe; nucleic acid detection;
KW target-complementary sequence; flavivirus; West Nile virus; WNV;
KW RNA virus; infection; meningitis; encephalitis;
KW high throughput screening; probe; ss.
XX
XX West Nile virus.
OS
XX WO2004036190-A2.
PN
XX 29-APR-2004.
PD
XX 10-OCT-2003; 2003WO-US033639.
PF
XX 16-OCT-2002; 2002US-0418891P.
XX 25-NOV-2002; 2002US-0429006P.
PR

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PR 24-FEB-2003; 2003US-0449810P.
XX
XX (GENP-) GEN-PROBE INC.
PA
XX Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX WPI; 2004-389590/36.
XX
XX New hybridization assay probe comprising target-complementary sequence of
PT bases, useful in detecting flavivirus, e.g. West Nile virus.
PT
XX Claim 26; SEQ ID NO 75; 135pp; English.
PS
XX This invention relates to a novel hybridisation assay probe, for
CC detecting a nucleic acid, which is a probe sequence that comprises a
CC target-complementary sequence of bases, and optionally one or more base
CC sequences that are not complementary to the nucleic acid that is to be
CC detected. The hybridisation assay probes and the kits are useful in
CC detecting and amplifying a target nucleic acid sequence, for example
CC flavivirus like West Nile virus, that may be present in a biological
CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC birds and culex mosquitoes, with humans and horses serving as incidental
CC hosts. Infection of humans can lead to meningitis or encephalitis. The
CC invention may allow for accurate and efficient high throughput screening.
CC The present sequence is that of an oligonucleotide probe which is related
CC to the invention.
XX
XX Sequence 24 BP; 4 A; 6 C; 8 G; 6 T; 0 U; 0 Other;
SQ
Query Match 50.0%; Score 24; DB 12; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTGAGGCTTAC 24
Db 1 TCCGAGACGGTCTGAGGCTTAC 24

RESULT 12
ADN36762
ID ADN36762 standard; DNA; 51 BP.
XX
XX ADN36762;
AC
XX 15-JUL-2004 (first entry)
XX
XX West Nile virus detection-related oligonucleotide probe SeqID84.
DE
XX hybridisation assay probe; nucleic acid detection;
KW target-complementary sequence; flavivirus; West Nile virus; WNV;
KW RNA virus; infection; meningitis; encephalitis;
KW high throughput screening; probe; ss.
XX
XX West Nile virus.
OS
XX Enterobacteria phage T7.
XX
XX Key Location/Qualifiers
FH misc_feature 1..27
FT /tag= a
FT /note= "T7 promoter sequence"
FT misc_feature 28..51
FT /tag= b
FT /note= "WNV-complimentary sequence"
XX
XX WO2004036190-A2.
PN
XX 29-APR-2004.
PD
XX 10-OCT-2003; 2003WO-US033639.
PF
XX 16-OCT-2002; 2002US-0418891P.
PR 25-NOV-2002; 2002US-0429006P.
PR 24-FEB-2003; 2003US-0449810P.

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XX (GENP-) GEN-PROBE INC.
XX Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX WPI; 2004-389590/36.
XX
XX New hybridization assay probe comprising target-complementary sequence of
XX bases, useful in detecting flavivirus, e.g. West Nile virus.
XX
XX Disclosure; SEQ ID NO 84; 135pp; English.
XX
XX This invention relates to a novel hybridisation assay probe, for
XX detecting a nucleic acid, which is a probe sequence that comprises a
XX target-complementary sequence of bases, and optionally one or more base
XX sequences that are not complementary to the nucleic acid that is to be
XX detected. The hybridisation assay probes and the kits are useful in
XX detecting and amplifying a target nucleic acid sequence, for example
XX flavivirus like West Nile virus, that may be present in a biological
XX sample. West Nile virus (WNV) is an RNA virus that primarily infects
XX birds and culex mosquitoes, with humans and horses serving as incidental
XX hosts. Infection of humans can lead to meningitis or encephalitis. The
XX invention may allow for accurate and efficient high throughput screening.
XX The present sequence is that of an oligonucleotide probe which is related
XX to the invention.
XX
XX Sequence 51 BP; 15 A; 10 C; 13 G; 13 T; 0 U; 0 Other;
XX
XX Query Match 50.0%; Score 24; DB 12; Length 51;
XX Best Local Similarity 100.0%; Pred. No. 0.002;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TCCGAGACGGTTCGAGGCTTAC 24
XX |||||||||||||||||||||||||
XX Db 28 TCCGAGACGGTTCGAGGCTTAC 51
XX
XX RESULT 13
XX ADK13681/c
XX ID ADK13681 standard; DNA; 10962 BP.
XX
XX AC ADK13681;
XX
XX 20-MAY-2004 (first entry)
XX
XX DE West Nile virus DNA sequence, SEQ ID 1.
XX
XX KW Virucide; Immunostimulant; flavivirus;
XX envelope protein domain III polypeptide; envelope protein; gene; ss.
XX
XX OS West Nile virus.
XX
XX FH Key Location/Qualifiers
XX CDS 97..10389
XX /*tag= a
XX /product= "West Nile Virus protein"
XX
XX WO2004016586-A2.
XX
XX PD 26-FEB-2004.
XX
XX PF 18-AUG-2003; 2003WO-US025681.
XX
XX PR 16-AUG-2002; 2002US-0403893P.
XX 06-FEB-2003; 2003US-0445581P.
XX
XX (TEXA ) UNIV TEXAS SYSTEM.
XX
XX Barrett A, Beasley D, Holbrook M;
XX
XX WPI; 2004-203756/19.
XX P-PSDB; ADK13682.
XX

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PT Diagnosing flavivirus infection by contacting a sample from a human or
PT animal with a flavivirus envelope protein domain III polypeptide, and
PT detecting formation of a immunocomplex between the envelope protein and
PT antibodies in the sample.
XX
XX PS Disclosure; SEQ ID NO 1; 110pp; English.
XX
XX The present invention relates to a method for screening for a flavivirus
XX in a subject or animal host. The method comprises: contacting a sample
XX from the subject with a composition comprising a flavivirus envelope
XX protein domain III polypeptide (ADK13683-ADK13701) under conditions that
XX permit formation of specific immunocomplex between an antibody in the
XX sample and the envelope protein domain III polypeptide; and detecting
XX whether a specific immunocomplex is formed. The present sequence is the
XX coding sequence for West Nile Virus protein, from which E protein
XX envelope protein domain III polypeptide (ADK13683) is derived.
XX
XX SQ Sequence 10962 BP; 2997 A; 2497 C; 3100 G; 2368 T; 0 U; 0 Other;
XX
XX Query Match 50.0%; Score 24; DB 12; Length 10962;
XX Best Local Similarity 100.0%; Pred. No. 0.0016;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TCCGAGACGGTTCGAGGCTTAC 24
XX |||||||||||||||||||||||||
XX Db 10564 TCCGAGACGGTTCGAGGCTTAC 10541
XX
XX RESULT 14
XX ADN36827
XX ID ADN36827 standard; RNA; 23 BP.
XX
XX AC ADN36827;
XX
XX DT 15-JUL-2004 (first entry)
XX
XX DE West Nile virus detection-related oligonucleotide probe SeqID149.
XX
XX KW hybridisation assay probe; nucleic acid detection;
XX target-complementary sequence; flavivirus; West Nile virus; WNV;
XX RNA virus; infection; meningitis; encephalitis;
XX high throughput screening; probe; ss.
XX
XX OS West Nile virus.
XX
XX FH Key Location/Qualifiers
XX modified_base 1..23
XX /*tag= a
XX /mod_base= OTHER
XX /note= "OTHER= 2'-methoxyethoxy (2'-MOE) nucleotides"
XX
XX WO2004036190-A2.
XX
XX PD 29-APR-2004.
XX
XX PF 10-OCT-2003; 2003WO-US033639.
XX
XX PR 16-OCT-2002; 2002US-0418891P.
XX 25-NOV-2002; 2002US-0429006P.
XX 24-FEB-2003; 2003US-0449810P.
XX
XX (GENP-) GEN-PROBE INC.
XX
XX Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX
XX WPI; 2004-389590/36.
XX
XX New hybridization assay probe comprising target-complementary sequence of
XX bases, useful in detecting flavivirus, e.g. West Nile virus.
XX
XX Example 1; SEQ ID NO 149; 135pp; English.
XX
XX This invention relates to a novel hybridisation assay probe, for

```

this infection it was not possible to identify the sequence of the target
 detecting a nucleic acid, which is a probe sequence that comprises a
 target-complementary sequence of bases, and optionally one or more base
 sequences that are not complementary to the nucleic acid that is to be
 detected. The hybridisation assay probes and the kits are useful in
 detecting and amplifying a target nucleic acid sequence, for example
 flavivirus like West Nile virus, that may be present in a biological
 sample. West Nile virus (WNV) is an RNA virus that primarily infects
 birds and culex mosquitoes, with humans and horses serving as incidental
 hosts. Infection of humans can lead to meningitis or encephalitis. The
 invention may allow for accurate and efficient high throughput screening.
 The present sequence is that of a PCR primer which is related to the

```
CC invention.
XX
SQ Sequence 50 BP; 15 A; 9 C; 13 G; 13 T; 0 U; 0 Other;

Query Match      47.9%; Score 23; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.0072;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTGAGGGCTT 23
    |||||
Db 28 TCCGAGACGGTTCTGAGGGCTT 50

RESULT 17
ADN36755
ID ADN36755 standard; DNA; 22 BP.
XX
AC ADN36755;
XX
DT 15-JUL-2004 (first entry)
XX
DE West Nile virus detection-related oligonucleotide probe SeqID77.
XX
KW hybridisation assay probe; nucleic acid detection;
KW target-complementary sequence; flavivirus; West Nile virus; WNV;
KW RNA virus; infection; meningitis; encephalitis;
KW high throughput screening; probe; ss.
XX
OS West Nile virus.
XX
PN WO2004036190-A2.
XX
PD 29-APR-2004.
XX
PF 10-OCT-2003; 2003WO-US033639.
XX
PR 16-OCT-2002; 2002US-0418891P.
PR 25-NOV-2002; 2002US-0429006P.
PR 24-FEB-2003; 2003US-0449810P.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX WPI; 2004-389590/36.
XX
DR
XX
PT New hybridization assay probe comprising target-complementary sequence of
PT bases, useful in detecting flavivirus, e.g. West Nile virus.
XX
PS Claim 26; SEQ ID NO 77; 135pp; English.
XX
CC This invention relates to a novel hybridisation assay probe, for
CC detecting a nucleic acid, which is a probe sequence that comprises a
CC target-complementary sequence of bases, and optionally one or more base
CC sequences that are not complementary to the nucleic acid that is to be
CC detected. The hybridisation assay probes and the kits are useful in
CC detecting and amplifying a target nucleic acid sequence, for example
CC flavivirus like West Nile virus, that may be present in a biological
CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC birds and culex mosquitoes, with humans and horses serving as incidental
CC hosts. Infection of humans can lead to meningitis or encephalitis. The
CC invention may allow for accurate and efficient high throughput screening.
CC The present sequence is that of an oligonucleotide probe which is related
CC to the invention.
XX
SQ Sequence 22 BP; 3 A; 5 C; 8 G; 6 T; 0 U; 0 Other;

Query Match      45.8%; Score 22; DB 12; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTGAGGGCTT 22
    |||||
Db 28 TCCGAGACGGTTCTGAGGGCTT 49

Db 1 TCCGAGACGGTTCTGAGGGCTT 22

RESULT 18
ADN36764
ID ADN36764 standard; DNA; 49 BP.
XX
AC ADN36764;
XX
DT 15-JUL-2004 (first entry)
XX
DE West Nile virus detection-related oligonucleotide probe SeqID86.
XX
KW hybridisation assay probe; nucleic acid detection;
KW target-complementary sequence; flavivirus; West Nile virus; WNV;
KW RNA virus; infection; meningitis; encephalitis;
KW high throughput screening; probe; ss.
XX
OS West Nile virus.
XX
PN WO2004036190-A2.
XX
PD 29-APR-2004.
XX
PF 10-OCT-2003; 2003WO-US033639.
XX
PR 16-OCT-2002; 2002US-0418891P.
PR 25-NOV-2002; 2002US-0429006P.
PR 24-FEB-2003; 2003US-0449810P.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX WPI; 2004-389590/36.
XX
DR
XX
PT New hybridization assay probe comprising target-complementary sequence of
PT bases, useful in detecting flavivirus, e.g. West Nile virus.
XX
PS Disclosure; SEQ ID NO 86; 135pp; English.
XX
CC This invention relates to a novel hybridisation assay probe, for
CC detecting a nucleic acid, which is a probe sequence that comprises a
CC target-complementary sequence of bases, and optionally one or more base
CC sequences that are not complementary to the nucleic acid that is to be
CC detected. The hybridisation assay probes and the kits are useful in
CC detecting and amplifying a target nucleic acid sequence, for example
CC flavivirus like West Nile virus, that may be present in a biological
CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC birds and culex mosquitoes, with humans and horses serving as incidental
CC hosts. Infection of humans can lead to meningitis or encephalitis. The
CC invention may allow for accurate and efficient high throughput screening.
CC The present sequence is that of an oligonucleotide probe which is related
CC to the invention.
XX
SQ Sequence 49 BP; 14 A; 9 C; 13 G; 13 T; 0 U; 0 Other;

Query Match      45.8%; Score 22; DB 12; Length 49;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCTGAGGGCTT 22
    |||||
Db 28 TCCGAGACGGTTCTGAGGGCTT 49
```


RESULT 19

ADO07431/c

ID ADO07431 standard; DNA; 10818 BP.

XX AC ADO07431;

XX DT 15-JUL-2004 (first entry)

XX DE Japanese Encephalitis virus JEV coding sequence SEQ ID NO: 9.

XX DE antiinflammatory; neuroprotective; gene therapy;

XX KW Japanese Encephalitis virus; JEV; ds; gene; vaccine;

XX KW Japanese encephalitis.

XX OS Japanese encephalitis virus.

XX PN WO2004033690-A1.

XX PD 22-APR-2004.

XX PF 09-OCT-2003; 2003WO-KR002081.

XX PR 09-OCT-2002; 2002KR-00061589.

XX PA (CIBC-) CID CO LTD.

XX PA (LEES/) LEE S H.

XX PI Lee SH, Lee Y, Yun S;

XX DR WPI; 2004-340933/31.

XX PT New Japanese encephalitis virus genomic RNA, useful in developing

XX PT vaccines for and in diagnosing and treating Japanese encephalitis.

XX PS Example 2; Page 145-152; 265pp; English.

XX CC The present invention relates to a genomic RNA of the Korean Japanese

XX CC Encephalitis Virus (JEV) isolate, composed of a 5' and 3' nontranslated

XX CC region (NTR) and a single polypeptide coding region. The JEV genomic RNA,

XX CC JEV cDNA and reagents are useful in developing vaccines for and in

XX CC diagnosing and treating Japanese encephalitis. The present sequence is a

XX CC sequence of the invention.

XX SQ Sequence 10818 BP; 2991 A; 2491 C; 3075 G; 2261 T; 0 U; 0 Other;

XX Query Match 45.8%; Score 22; DB 12; Length 10818;

XX Best Local Similarity 100.0%; Pred. No. 0.021;

XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCCGAGACGGTCTCTGAGGGCTT 22

DB 10523 TCCGAGACGGTCTCTGAGGGCTT 10502

RESULT 20

ADO07437/c

ID ADO07437 standard; DNA; 10968 BP.

XX AC ADO07437;

XX DT 15-JUL-2004 (first entry)

XX DE Japanese Encephalitis virus JEV coding sequence SEQ ID NO: 15.

XX DE antiinflammatory; neuroprotective; gene therapy;

XX KW Japanese Encephalitis virus; JEV; ds; gene; vaccine;

XX KW Japanese encephalitis.

XX OS Japanese encephalitis virus.

XX PN WO2004033690-A1.

XX

XX PD 22-APR-2004.

XX PF 09-OCT-2003; 2003WO-KR002081.

XX PR 09-OCT-2002; 2002KR-00061589.

XX PA (CIBC-) CID CO LTD.

XX PA (LEES/) LEE S H.

XX PI Lee SH, Lee Y, Yun S;

XX DR WPI; 2004-340933/31.

XX PT New Japanese encephalitis virus genomic RNA, useful in developing

XX PT vaccines for and in diagnosing and treating Japanese encephalitis.

XX PS Claim 3; Page 154-161; 265pp; English.

XX CC

XX CC The present invention relates to a genomic RNA of the Korean Japanese

XX CC Encephalitis Virus (JEV) isolate, composed of a 5' and 3' nontranslated

XX CC region (NTR) and a single polypeptide coding region. The JEV genomic RNA,

XX CC JEV cDNA and reagents are useful in developing vaccines for and in

XX CC diagnosing and treating Japanese encephalitis. The present sequence is a

XX CC sequence of the invention.

XX SQ Sequence 10968 BP; 3032 A; 2518 C; 3117 G; 2301 T; 0 U; 0 Other;

XX Query Match 45.8%; Score 22; DB 12; Length 10968;

XX Best Local Similarity 100.0%; Pred. No. 0.021;

XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCCGAGACGGTCTCTGAGGGCTT 22

DB 10573 TCCGAGACGGTCTCTGAGGGCTT 10552

RESULT 21

ADO07466/c

ID ADO07466 standard; DNA; 18563 BP.

XX AC ADO07466;

XX DT 15-JUL-2004 (first entry)

XX DE Japanese Encephalitis virus JEV coding sequence SEQ ID NO: 44.

XX KW antiinflammatory; neuroprotective; gene therapy;

XX KW Japanese Encephalitis virus; JEV; ds; gene; vaccine;

XX KW Japanese encephalitis.

XX OS Japanese encephalitis virus.

XX PN WO2004033690-A1.

XX PD 22-APR-2004.

XX PF 09-OCT-2003; 2003WO-KR002081.

XX PR 09-OCT-2002; 2002KR-00061589.

XX PA (CIBC-) CID CO LTD.

XX PA (LEES/) LEE S H.

XX PI Lee SH, Lee Y, Yun S;

XX DR WPI; 2004-340933/31.

XX PT New Japanese encephalitis virus genomic RNA, useful in developing

XX PT vaccines for and in diagnosing and treating Japanese encephalitis.

XX PS Claim 12; Page 193-206; 265pp; English.

CC The present invention relates to a genomic RNA of the Korean Japanese
 CC Encephalitis Virus (JEV) isolate, composed of a 5' and 3' nontranslated
 CC region (NTR) and a single polypeptide coding region. The JEV genomic RNA,
 CC JEV cDNA and reagents are useful in developing vaccines for and in
 CC diagnosing and treating Japanese encephalitis. The present sequence is a
 CC sequence of the invention.
 XX

SQ Sequence 18563 BP; 4943 A; 4211 C; 4929 G; 4480 T; 0 U; 0 Other;
 Query Match 45.8%; Score 22; DB 12; Length 18563;
 Best Local Similarity 100.0%; Pred. No. 0.02;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTCTCTGAGGGCTT 22
 |||||
 Db 10573 TCCGAGACGGTCTCTGAGGGCTT 10552

RESULT 22

ADO07465/c
 ID ADO07465 standard; DNA; 18563 BP.

XX
 AC ADO07465;

DT 15-JUL-2004 (first entry)

DE Japanese Encephalitis virus JEV coding sequence SEQ ID NO: 43.

XX antiinflammatory; neuroprotective; gene therapy;
 KW Japanese Encephalitis virus; JEV; ds; gene; vaccine;
 XX Japanese encephalitis.

OS Japanese encephalitis virus.

XX WO2004033690-A1.

XX 22-APR-2004.

PF 09-OCT-2003; 2003WO-KR002081.

XX 09-OCT-2002; 2002KR-00061589.

XX (CIDC-) CID CO LTD.

PA (LEES/) LEE S H.

XX Lee SH, Lee Y, Yun S;

XX WPI; 2004-340933/31.

XX New Japanese encephalitis virus genomic RNA, useful in developing
 PT vaccines for and in diagnosing and treating Japanese encephalitis.

XX Claim 12; Page 180-193; 265pp; English.

XX The present invention relates to a genomic RNA of the Korean Japanese
 CC Encephalitis Virus (JEV) isolate, composed of a 5' and 3' nontranslated
 CC region (NTR) and a single polypeptide coding region. The JEV genomic RNA,
 CC JEV cDNA and reagents are useful in developing vaccines for and in
 CC diagnosing and treating Japanese encephalitis. The present sequence is a
 CC sequence of the invention.
 XX

SQ Sequence 18563 BP; 4944 A; 4211 C; 4929 G; 4479 T; 0 U; 0 Other;

Query Match 45.8%; Score 22; DB 12; Length 18563;
 Best Local Similarity 100.0%; Pred. No. 0.02;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTCTCTGAGGGCTT 22
 |||||
 Db 10573 TCCGAGACGGTCTCTGAGGGCTT 10552

RESULT 23

ADO07467/c

ID ADO07467 standard; DNA; 18565 BP.

XX ADO07467;

XX 15-JUL-2004 (first entry)

XX Japanese Encephalitis virus JEV coding sequence SEQ ID NO: 45.

XX antiinflammatory; neuroprotective; gene therapy;
 KW Japanese Encephalitis virus; JEV; ds; gene; vaccine;
 XX Japanese encephalitis.

XX Japanese encephalitis virus.

XX WO2004033690-A1.

XX 22-APR-2004.

PF 09-OCT-2003; 2003WO-KR002081.

XX 09-OCT-2002; 2002KR-00061589.

XX (CIDC-) CID CO LTD.

XX (LEES/) LEE S H.

XX Lee SH, Lee Y, Yun S;

XX WPI; 2004-340933/31.

XX New Japanese encephalitis virus genomic RNA, useful in developing
 PT vaccines for and in diagnosing and treating Japanese encephalitis.

XX Claim 12; Page 206-219; 265pp; English.

XX The present invention relates to a genomic RNA of the Korean Japanese
 CC Encephalitis Virus (JEV) isolate, composed of a 5' and 3' nontranslated
 CC region (NTR) and a single polypeptide coding region. The JEV genomic RNA,
 CC JEV cDNA and reagents are useful in developing vaccines for and in
 CC diagnosing and treating Japanese encephalitis. The present sequence is a
 CC sequence of the invention.
 XX

SQ Sequence 18565 BP; 4944 A; 4211 C; 4929 G; 4481 T; 0 U; 0 Other;

Query Match 45.8%; Score 22; DB 12; Length 18565;
 Best Local Similarity 100.0%; Pred. No. 0.02;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTCTCTGAGGGCTT 22
 |||||
 Db 10573 TCCGAGACGGTCTCTGAGGGCTT 10552

RESULT 24

ADO07468/c

ID ADO07468 standard; DNA; 19038 BP.

XX ADO07468;

XX 15-JUL-2004 (first entry)

XX Japanese Encephalitis virus JEV coding sequence SEQ ID NO: 46.

XX antiinflammatory; neuroprotective; gene therapy;
 KW Japanese Encephalitis virus; JEV; ds; gene; vaccine;
 XX Japanese encephalitis.

XX Japanese encephalitis virus.

XX WO2004033690-A1.

XX 22-APR-2004.

XX

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PF 09-OCT-2003; 2003WO-KR002081.
XX
XX
XX 09-OCT-2002; 2002KR-00061589.
XX
XX (CIDC-) CID CO LTD.
XX (LEES/) LEE S H.
XX Lee SH, Lee Y, Yun S;
XX WPI; 2004-340933/31.
XX
XX New Japanese encephalitis virus genomic RNA, useful in developing
PT vaccines for and in diagnosing and treating Japanese encephalitis.
XX
XX Claim 12; Page 219-232; 265pp; English.
XX
XX The present invention relates to a genomic RNA of the Korean Japanese
CC Encephalitis Virus (JEV) isolate, composed of a 5' and 3' nontranslated
CC region (NTR) and a single polypeptide coding region. The JEV genomic RNA,
CC JEV cDNA and reagents are useful in developing vaccines for and in
CC diagnosing and treating Japanese encephalitis. The present sequence is a
CC sequence of the invention.
XX
XX Sequence 19038 BP; 5059 A; 4310 C; 5055 G; 4613 T; 0 U; 0 Other;
SQ
Query Match 45.8%; Score 22; DB 12; Length 19038;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCGAGACGGTTCGTGAGGCTT 22
DB 10573 TCCGAGACGGTTCGTGAGGCTT 10552
RESULT 25
AD007469/C
ID ADO07469 standard; DNA; 19038 BP.
XX
XX ADO07469;
XX
XX 15-JUL-2004 (first entry)
XX
XX Japanese Encephalitis virus JEV coding sequence SEQ ID NO: 47.
DE antiinflammatory; neuroprotective; gene therapy;
KW Japanese Encephalitis virus; JEV; ds; gene; vaccine;
KW Japanese encephalitis.
XX
XX Japanese encephalitis virus.
OS
XX WO2004033690-A1.
XX
XX 22-APR-2004.
XX
XX 09-OCT-2003; 2003WO-KR002081.
XX
XX 09-OCT-2002; 2002KR-00061589.
XX (CIDC-) CID CO LTD.
XX (LEES/) LEE S H.
XX
XX Lee SH, Lee Y, Yun S;
XX WPI; 2004-340933/31.
XX
XX New Japanese encephalitis virus genomic RNA, useful in developing
PT vaccines for and in diagnosing and treating Japanese encephalitis.
XX
XX Claim 12; Page 245-258; 265pp; English.
XX
XX The present invention relates to a genomic RNA of the Korean Japanese
CC Encephalitis Virus (JEV) isolate, composed of a 5' and 3' nontranslated
CC region (NTR) and a single polypeptide coding region. The JEV genomic RNA,
CC JEV cDNA and reagents are useful in developing vaccines for and in
CC diagnosing and treating Japanese encephalitis. The present sequence is a
CC sequence of the invention.
XX
XX Sequence 19040 BP; 5060 A; 4310 C; 5055 G; 4615 T; 0 U; 0 Other;
SQ
Query Match 45.8%; Score 22; DB 12; Length 19040;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCGAGACGGTTCGTGAGGCTT 22
DB 10573 TCCGAGACGGTTCGTGAGGCTT 10552
RESULT 27
ADN36873
ID ADN36873 standard; RNA; 36 BP.
XX
XX
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AC XX ADN36873;
DE XX 15-JUL-2004 (first entry)
XX XX
XX XX West Nile virus detection-related oligonucleotide probe SeqID195.
DE XX hybridisation assay probe; nucleic acid detection;
XX XX target-complementary sequence; flavivirus; West Nile virus; WNV;
KW KW RNA virus; infection; meningitis; encephalitis;
KW KW high throughput screening; probe; ss.
XX XX West Nile virus.
OS XX
XX XX
XX XX Key Location/Qualifiers
FH modified_base 1..36
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= 2'-methoxyethoxy (2'-MOE) nucleotides"
XX XX
XX XX WO2004036190-A2.
XX XX
XX XX 29-APR-2004.
XX XX
XX XX 10-OCT-2003; 2003WO-US033639.
XX XX
XX XX 16-OCT-2002; 2002US-0418891P.
XX XX 25-NOV-2002; 2002US-0429006P.
XX XX 24-FEB-2003; 2003US-0449810P.
XX XX
XX XX (GENP-) GEN-PROBE INC.
XX XX
XX XX Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX XX WPI; 2004-389590/36.
XX XX
XX XX New hybridization assay probe comprising target-complementary sequence of
XX XX bases, useful in detecting flavivirus, e.g. West Nile virus.
XX XX
XX XX Example 1; SEQ ID NO 195; 135pp; English.
XX XX
XX XX This invention relates to a novel hybridisation assay probe, for
XX XX detecting a nucleic acid, which is a probe sequence that comprises a
XX XX target-complementary sequence of bases, and optionally one or more base
XX XX sequences that are not complementary to the nucleic acid that is to be
XX XX detected. The hybridisation assay probes and the kits are useful in
XX XX detecting and amplifying a target nucleic acid sequence, for example
XX XX flavivirus like West Nile virus, that may be present in a biological
XX XX sample. West Nile virus (WNV) is an RNA virus that primarily infects
XX XX birds and culex mosquitoes, with humans and horses serving as incidental
XX XX hosts. Infection of humans can lead to meningitis or encephalitis. The
XX XX invention may allow for accurate and efficient high throughput screening.
XX XX The present sequence is that of an oligonucleotide probe which is related
XX XX to the invention.
XX XX
XX XX Sequence 36 BP; 5 A; 13 C; 7 G; 0 T; 11 U; 0 Other;
SQ
Query Match 43.8%; Score 21; DB 12; Length 36;
Best Local Similarity 61.9%; Pred. No. 0.094;
Matches 13; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
QY 28 GATCACTTCGACGCTTTC 48
Db 1 GAUCACUUCGACGUUUC 21
RESULT 28
ADN36794/c
ID ADN36794 standard; DNA; 19 BP.
XX XX
XX XX ADN36794;
XX XX
XX XX 15-JUL-2004 (first entry)
XX XX
XX XX West Nile virus detection-related oligonucleotide probe SeqID195.
XX XX hybridisation assay probe; nucleic acid detection;
XX XX target-complementary sequence; flavivirus; West Nile virus; WNV;
XX XX RNA virus; infection; meningitis; encephalitis;
XX XX high throughput screening; probe; ss.
XX XX West Nile virus.
OS XX
XX XX
XX XX Key Location/Qualifiers
FH modified_base 1..36
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= 2'-methoxyethoxy (2'-MOE) nucleotides"
XX XX
XX XX WO2004036190-A2.
XX XX
XX XX 29-APR-2004.
XX XX
XX XX 10-OCT-2003; 2003WO-US033639.
XX XX
XX XX 16-OCT-2002; 2002US-0418891P.
XX XX 25-NOV-2002; 2002US-0429006P.
XX XX 24-FEB-2003; 2003US-0449810P.
XX XX
XX XX (GENP-) GEN-PROBE INC.
XX XX
XX XX Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX XX WPI; 2004-389590/36.
XX XX
XX XX New hybridization assay probe comprising target-complementary sequence of
XX XX bases, useful in detecting flavivirus, e.g. West Nile virus.
XX XX
XX XX Example 1; SEQ ID NO 195; 135pp; English.
XX XX
XX XX This invention relates to a novel hybridisation assay probe, for
XX XX detecting a nucleic acid, which is a probe sequence that comprises a
XX XX target-complementary sequence of bases, and optionally one or more base
XX XX sequences that are not complementary to the nucleic acid that is to be
XX XX detected. The hybridisation assay probes and the kits are useful in
XX XX detecting and amplifying a target nucleic acid sequence, for example
XX XX flavivirus like West Nile virus, that may be present in a biological
XX XX sample. West Nile virus (WNV) is an RNA virus that primarily infects
XX XX birds and culex mosquitoes, with humans and horses serving as incidental
XX XX hosts. Infection of humans can lead to meningitis or encephalitis. The
XX XX invention may allow for accurate and efficient high throughput screening.
XX XX The present sequence is that of an oligonucleotide probe which is related
XX XX to the invention.
XX XX
XX XX Sequence 36 BP; 5 A; 13 C; 7 G; 0 T; 11 U; 0 Other;
SQ
Query Match 43.8%; Score 21; DB 12; Length 36;
Best Local Similarity 61.9%; Pred. No. 0.094;
Matches 13; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
QY 28 GATCACTTCGACGCTTTC 48
Db 1 GAUCACUUCGACGUUUC 21

```

```

DE XX West Nile virus detection-related oligonucleotide probe SeqID116.
XX XX hybridisation assay probe; nucleic acid detection;
KW KW target-complementary sequence; flavivirus; West Nile virus; WNV;
KW KW RNA virus; infection; meningitis; encephalitis;
KW KW high throughput screening; probe; ss.
XX XX West Nile virus.
OS XX
XX XX
XX XX Key Location/Qualifiers
FH modified_base 1..19
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= 2'-methoxyethoxy (2'-MOE) nucleotides"
XX XX
XX XX WO2004036190-A2.
XX XX
XX XX 29-APR-2004.
XX XX
XX XX 10-OCT-2003; 2003WO-US033639.
XX XX
XX XX 16-OCT-2002; 2002US-0418891P.
XX XX 25-NOV-2002; 2002US-0429006P.
XX XX 24-FEB-2003; 2003US-0449810P.
XX XX
XX XX (GENP-) GEN-PROBE INC.
XX XX
XX XX Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX XX WPI; 2004-389590/36.
XX XX
XX XX New hybridization assay probe comprising target-complementary sequence of
XX XX bases, useful in detecting flavivirus, e.g. West Nile virus.
XX XX
XX XX Example 1; SEQ ID NO 116; 135pp; English.
XX XX
XX XX This invention relates to a novel hybridisation assay probe, for
XX XX detecting a nucleic acid, which is a probe sequence that comprises a
XX XX target-complementary sequence of bases, and optionally one or more base
XX XX sequences that are not complementary to the nucleic acid that is to be
XX XX detected. The hybridisation assay probes and the kits are useful in
XX XX detecting and amplifying a target nucleic acid sequence, for example
XX XX flavivirus like West Nile virus, that may be present in a biological
XX XX sample. West Nile virus (WNV) is an RNA virus that primarily infects
XX XX birds and culex mosquitoes, with humans and horses serving as incidental
XX XX hosts. Infection of humans can lead to meningitis or encephalitis. The
XX XX invention may allow for accurate and efficient high throughput screening.
XX XX The present sequence is that of an oligonucleotide probe which is related
XX XX to the invention.
XX XX
XX XX Sequence 19 BP; 5 A; 7 C; 4 G; 3 T; 0 U; 0 Other;
SQ
Query Match 39.6%; Score 19; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 GACGGTCTGAGGCTTAC 24
Db 19 GACGGTCTGAGGCTTAC 1
RESULT 29
ADN36792/c
ID ADN36792 standard; DNA; 20 BP.
XX XX
XX XX ADN36792;
XX XX
XX XX 15-JUL-2004 (first entry)
XX XX
XX XX West Nile virus detection-related oligonucleotide probe SeqID114.
XX XX hybridisation assay probe; nucleic acid detection;
XX XX target-complementary sequence; flavivirus; West Nile virus; WNV;
XX XX

```

KW RNA virus; infection; meningitis; encephalitis;
 XX high throughput screening; probe; ss.
 OS West Nile virus.
 XX
 PH Key Location/Qualifiers
 FT modified_base 1..20
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER= 2'-methoxyethoxy (2'-MOE) nucleotides"
 XX
 XX WO2004036190-A2.
 XX
 XX 29-APR-2004.
 XX
 XX 10-OCT-2003; 2003WO-US033639.
 XX
 XX 16-OCT-2002; 2002US-0418891P.
 PR 25-NOV-2002; 2002US-0429006P.
 PR 24-FEB-2003; 2003US-0449810P.
 XX
 XX (GENP-) GEN-PROBE INC.
 XX
 XX Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
 PI WPI; 2004-389590/36.
 DR
 XX New hybridization assay probe comprising target-complementary sequence of
 PT bases, useful in detecting flavivirus, e.g. West Nile virus.
 PT
 XX Claim 17; SEQ ID NO 114; 135pp; English.
 PS
 XX This invention relates to a novel hybridisation assay probe, for
 CC detecting a nucleic acid, which is a probe sequence that comprises a
 CC target-complementary sequence of bases, and optionally one or more base
 CC sequences that are not complementary to the nucleic acid that is to be
 CC detected. The hybridisation assay probes and the kits are useful in
 CC detecting and amplifying a target nucleic acid sequence, for example
 CC flavivirus like West Nile virus, that may be present in a biological
 CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
 CC birds and culex mosquitoes, with humans and horses serving as incidental
 CC hosts. Infection of humans can lead to meningitis or encephalitis. The
 CC invention may allow for accurate and efficient high throughput screening.
 CC The present sequence is that of an oligonucleotide probe which is related
 CC to the invention.
 XX
 SQ Sequence 20 BP; 7 A; 3 C; 7 G; 3 T; 0 U; 0 Other;
 Query Match 37.5%; Score 18; DB 12; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.5;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 31 CACTTCGCGAGCTTGTTC 48
 DB 20 CACTTCGCGAGCTTGTTC 3
 RESULT 30
 ACN03369/c
 ID ACN03369 standard; RNA; 17 BP.
 XX
 AC ACN03369;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE WNV Inozyme substrate SEQ ID NO 3372.
 XX
 XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
 KW Amberzyme; Zinzyme; ss.
 XX

OS West Nile Virus.
 XX
 PN WO200268637-A2.
 XX
 PD 06-SEP-2002.
 XX
 PF 19-OCT-2001; 2001WO-US048350.
 XX
 PR 20-OCT-2000; 2000US-0242411P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 XX
 PI Blatt L, Mcswiggen JA;
 XX
 XX WPI; 2002-706994/76.
 DR
 XX New nucleic acid molecule that modulates replication of West Nile Virus
 PT (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 XX
 PS Claim 23; SEQ ID NO 3372; 495pp; English.
 XX
 CC The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention
 XX
 SQ Sequence 17 BP; 4 A; 6 C; 4 G; 0 T; 3 U; 0 Other;
 Query Match 35.4%; Score 17; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCCGAGACGGTCTGAG 17
 DB 17 TCCGAGACGGTCTGAG 1
 RESULT 31
 ACN03364/c
 ID ACN03364 standard; RNA; 17 BP.
 XX
 AC ACN03364;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE WNV Inozyme substrate SEQ ID NO 3367.
 XX
 XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
 KW Amberzyme; Zinzyme; ss.
 XX
 OS West Nile Virus.
 XX
 PN WO200268637-A2.
 XX
 PD 06-SEP-2002.
 XX
 PF 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-0242411P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 XX Blatt L, Mcswiggen JA;
 PI WPI; 2002-706994/76.
 XX
 XX New nucleic acid molecule that modulates replication of West Nile Virus
 PT (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 XX
 PS Claim 23; SEQ ID NO 3367; 495pp; English.
 XX
 XX The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention
 XX
 SQ Sequence 17 BP; 5 A; 4 C; 4 G; 0 T; 4 U; 0 Other;
 Query Match 35.4%; Score 17; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 18 GGCTTACATGGATCACT 34
 Db 17 GGCTTACATGGATCACT 1
 RESULT 32
 ACN05430/c
 ID ACN05430 standard; RNA; 17 BP.
 XX ACN05430;
 AC
 XX 22-APR-2004 (first entry)
 DT
 XX WNV DNazyme substrate SEQ ID NO 5433.
 DE
 XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
 KW Amberzyme; Zinzyme; ss.
 XX
 XX West Nile Virus.
 OS
 XX WO200268637-A2.
 PN
 XX 06-SEP-2002.
 PD
 XX 19-OCT-2001; 2001WO-US048350.
 PF
 XX 20-OCT-2000; 2000US-0242411P.
 PR
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 XX Blatt L, Mcswiggen JA;
 PI WPI; 2002-706994/76.
 XX
 XX New nucleic acid molecule that modulates replication of West Nile Virus
 PT (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 XX

PI Blatt L, Mcswiggen JA;
 XX WPI; 2002-706994/76.
 XX
 XX New nucleic acid molecule that modulates replication of West Nile Virus
 PT (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 XX
 PS Claim 23; SEQ ID NO 5433; 495pp; English.
 XX
 XX The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention
 XX
 SQ Sequence 17 BP; 5 A; 3 C; 5 G; 0 T; 4 U; 0 Other;
 Query Match 35.4%; Score 17; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 22 TACATGGATCACTTCGC 38
 Db 17 TACATGGATCACTTCGC 1
 RESULT 33
 ACN09609
 ID ACN09609 standard; RNA; 17 BP.
 XX ACN09609;
 AC
 XX 22-APR-2004 (first entry)
 DT
 XX WNV minus strand Inozyme substrate SEQ ID NO 9612.
 DE
 XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
 KW Amberzyme; Zinzyme; ss.
 XX
 XX West Nile Virus.
 OS
 XX WO200268637-A2.
 PN
 XX 06-SEP-2002.
 PD
 XX 19-OCT-2001; 2001WO-US048350.
 PF
 XX 20-OCT-2000; 2000US-0242411P.
 PR
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 XX Blatt L, Mcswiggen JA;
 PI WPI; 2002-706994/76.
 XX
 XX New nucleic acid molecule that modulates replication of West Nile Virus
 PT (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 XX

XX Claim 23; SEQ ID NO 9612; 495pp; English.
 XX
 XX The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention
 XX
 SQ Sequence 17 BP; 4 A; 4 C; 5 G; 0 T; 4 U; 0 Other;
 Query Match 35.4%; Score 17; DB 6; Length 17;
 Best Local Similarity 76.5%; Pred. No. 16;
 Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 17 GGCTTACATGGATCAC 33
 DB 1 GGCGUACAUUGGAUCAC 17
 RESULT 34
 ACN13634
 ID ACN13634 standard; RNA; 17 BP.
 XX
 AC ACN13634;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE WNV minus strand DNazyme substrate SEQ ID NO 13637.
 XX
 KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
 KW Amberzyme; Zinzyme; ss.
 XX
 OS West Nile Virus.
 XX
 PN WO200268637-A2.
 XX
 PD 06-SEP-2002.
 XX
 PF 19-OCT-2001; 2001WO-US048350.
 XX
 PR 20-OCT-2000; 2000US-0242411P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 XX
 PI Blatt L, Mcswiggen JA;
 XX
 DR WPI; 2002-706994/76.
 XX
 XX New nucleic acid molecule that modulates replication of West Nile Virus
 PT (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 XX
 PS Claim 23; SEQ ID NO 13637; 495pp; English.
 XX
 XX The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, hepatocellular carcinoma or cirrhosis.

CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention
 XX
 SQ Sequence 17 BP; 4 A; 4 C; 3 G; 0 T; 6 U; 0 Other;
 Query Match 35.4%; Score 17; DB 6; Length 17;
 Best Local Similarity 64.7%; Pred. No. 16;
 Matches 11; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
 QY 21 TTACATGGATTCATTCG 37
 DB 1 UUACAUUGGAUCACUUGC 17
 RESULT 35
 ACN14220
 ID ACN14220 standard; RNA; 17 BP.
 XX
 AC ACN14220;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE WNV minus strand Amberzyme substrate SEQ ID NO 14223.
 XX
 KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
 KW Amberzyme; Zinzyme; ss.
 XX
 OS West Nile Virus.
 XX
 PN WO200268637-A2.
 XX
 PD 06-SEP-2002.
 XX
 PF 19-OCT-2001; 2001WO-US048350.
 XX
 PR 20-OCT-2000; 2000US-0242411P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 XX
 PI Blatt L, Mcswiggen JA;
 XX
 DR WPI; 2002-706994/76.
 XX
 XX New nucleic acid molecule that modulates replication of West Nile Virus
 PT (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 XX
 PS Claim 23; SEQ ID NO 14223; 495pp; English.
 XX
 XX The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080


```

RESULT 38
ACN14217
ID ACN14217 standard; RNA; 17 BP.
XX
XX
AC ACN14217;
XX
XX
DT 22-APR-2004 (first entry)
XX
XX
WNV minus strand Amberzyme substrate SEQ ID NO 14220.
DE
XX
XX
WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
KW Amberzyme; Zinzyme; ss.
XX
XX
OS West Nile Virus.
XX
XX
WO200268637-A2.
PN
XX
XX
PD 06-SEP-2002.
XX
XX
PF 19-OCT-2001; 2001WO-US048350.
XX
XX
PR 20-OCT-2000; 2000US-0242411P.
XX
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
XX
XX
PI Blatt L, Mcswiggen JA;
XX
XX
WPI; 2002-706994/76.
XX
XX
New nucleic acid molecule that modulates replication of West Nile Virus
PT (WNV), useful for treating a condition related to WNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
XX
PS Claim 23; SEQ ID NO 14220; 495pp; English.
XX
XX
The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-Cleaver, DNazyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
XX
Sequence 17 BP; 3 A; 3 C; 6 G; 0 T; 5 U; 0 Other;
SQ
Query Match 35.4%; Score 17; DB 6; Length 17;
Best Local Similarity 70.6%; Pred. No. 16;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACGGTTCTGAGGGCTTA 23
DB 1 ACGGUUCUGAGGGCUUA 17
|||||:|||||:|

RESULT 39
ACN04659/C
ID ACN04659 standard; RNA; 17 BP.
XX
XX
AC ACN04659;
XX
XX

```

```

DT 22-APR-2004 (first entry)
XX
XX
WNV Zinzyme substrate SEQ ID NO 4662.
XX
XX
WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
KW Amberzyme; Zinzyme; ss.
XX
XX
OS West Nile Virus.
XX
XX
WO200268637-A2.
PN
XX
XX
PD 06-SEP-2002.
XX
XX
PF 19-OCT-2001; 2001WO-US048350.
XX
XX
PR 20-OCT-2000; 2000US-0242411P.
XX
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
XX
XX
PI Blatt L, Mcswiggen JA;
XX
XX
WPI; 2002-706994/76.
XX
XX
New nucleic acid molecule that modulates replication of West Nile Virus
PT (WNV), useful for treating a condition related to WNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
XX
PS Claim 23; SEQ ID NO 4662; 495pp; English.
XX
XX
The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-Cleaver, DNazyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
XX
Sequence 17 BP; 4 A; 5 C; 3 G; 0 T; 5 U; 0 Other;
SQ
Query Match 35.4%; Score 17; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ACGGCTTACATGATCA 32
DB 17 ACGGCTTACATGATCA 1
|||||:|||||:|

RESULT 40
ACN14221
ID ACN14221 standard; RNA; 17 BP.
XX
XX
AC ACN14221;
XX
XX
DT 22-APR-2004 (first entry)
XX
XX
WNV minus strand Amberzyme substrate SEQ ID NO 14224.
DE
XX
XX
WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW

```

KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
 XX Amberzyme; Zinzyne; ss.

OS West Nile Virus.

XX WO200268637-A2.

XX 06-SEP-2002.

XX 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.

XX (BLAT/) BLATT L.

XX (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus

XX (WNV), useful for treating a condition related to WNV infection e.g.

XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX Claim 23; SEQ ID NO 14224; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication

XX of the West Nile Virus (WNV). The nucleic acid molecules are useful for

XX treating a condition related to WNV infection e.g. pancreatitis,

XX encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,

XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid

XX molecule is selected from the group of ribozymes consisting of

XX Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyne. The

XX nucleic acid molecules further comprise at least five ribose residues, at

XX least ten 2'-O-methyl modifications, phosphorothioate linkages on at

XX least three of the 5' terminal nucleotides and a 3' end modification of a

XX 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080

XX are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given

XX in the specification. The present sequence is that of a nucleic acid

XX molecule of the invention

XX Sequence 17 BP; 4 A; 5 C; 2 G; 0 T; 6 U; 0 Other;

XX Query Match 35.4%; Score 17; DB 6; Length 17;

XX Best Local Similarity 64.7%; Pred. No. 16;

XX Matches 11; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

XX QY 20 CTTACATGGATCACTTC 36

XX Db 1 CUUACAUGGACUACUUC 17

XX RESULT 41

XX ACN03363/c

XX ID ACN03363 standard; RNA; 17 BP.

XX AC ACN03363;

XX XX 22-APR-2004 (first entry)

XX XX WNV Inozyme substrate SEQ ID NO 3366.

XX XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;

XX virucide; neuroprotective; antibacterial; replication; pancreatitis;

XX encephalitis; myocarditis; meningitis; infection; hepatitis;

XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;

XX Amberzyme; Zinzyne; ss.

XX West Nile Virus.

XX WO200268637-A2.

XX 06-SEP-2002.

XX 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.

XX (BLAT/) BLATT L.

XX (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus

XX (WNV), useful for treating a condition related to WNV infection e.g.

XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX Claim 23; SEQ ID NO 14224; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication

XX of the West Nile Virus (WNV). The nucleic acid molecules are useful for

XX treating a condition related to WNV infection e.g. pancreatitis,

XX encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,

XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid

XX molecule is selected from the group of ribozymes consisting of

XX Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyne. The

PD 06-SEP-2002.

XX 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.

XX (BLAT/) BLATT L.

XX (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus

XX (WNV), useful for treating a condition related to WNV infection e.g.

XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX Claim 23; SEQ ID NO 3366; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication

XX of the West Nile Virus (WNV). The nucleic acid molecules are useful for

XX treating a condition related to WNV infection e.g. pancreatitis,

XX encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,

XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid

XX molecule is selected from the group of ribozymes consisting of

XX Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyne. The

XX nucleic acid molecules further comprise at least five ribose residues, at

XX least ten 2'-O-methyl modifications, phosphorothioate linkages on at

XX least three of the 5' terminal nucleotides and a 3' end modification of a

XX 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080

XX are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given

XX in the specification. The present sequence is that of a nucleic acid

XX molecule of the invention

XX Sequence 17 BP; 6 A; 3 C; 4 G; 0 T; 4 U; 0 Other;

XX Query Match 35.4%; Score 17; DB 6; Length 17;

XX Best Local Similarity 100.0%; Pred. No. 16;

XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 19 GCTTACATGGATCACTT 35

XX Db 17 GCTTACATGGATCACTT 1

XX RESULT 42

XX ACN14216

XX ID ACN14216 standard; RNA; 17 BP.

XX AC ACN14216;

XX XX 22-APR-2004 (first entry)

XX XX WNV minus strand Amberzyme substrate SEQ ID NO 14219.

XX XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;

XX virucide; neuroprotective; antibacterial; replication; pancreatitis;

XX encephalitis; myocarditis; meningitis; infection; hepatitis;

XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;

XX Amberzyme; Zinzyne; ss.

XX West Nile Virus.

XX WO200268637-A2.

XX 06-SEP-2002.

XX 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.

XX (BLAT/) BLATT L.

XX (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus

XX (WNV), useful for treating a condition related to WNV infection e.g.

XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX Claim 23; SEQ ID NO 3366; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication

XX of the West Nile Virus (WNV). The nucleic acid molecules are useful for

XX treating a condition related to WNV infection e.g. pancreatitis,

XX encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,

XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid

XX molecule is selected from the group of ribozymes consisting of

XX Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyne. The

XX nucleic acid molecules further comprise at least five ribose residues, at

XX least ten 2'-O-methyl modifications, phosphorothioate linkages on at

XX least three of the 5' terminal nucleotides and a 3' end modification of a

XX 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080

XX are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given

PA (BLAT/) BLATT L.
 XX (MCSW/) MCSWIGGEN J A.
 XX Blatt L, Mcswiggen JA;
 XX WPI; 2002-706994/76.
 DR
 XX
 XX New nucleic acid molecule that modulates replication of West Nile Virus
 PT (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 XX
 XX Claim 23; SEQ ID NO 14219; 495pp; English.
 XX
 CC The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention
 XX
 XX Sequence 17 BP; 3 A; 4 C; 6 G; 0 T; 4 U; 0 Other;
 SQ
 Query Match 35.4%; Score 17; DB 6; Length 17;
 Best Local Similarity 76.5%; Pred. No. 16;
 Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCCGAGACGGTCTTGAG 17
 Db :|||||||:|:|:|
 1 UCCGAGACGGUUCUGAG 17
 RESULT 43
 ACN01375/C
 ID ACN01375 standard; RNA; 17 BP.
 XX
 AC ACN01375;
 XX
 XX 22-APR-2004 (first entry)
 DT
 XX
 DE WNV Hammerhead Ribozyme substrate SEQ ID NO 1365.
 XX
 XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
 KW Amberzyme; Zinzyme; ss.
 XX
 OS West Nile Virus.
 XX
 XX WO200268637-A2.
 PN
 XX 06-SEP-2002.
 PD
 XX
 PF 19-OCT-2001; 2001WO-US048350.
 XX
 XX 20-OCT-2000; 2000US-0242411P.
 PR
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 XX
 XX Blatt L, Mcswiggen JA;
 PI
 XX WPI; 2002-706994/76.
 DR
 XX

PT New nucleic acid molecule that modulates replication of West Nile Virus
 PT (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 XX
 XX Claim 23; SEQ ID NO 1365; 495pp; English.
 XX
 CC The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention
 XX
 XX Sequence 17 BP; 6 A; 2 C; 5 G; 0 T; 4 U; 0 Other;
 SQ
 Query Match 35.4%; Score 17; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 20 CTTACATGGATCACTTC 36
 Db |||||||||
 17 CTTACATGGATCACTTC 1
 RESULT 44
 ACN07449
 ID ACN07449 standard; RNA; 17 BP.
 XX
 AC ACN07449;
 XX
 XX 22-APR-2004 (first entry)
 DT
 XX
 DE WNV minus strand Hammerhead Ribozyme substrate SEQ ID NO 7452.
 XX
 XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
 KW Amberzyme; Zinzyme; ss.
 XX
 OS West Nile Virus.
 XX
 XX WO200268637-A2.
 PN
 XX 06-SEP-2002.
 PD
 XX
 PF 19-OCT-2001; 2001WO-US048350.
 XX
 XX 20-OCT-2000; 2000US-0242411P.
 PR
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 XX
 XX Blatt L, Mcswiggen JA;
 PI
 XX WPI; 2002-706994/76.
 DR
 XX
 XX New nucleic acid molecule that modulates replication of West Nile Virus
 PT (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 XX
 XX Claim 23; SEQ ID NO 7452; 495pp; English.
 XX
 CC The invention relates to nucleic acid molecules that modulate replication

CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, inozyme, G-cleaver, DNzyme, Amberzyme and Zinzyme. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention

XX
 SQ Sequence 17 BP; 4 A; 3 C; 6 G; 0 T; 4 U; 0 Other;

Query Match 35.4%; Score 17; DB 6; Length 17;
 Best Local Similarity 76.5%; Pred. No. 16;
 Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 15 GAGGGCTTACATGGATC 31
 .|||||:||||:||||:
 Db 1 GAGGGCUUACUAGGAUC 17

RESULT 45
 ACN03368/c
 ID ACN03368 standard; RNA; 17 BP.
 AC ACN03368;
 XX
 XX 22-APR-2004 (first entry)
 DT
 XX
 DE WNV Inozyme substrate SEQ ID NO 3371.
 XX
 XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNzyme;
 KW Amberzyme; Zinzyme; ss.

OS West Nile Virus.
 XX
 XX WO200268637-A2.
 PN
 XX
 PD 06-SEP-2002.
 XX
 XX 19-OCT-2001; 2001WO-US048350.
 PF
 XX
 XX 20-OCT-2000; 2000US-0242411P.
 PR
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 XX
 XX Blatt L, Mcswiggen JA;
 PI
 XX
 XX WPI; 2002-706994/76.
 DR
 XX
 XX New nucleic acid molecule that modulates replication of West Nile Virus
 PT (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 PT
 XX
 PS Claim 23; SEQ ID NO 3371; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, inozyme, G-cleaver, DNzyme, Amberzyme and Zinzyme. The
 CC nucleic acid molecules further comprise at least five ribose residues, at

CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention

XX
 SQ Sequence 17 BP; 5 A; 7 C; 3 G; 0 T; 2 U; 0 Other;

Query Match 35.4%; Score 17; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GACGGTTCGAGGGCTT 22
 |||||:|||||:
 Db 17 GACGGTTCGAGGGCTT 1

RESULT 46
 ACN12333
 ID ACN12333 standard; RNA; 17 BP.
 XX
 XX ACN12333;
 XX
 XX 22-APR-2004 (first entry)
 DT
 XX
 DE WNV minus strand Zinzyme substrate SEQ ID NO 12336.
 XX
 XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNzyme;
 KW Amberzyme; Zinzyme; ss.

OS West Nile Virus.
 XX
 XX WO200268637-A2.
 PN
 XX
 PD 06-SEP-2002.
 XX
 XX 19-OCT-2001; 2001WO-US048350.
 PF
 XX
 XX 20-OCT-2000; 2000US-0242411P.
 PR
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 XX
 XX Blatt L, Mcswiggen JA;
 PI
 XX
 XX WPI; 2002-706994/76.
 DR
 XX
 XX New nucleic acid molecule that modulates replication of West Nile Virus
 PT (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 PT
 XX
 PS Claim 23; SEQ ID NO 12336; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, inozyme, G-cleaver, DNzyme, Amberzyme and Zinzyme. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention

SQ Sequence 17 BP; 3 A; 4 C; 7 G; 0 T; 3 U; 0 Other;

Query Match 35.4%; Score 17; DB 6; Length 17;
Best Local Similarity 82.4%; Pred. No. 16;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCGAGACGGTTCGAGG 18
DB 1 CCGAGACGGUUCUGAGG 17

RESULT 47

ACN01376/c
ID ACN01376 standard; RNA; 17 BP.

XX ACN01376;

DT 22-APR-2004 (first entry)

XX WNV Hammerhead Ribozyme substrate SEQ ID NO 1366.

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
KW Amberzyme; Zinzyme; ss.

XX West Nile Virus.

XX WO200268637-A2.

XX 06-SEP-2002.

XX 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus
(WNV), useful for treating a condition related to WNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX Claim 23; SEQ ID NO 1366; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication
of the West Nile Virus (WNV). The nucleic acid molecules are useful for
treating a condition related to WNV infection e.g. pancreatitis,
encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
molecule is selected from the group of ribozymes consisting of
Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
nucleic acid molecules further comprise at least five ribose residues, at
least ten 2'-O-methyl modifications, phosphorothioate linkages on at
least three of the 5' terminal nucleotides and a 3' end modification of a
3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
in the specification. The present sequence is that of a nucleic acid
molecule of the invention

XX Sequence 17 BP; 5 A; 6 C; 2 G; 0 T; 4 U; 0 Other;

Query Match 35.4%; Score 17; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TGAGGGCTTACATGGAT 30

DB 17 TGAGGGCTTACATGGAT 1

RESULT 48

ACN03365/c
ID ACN03365 standard; RNA; 17 BP.

XX ACN03365;

XX 22-APR-2004 (first entry)

XX WNV Inozyme substrate SEQ ID NO 3368.

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
KW Amberzyme; Zinzyme; ss.

XX West Nile Virus.

XX WO200268637-A2.

XX 06-SEP-2002.

XX 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus
(WNV), useful for treating a condition related to WNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX Claim 23; SEQ ID NO 3368; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication
of the West Nile Virus (WNV). The nucleic acid molecules are useful for
treating a condition related to WNV infection e.g. pancreatitis,
encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
molecule is selected from the group of ribozymes consisting of
Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
nucleic acid molecules further comprise at least five ribose residues, at
least ten 2'-O-methyl modifications, phosphorothioate linkages on at
least three of the 5' terminal nucleotides and a 3' end modification of a
3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
in the specification. The present sequence is that of a nucleic acid
molecule of the invention

XX Sequence 17 BP; 6 A; 5 C; 3 G; 0 T; 3 U; 0 Other;

Query Match 35.4%; Score 17; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTTCTGAGGGCTTACAT 26

DB 17 GTTCTGAGGGCTTACAT 1

RESULT 49

ACN03366/c
ID ACN03366 standard; RNA; 17 BP.

```

XX AC ACN03366;
XX DT 22-APR-2004 (first entry)
XX DE WNV Inozyme substrate SEQ ID NO 3369.
XX KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
XX KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
XX KW encephalitis; myocarditis; meningitis; infection; hepatitis;
XX KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
XX KW Amberzyme; Zinzyme; ss.
XX OS West Nile Virus.
XX PN WO200268637-A2.
XX PD 06-SEP-2002.
XX PF 19-OCT-2001; 2001WO-US048350.
XX PR 20-OCT-2000; 2000US-0242411P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (BLAT/) BLATT L.
XX PA (MCSW/) MCSWIGGEN J A.
XX PI Blatt L, Mcswiggen JA;
XX PS WPI; 2002-706994/76.
XX CC New nucleic acid molecule that modulates replication of West Nile Virus
XX CC (WNV), useful for treating a condition related to WNV infection e.g.
XX CC pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX PS Claim 23; SEQ ID NO 3369; 495pp; English.
XX CC The invention relates to nucleic acid molecules that modulate replication
XX CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
XX CC treating a condition related to WNV infection e.g. pancreatitis,
XX CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
XX CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
XX CC molecule is selected from the group of ribozymes consisting of
XX CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
XX CC nucleic acid molecules further comprise at least five ribose residues, at
XX CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
XX CC least three of the 5' terminal nucleotides and a 3' end modification of a
XX CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
XX CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
XX CC in the specification. The present sequence is that of a nucleic acid
XX CC molecule of the invention
XX SQ Sequence 17 BP; 5 A; 6 C; 3 G; 0 T; 3 U; 0 Other;

Query Match 35.4%; Score 17; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGTTCGTAGGGCTTACA 25
DB 17 GGTTCGTAGGGCTTACA 1

RESULT 50
ACN04660/c
ID ACN04660 standard; RNA; 17 BP.
XX AC ACN04660;
XX DT 22-APR-2004 (first entry)
XX DE WNV Zinzyme substrate SEQ ID NO 4663.
XX

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KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
KW Amberzyme; Zinzyme; ss.
XX OS West Nile Virus.
XX PN WO200268637-A2.
XX PD 06-SEP-2002.
XX PF 19-OCT-2001; 2001WO-US048350.
XX PR 20-OCT-2000; 2000US-0242411P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (BLAT/) BLATT L.
XX PA (MCSW/) MCSWIGGEN J A.
XX PI Blatt L, Mcswiggen JA;
XX PS WPI; 2002-706994/76.
XX CC New nucleic acid molecule that modulates replication of West Nile Virus
XX CC (WNV), useful for treating a condition related to WNV infection e.g.
XX CC pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX PS Claim 23; SEQ ID NO 4663; 495pp; English.
XX CC The invention relates to nucleic acid molecules that modulate replication
XX CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
XX CC treating a condition related to WNV infection e.g. pancreatitis,
XX CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
XX CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
XX CC molecule is selected from the group of ribozymes consisting of
XX CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
XX CC nucleic acid molecules further comprise at least five ribose residues, at
XX CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
XX CC least three of the 5' terminal nucleotides and a 3' end modification of a
XX CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
XX CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
XX CC in the specification. The present sequence is that of a nucleic acid
XX CC molecule of the invention
XX SQ Sequence 17 BP; 5 A; 6 C; 3 G; 0 T; 3 U; 0 Other;

Query Match 35.4%; Score 17; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TCTGAGGGCTTACATGG 28
DB 17 TCTGAGGGCTTACATGG 1

Search completed: March 25, 2005, 08:13:37
Job time : 284.253 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 25, 2005, 04:27:15 ; Search time 1913.92 Seconds
(without alignments)
954.628 Million cell updates/sec

Title: US-10-688-489-73

Perfect score: 48

Sequence: 1 tcgcgagcgttctgaggc.....atcacttcgagctttgttc 48

Scoring table: OLIGO NUC

Gapop_60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gsa1:*

9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	19	39.6	916	4	B1100670 602885941
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C 4	17	35.4	133	2	AW839969 MR4-LT007
C 5	17	35.4	222	9	CE600009 tigr-gss-
C 6	17	35.4	235	9	CE381828 tigr-gss-
C 7	17	35.4	278	9	CE403157 tigr-gss-
C 8	17	35.4	353	9	CE621983 tigr-gss-
C 9	17	35.4	381	9	CE737260 tigr-gss-
C 10	17	35.4	401	9	CE052353 tigr-gss-
C 11	17	35.4	406	9	CE025163 tigr-gss-
C 12	17	35.4	409	9	CE778541 tigr-gss-
C 13	17	35.4	410	9	CE468568 tigr-gss-
C 14	17	35.4	413	9	CE206168 tigr-gss-
C 15	17	35.4	426	9	CE267316 tigr-gss-
C 16	17	35.4	431	9	CE218594 tigr-gss-
C 17	17	35.4	460	9	CE111389 tigr-gss-
C 18	17	35.4	462	9	CE015704 tigr-gss-
C 19	17	35.4	468	9	CE235142 tigr-gss-
C 20	17	35.4	471	9	CE724068 tigr-gss-
C 21	17	35.4	498	9	CE788674 tigr-gss-
C 22	17	35.4	544	9	CE679750 tigr-gss-
C 23	17	35.4	556	9	CE411475 tigr-gss-
C 24	17	35.4	565	9	CE274341 tigr-gss-

C 25	17	35.4	566	9	CE671584 tigr-gss-
C 26	17	35.4	582	9	CE371722 tigr-gss-
C 27	17	35.4	589	9	CE076080 tigr-gss-
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C 29	17	35.4	600	6	CA229401 SCAGFL302
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C 31	17	35.4	612	9	CE069149 tigr-gss-
C 32	17	35.4	612	9	CE183667 tigr-gss-
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C 39	17	35.4	673	8	BH145540 TDGEX60TH
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C 47	17	35.4	821	5	BU467348 603371996
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C 49	17	35.4	825	5	CR241446 Reverse s
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C 90	16	33.3	602	4	BG453197 NF089H12L
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C 96	16	33.3	628	9	CB636722 OSJNE8021
C 97	16	33.3	629	9	CG206431 TOS0636 T

C 98	16	33.3	634	8	A2717026	A2717026	RPCI-24-1	171	15	31.2	245	9	CE314130	CE314130	tigr-g88-
C 99	16	33.3	635	9	CC880281	CC880281	ZMBB0021	172	15	31.2	246	9	CE113530	CE113530	tigr-g88-
C 100	16	33.3	636	7	CN881360	CN881360	1010427AAS	173	15	31.2	247	1	AV087444	AV087444	OM3-IT004
C 101	16	33.3	637	9	CE565095	CE565095	tigr-g88-	174	15	31.2	254	2	BF772925	BF772925	CW3-IT004
C 102	16	33.3	638	9	CL825006	CL825006	OR_CBA004	175	15	31.2	254	9	CE233690	CE233690	tigr-g88-
C 103	16	33.3	639	8	BH484787	BH484787	BOGHDA3TF	176	15	31.2	254	9	CE850304	CE850304	tigr-g88-
C 104	16	33.3	639	6	CA452447	CA452447	Rxo-2_C09	177	15	31.2	254	9	CE401347	CE401347	tigr-g88-
C 105	16	33.3	639	6	BH966029	BH966029	10420N05	178	15	31.2	257	9	CE482232	CE482232	tigr-g88-
C 106	16	33.3	639	7	CL176655	CL176655	oh3383_1	178	15	31.2	257	9	CE677702	CE677702	tigr-g88-
C 107	16	33.3	723	7	CL474321	CL474321	AGENCOURT	180	15	31.2	260	9	CE008552	CE008552	tigr-g88-
C 108	16	33.3	723	9	CL544011	CL544011	OB_Ba007	181	15	31.2	260	9	CE432060	CE432060	tigr-g88-
C 109	16	33.3	732	9	AG360335	AG360335	Mus_muscu	182	15	31.2	266	9	CE421620	CE421620	tigr-g88-
C 110	16	33.3	732	9	CL781167	CL781167	OR_Ba009	183	15	31.2	269	9	AB082339	AB082339	Drosophila
C 111	16	33.3	737	7	CD826182	CD826182	BN25_063A	184	15	31.2	271	9	CE044025	CE044025	tigr-g88-
C 112	16	33.3	745	8	BZ676878	BZ676878	PUBH50TD	185	15	31.2	273	2	AW454040	AW454040	zeh10853
C 113	16	33.3	750	5	BU252574	BU252574	603745432	186	15	31.2	273	9	CL161415	CL161415	104_352_1
C 114	16	33.3	750	7	CO894483	CO894483	BovGen_22	187	15	31.2	274	1	AA488234	AA488234	ad08C08r
C 115	16	33.3	758	7	CO572794	CO572794	AGENCOURT	188	15	31.2	275	1	AV087644	AV087644	AV087644
C 116	16	33.3	767	6	CB648974	CB648974	OSJNEB12K	189	15	31.2	276	9	CE468170	CE468170	tigr-g88-
C 117	16	33.3	779	6	CF719567	CF719567	CCAGY20TR	190	15	31.2	277	1	AV087687	AV087687	AV087687
C 118	16	33.3	782	7	CD442333	CD442333	EL01N0408	191	15	31.2	280	1	AV090463	AV090463	AV090463
C 119	16	33.3	806	6	CC802540	CC802540	ih31d01.b	192	15	31.2	281	1	AI616557	AI616557	zeh00246
C 120	16	33.3	808	6	CD439001	CD439001	EL01N0519	193	15	31.2	286	9	CE707225	CE707225	tigr-g88-
C 121	16	33.3	808	7	CF346064	CF346064	AGENCOURT	194	15	31.2	288	8	AZ253297	AZ253297	RPCI-23-9
C 122	16	33.3	812	6	CB658330	CB658330	OSJNEB14E	195	15	31.2	290	1	AI618295	AI618295	zeh00053
C 123	16	33.3	837	6	CB635448	CB635448	OSJNEB15N	196	15	31.2	291	6	CB276655	CB276655	pl34h01.y
C 124	16	33.3	852	9	CR812154	CR812154	GR0AAA36B	197	15	31.2	291	9	CE475105	CE475105	tigr-g88-
C 125	16	33.3	853	7	CO435611	CO435611	OSMR677_5	198	15	31.2	291	9	CE772495	CE772495	tigr-g88-
C 126	16	33.3	853	7	CL484057	CL484057	SAIL_390	199	15	31.2	295	2	AW453716	AW453716	zeh10374
C 127	16	33.3	870	8	BH514604	BH514604	BOG058TF	200	15	31.2	295	2	CE127265	CE127265	tigr-g88-
C 128	16	33.3	877	9	CR098487	CR098487	Reverse_8	201	15	31.2	297	9	CE013144	CE013144	tigr-g88-
C 129	16	33.3	916	9	CR132303	CR132303	Reverse_8	202	15	31.2	298	8	AQ073531	AQ073531	EP(2)2369
C 130	16	33.3	916	9	CG154491	CG154491	PUKCT05TD	203	15	31.2	298	8	AQ254813	AQ254813	EP(2)0816
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C 132	16	33.3	1013	9	BU378222	BU378222	603813104	205	15	31.2	305	9	CE290082	CE290082	tigr-g88-
C 133	16	33.3	1029	5	CC243337	CC243337	CH261-148	206	15	31.2	311	1	AI353436	AI353436	zeh0497.8
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C 137	16	33.3	1617	3	CNSOAA4V4	CNSOAA4V4	Arabidops	210	15	31.2	314	9	CE793686	CE793686	SALK_0174
C 138	16	33.3	1721	3	CNSOAA72U	CNSOAA72U	Arabidops	211	15	31.2	316	9	CE752252	CE752252	tigr-g88-
C 139	16	33.3	1764	3	CNSOAA736	CNSOAA736	Arabidops	212	15	31.2	317	9	CE821716	CE821716	tigr-g88-
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C 151	15	31.2	185	9	CE522238	CE522238	tigr-g88-	224	15	31.2	334	6	CD584966	CD584966	RK028A4F0
C 152	15	31.2	190	9	DM545759	DM545759	Drosophila	225	15	31.2	335	6	CE592011	CE592011	RK068A2D0
C 153	15	31.2	190	9	CE301049	CE301049	tigr-g88-	226	15	31.2	340	9	CE102616	CE102616	tigr-g88-
C 154	15	31.2	195	9	CE687400	CE687400	tigr-g88-	227	15	31.2	340	9	CE515000	CE515000	tigr-g88-
C 155	15	31.2	197	9	CE346908	CE346908	tigr-g88-	228	15	31.2	344	3	AY432736	AY432736	Aedes aeg
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C 158	15	31.2	205	2	AW454664	AW454664	zeh11869	231	15	31.2	352	6	CD196017	CD196017	MS1-0091T
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C 161	15	31.2	222	9	CE160869	CE160869	tigr-g88-	234	15	31.2	356	9	CL375560	CL375560	RPCI4_47
C 162	15	31.2	228	9	CE654039	CE654039	tigr-g88-	235	15	31.2	357	9	CE272729	CE272729	tigr-g88-
C 163	15	31.2	230	7	CV372791	CV372791	PM3-ET026	236	15	31.2	358	9	CE204069	CE204069	tigr-g88-
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C 165	15	31.2	236	2	AW320339	AW320339	uol7e10.y	238	15	31.2	368	8	AQ971791	AQ971791	RPCI-23-3
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C 167	15	31.2	240	8	BZ765024	BZ765024	SALK_1279	240	15	31.2	369	9	CE310662	CE310662	tigr-g88-
C 168	15	31.2	242	9	CE032616	CE032616	tigr-g88-	241	15	31.2	372	9	CE409610	CE409610	tigr-g88-
C 169	15	31.2	242	9	CE380872	CE380872	tigr-g88-	242	15	31.2	375	9	CE086627	CE086627	tigr-g88-
C 170	15	31.2	245	1	AV272638	AV272638	AV272638	243	15	31.2	379	9	CE193502	CE193502	tigr-g88-

244	15	31.2	382	9	CE487581	tigr-g88-	317	15	31.2	459	9	CE693412	tigr-g88-
245	15	31.2	384	9	CE440273	tigr-g88-	C 318	15	31.2	460	9	CE575511	tigr-g88-
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ALIGNMENTS

BI100670 916 bp mRNA linear EST 26-JUN-2001
 602885941F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:5041067
 5', mRNA sequence.

BI100670
 BI100670.1 GI:14551563

EST.
 Mus musculus (house mouse)

ORGANISM
 Mus musculus

REFERENCE
 1 (bases 1 to 916)

AUTHORS
 NIH-MGC http://mgs.nci.nih.gov/.

TITLE
 National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabps-remail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLML)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLML at:
 http://image.lnl.gov
 Plate: L1AM1113 Row: b Column: 12
 High quality sequence stop: 513.
 Location/Qualifiers
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RESULT 1

BI100670/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

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Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

ORIGIN
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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTTCTGAGGCTTACATGG 28
Db 514 GTTCTGAGGCTTACATGG 496

RESULT 2
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LOCUS RUB008B11.ab1 RJtestis Gallus gallus cDNA 5', mRNA sequence.
ACCESSION CN226960
VERSION CN226960.1 GI:46330704
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 413)
AUTHORS Savolainen,P., Fitzsimmons,C.J., Arvestad,L., Andersson,L. and
Lundberg,J.
TITLE EST analysis of brain and testis cDNA libraries from White leghorn
and Red Jungle Fowl
JOURNAL Unpublished (2004)
COMMENT Contact: Peter Savolainen
Department of Biotechnology
Royal Institute of Technology, KTH
SE-106 91 Stockholm, SWEDEN
Tel: +46 (0)8 5537 8481
Fax: +46 (0)8 5537 8335
Email: Peter.Savolainen@biotech.kth.se
Seq primer: M13 reverse primer.
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RESULT 3
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LOCUS
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DEFINITION tigr-gss-dog-17000322656173 Dog Library Canis familiaris genomic,
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VERSION CE067576.1 GI:35125996
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SOURCE Canis familiaris (dog)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 154)
AUTHORS Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
MEDLINE 22875432
PUBMED 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
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peripheral blood"
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Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 4 GAGACGGTTCTGAGGCG 20
Db 28 GAGACGGTTCTGAGGCG 44
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RESULT 4
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LOCUS MR4-LT0077-150200-101-h10 LT0077 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW839969
VERSION AW839969.1 GI:7933943
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 193)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baig,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
```

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TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
```

Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimponeludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=et2=MR4-LT0077-150
 200-101-h10&t3=2000-02-15&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 19
 High quality sequence stop: 193.
 Location/Qualifiers
 1. .193
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="LT0077"
 /note="Organ: leiomyos; Vector: puc18; Site 1: SmaI;
 Site 2: SmaI; A mini-library was made by cloning products
 derived from ORSTS PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the puc 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

FEATURES
source

ORIGIN
 Query Match 35.4%; Score 17; DB 2; Length 193;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 ACTTCGAGCTTTGTTTC 48
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 Db 1 ACTTCGAGCTTTGTTTC 17

RESULT 5
 CE600009/c
 LOCUS
 DEFINITION tigr-gss-dog-1700036646390 Dog Library Canis familiaris genomic,
 genomic survey sequence.
 ACCESSION CE600009
 VERSION CE600009.1 GI:36916848
 KEYWORDS GSS.
 SOURCE Canis familiaris (dog)
 ORGANISM Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 REFERENCE 1 (bases 1 to 222)
 AUTHORS Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
 Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
 Venter,J.C.
 TITLE The dog genome: survey sequencing and comparative analysis
 JOURNAL Science 301 (5641), 1898-1903 (2003)
 MEDLINE 22875432
 PUBMED 14512627
 COMMENT Contact: Kirkness EF
 The Institute for Genomic Research
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
 Rockville, MD 20850, USA
 Tel: 301-838-0200
 Fax: 301-838-0208
 Email: ekirknes@tigr.org
 Class: shotgun.

FEATURES
source

Location/Qualifiers
 1. .222
 /organism="Canis familiaris"
 /mol_type="genomic DNA"
 /strain="Standard Poodle"
 /db_xref="taxon:9615"
 /clone_lib="Dog Library"
 /note="Site 1: BstXI; Libraries were prepared from
 peripheral blood"

ORIGIN

Query Match 35.4%; Score 17; DB 9; Length 222;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 GAGACGGTTCTGAGGCG 20
 |||||
 Db 213 GAGACGGTTCTGAGGCG 197

RESULT 6
CE381828/c

LOCUS
 DEFINITION tigr-gss-dog-17000334214632 Dog Library Canis familiaris genomic,
 genomic survey sequence.
 ACCESSION CE381828
 VERSION CE381828.1 GI:36613404
 KEYWORDS GSS.
 SOURCE Canis familiaris (dog)
 ORGANISM Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 REFERENCE 1 (bases 1 to 235)
 AUTHORS Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
 Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
 Venter,J.C.
 TITLE The dog genome: survey sequencing and comparative analysis
 JOURNAL Science 301 (5641), 1898-1903 (2003)
 MEDLINE 22875432
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 COMMENT Contact: Kirkness EF
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 Rockville, MD 20850, USA
 Tel: 301-838-0200
 Fax: 301-838-0208
 Email: ekirknes@tigr.org
 Class: shotgun.

FEATURES
source

Location/Qualifiers
 1. .235
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 /mol_type="genomic DNA"
 /strain="Standard Poodle"
 /db_xref="taxon:9615"
 /clone_lib="Dog Library"
 /note="Site 1: BstXI; Libraries were prepared from
 peripheral blood"

ORIGIN

Query Match 35.4%; Score 17; DB 9; Length 235;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 GAGACGGTTCTGAGGCG 20
 |||||
 Db 131 GAGACGGTTCTGAGGCG 115

RESULT 7
CE403157

LOCUS
 DEFINITION tigr-gss-dog-17000334744718 Dog Library Canis familiaris genomic,
 genomic survey sequence.
 ACCESSION CE403157
 VERSION CE403157.1 GI:36652971
 KEYWORDS GSS.
 SOURCE Canis familiaris (dog)
 ORGANISM Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 REFERENCE 1 (bases 1 to 278)
 AUTHORS Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
 Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and

Venter, J.C.
The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
MEDLINE 22875432
PUBMED 14512627
COMMENT Contact: Kirkness EF
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Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.

FEATURES
source
1. .278
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/notes="Site 1: BstXI; Libraries were prepared from
peripheral blood"

ORIGIN
Query Match 35.4%; Score 17; DB 9; Length 278;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGACGGTTCTGAGGCG 20
|||||
Db 138 GAGACGGTTCTGAGGCG 154

RESULT 8
CE621983/c
LOCUS
DEFINITION tigr-gss-dog-17000313638114 Dog Library Canis familiaris genomic,
genomic survey sequence.
ACCESSION CE621983.1 GI:36939358
VERSION
KEYWORDS
SOURCE
ORGANISM
Canis familiaris (dog)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 353)
AUTHORS Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
Venter, J.C.
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MEDLINE 22875432
PUBMED 14512627
COMMENT Contact: Kirkness EF
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Rockville, MD 20850, USA
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Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.

FEATURES
source
1. .353
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/notes="Site 1: BstXI; Libraries were prepared from
peripheral blood"

ORIGIN
Query Match 35.4%; Score 17; DB 9; Length 353;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 42;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGACGGTTCTGAGGCG 20
|||||
Db 162 GAGACGGTTCTGAGGCG 146

RESULT 9
CE737260
LOCUS
DEFINITION tigr-gss-dog-17000315462536 Dog Library Canis familiaris genomic,
genomic survey sequence.
ACCESSION CE737260.1 GI:37077455
VERSION
KEYWORDS
SOURCE
ORGANISM
Canis familiaris (dog)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 381)
AUTHORS Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
Venter, J.C.
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PUBMED 14512627
COMMENT Contact: Kirkness EF
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Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.

FEATURES
source
1. .381
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/notes="Site 1: BstXI; Libraries were prepared from
peripheral blood"

ORIGIN
Query Match 35.4%; Score 17; DB 9; Length 381;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTTCTGAGGCGTTACAT 26
|||||
Db 213 GTTCTGAGGCGTTACAT 229

RESULT 10
CE052353
LOCUS
DEFINITION tigr-gss-dog-17000358219219 Dog Library Canis familiaris genomic,
genomic survey sequence.
ACCESSION CE052353.1 GI:35095839
VERSION
KEYWORDS
SOURCE
ORGANISM
Canis familiaris (dog)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 401)
AUTHORS Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
Venter, J.C.
The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
MEDLINE 22875432
PUBMED 14512627
COMMENT Contact: Kirkness EF
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Email: ekirknes@tigr.org
Class: shotgun.

FEATURES
source
1. .353
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/notes="Site 1: BstXI; Libraries were prepared from
peripheral blood"

ORIGIN
Query Match 35.4%; Score 17; DB 9; Length 353;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

JOURNAL Science 301 (5641), 1898-1903 (2003)
 MEDLINE 22875432
 PUBMED 14512627
 COMMENT Contact: Kirkness EF

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 Fax: 301-838-0208
 Email: ekirknes@tigr.org
 Class: shotgun.

FEATURES

Location/Qualifiers
 1. .401
 /organism="Canis familiaris"
 /mol_type="genomic DNA"
 /strain="Standard Poodle"
 /db_xref="taxon:9615"
 /clone_lib="Dog Library"
 /note="Site 1: BstXI; Libraries were prepared from
 peripheral blood"

ORIGIN

Query Match 35.4%; Score 17; DB 9; Length 401;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAGACGGTTCTGAGGC 20
 |||||
 Db 262 GAGACGGTTCTGAGGC 278

RESULT 11
 CE025163 406 bp DNA linear GSS 24-SEP-2003
 LOCUS tigr-gss-dog-17000322362916 Dog Library Canis familiaris genomic,
 DEFINITION genomic survey sequence.

ACCESSION CE025163
 VERSION CE025163.1 GI:35041644
 KEYWORDS GSS.
 SOURCE Canis familiaris (dog)
 ORGANISM Canis familiaris

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 AUTHORS Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
 Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
 Venter,J.C.

TITLE The dog genome: survey sequencing and comparative analysis

JOURNAL Science 301 (5641), 1898-1903 (2003)
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 PUBMED 14512627
 COMMENT Contact: Kirkness EF

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 Fax: 301-838-0208
 Email: ekirknes@tigr.org
 Class: shotgun.

FEATURES

Location/Qualifiers
 1. .406
 /organism="Canis familiaris"
 /mol_type="genomic DNA"
 /strain="Standard Poodle"
 /db_xref="taxon:9615"
 /clone_lib="Dog Library"
 /note="Site 1: BstXI; Libraries were prepared from
 peripheral blood"

ORIGIN

Query Match 35.4%; Score 17; DB 9; Length 406;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAGACGGTTCTGAGGC 20
 |||||
 Db 302 GAGACGGTTCTGAGGC 318

RESULT 12
 CE778541/c
 LOCUS tigr-gss-dog-17000317030140 Dog Library Canis familiaris genomic,
 DEFINITION genomic survey sequence.

ACCESSION CE778541
 VERSION CE778541.1 GI:37119304
 KEYWORDS GSS.
 SOURCE Canis familiaris (dog)
 ORGANISM Canis familiaris

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 AUTHORS Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
 Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
 Venter,J.C.

TITLE The dog genome: survey sequencing and comparative analysis

JOURNAL Science 301 (5641), 1898-1903 (2003)
 MEDLINE 22875432
 PUBMED 14512627
 COMMENT Contact: Kirkness EF

The Institute for Genomic Research
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 Tel: 301-838-0200
 Fax: 301-838-0208
 Email: ekirknes@tigr.org
 Class: shotgun.

FEATURES

Location/Qualifiers
 1. .409
 /organism="Canis familiaris"
 /mol_type="genomic DNA"
 /strain="Standard Poodle"
 /db_xref="taxon:9615"
 /clone_lib="Dog Library"
 /note="Site 1: BstXI; Libraries were prepared from
 peripheral blood"

ORIGIN

Query Match 35.4%; Score 17; DB 9; Length 409;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAGACGGTTCTGAGGC 20
 |||||
 Db 301 GAGACGGTTCTGAGGC 285

RESULT 13
 CE468568

LOCUS tigr-gss-dog-17000363678786 Dog Library Canis familiaris genomic,
 DEFINITION genomic survey sequence.

ACCESSION CE468568
 VERSION CE468568.1 GI:36772018
 KEYWORDS GSS.
 SOURCE Canis familiaris (dog)
 ORGANISM Canis familiaris

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 AUTHORS Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
 Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
 Venter,J.C.

TITLE The dog genome: survey sequencing and comparative analysis

JOURNAL Science 301 (5641), 1898-1903 (2003)
 MEDLINE 22875432

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PUBMED 14512627
COMMENT Contact: Kirkness EF
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Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.

FEATURES
source
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Location/Qualifiers
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/notes="Site 1: BstXI; Libraries were prepared from
peripheral blood"

ORIGIN
Query Match 35.4%; Score 17; DB 9; Length 410;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAGACGGTTCTGAGGC 20
|||||
Db 372 GAGACGGTTCTGAGGC 388

RESULT 14
LOCUS CE206168/c 413 bp DNA linear GSS 25-SEP-2003
DEFINITION tigr-gss-dog-17000372648258 Dog Library Canis familiaris genomic,
genomic survey sequence.
ACCESSION CE206168.1 GI:35361823
VERSION CE206168
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 413)
AUTHORS Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
The dog genome: survey sequencing and comparative analysis
TITLE The dog genome: survey sequencing and comparative analysis
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MEDLINE 22875432
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COMMENT Contact: Kirkness EF
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Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.

FEATURES
source
1..413
Location/Qualifiers
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/notes="Site 1: BstXI; Libraries were prepared from
peripheral blood"

ORIGIN
Query Match 35.4%; Score 17; DB 9; Length 413;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAGACGGTTCTGAGGC 20
|||||
Db 372 GAGACGGTTCTGAGGC 388

RESULT 15
LOCUS CE267316/c 426 bp DNA linear GSS 26-SEP-2003
DEFINITION tigr-gss-dog-17000359912254 Dog Library Canis familiaris genomic,
genomic survey sequence.
ACCESSION CE267316.1 GI:35992555
VERSION CE267316
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 426)
AUTHORS Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
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TITLE The dog genome: survey sequencing and comparative analysis
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Email: ekirknes@tigr.org
Class: shotgun.

FEATURES
source
1..426
Location/Qualifiers
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/notes="Site 1: BstXI; Libraries were prepared from
peripheral blood"

ORIGIN
Query Match 35.4%; Score 17; DB 9; Length 426;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAGACGGTTCTGAGGC 20
|||||
Db 277 GAGACGGTTCTGAGGC 261

RESULT 16
LOCUS CE218594 431 bp DNA linear GSS 25-SEP-2003
DEFINITION tigr-gss-dog-17000326860586 Dog Library Canis familiaris genomic,
genomic survey sequence.
ACCESSION CE218594.1 GI:35374263
VERSION CE218594
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 431)
AUTHORS Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
The dog genome: survey sequencing and comparative analysis
TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
MEDLINE 22875432
PUBMED 14512627
COMMENT Contact: Kirkness EF

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Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.

FEATURES
source
1. .431
Location/Qualifiers
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"

ORIGIN

Query Match 35.4%; Score 17; DB 9; Length 431;
Best Local Similarity 100.0%; Pred. No. 42; Mismatches 0; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GAGACGGTTCTGAGGCG 20
|||||
DB 330 GAGACGGTTCTGAGGCG 346

RESULT 17

CE111389
LOCUS
DEFINITION
tigr-gss-dog-17000324922150 Dog Library Canis familiaris genomic,
genomic survey sequence.

ACCESSION
CE111389
VERSION
CE111389.1 GI:35178274
KEYWORDS
GSS.
SOURCE
Canis familiaris (dog)
ORGANISM
Canis familiaris

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 460)
Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.

TITLE
The dog genome: survey sequencing and comparative analysis

JOURNAL
Science 301 (5641), 1898-1903 (2003)

PUBMED
22875432

COMMENT
14512627

Contact: Kirkness EF
The Institute for Genomic Research
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Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.

FEATURES

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1. .460
Location/Qualifiers
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"

ORIGIN

Query Match 35.4%; Score 17; DB 9; Length 460;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GAGACGGTTCTGAGGCG 20
|||||
DB 322 GAGACGGTTCTGAGGCG 338

RESULT 18

CE015704/c
LOCUS
DEFINITION
tigr-gss-dog-17000321327472 Dog Library Canis familiaris genomic,
genomic survey sequence.

ACCESSION
CE015704
VERSION
CE015704.1 GI:35022697
KEYWORDS
GSS.
SOURCE
Canis familiaris (dog)
ORGANISM
Canis familiaris

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 462)
Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.

TITLE
The dog genome: survey sequencing and comparative analysis

JOURNAL
Science 301 (5641), 1898-1903 (2003)

PUBMED
22875432

COMMENT
14512627

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Rockville, MD 20850, USA
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Email: ekirknes@tigr.org
Class: shotgun.

FEATURES
source
1. .462
Location/Qualifiers
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"

ORIGIN

Query Match 35.4%; Score 17; DB 9; Length 462;
Best Local Similarity 100.0%; Pred. No. 42; Mismatches 0; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GAGACGGTTCTGAGGCG 20
|||||
DB 267 GAGACGGTTCTGAGGCG 251

RESULT 19

CE235142
LOCUS
DEFINITION
tigr-gss-dog-1700033378589 Dog Library Canis familiaris genomic,
genomic survey sequence.

ACCESSION
CE235142
VERSION
CE235142.1 GI:35390900
KEYWORDS
GSS.
SOURCE
Canis familiaris (dog)
ORGANISM
Canis familiaris

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 468)
Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.

TITLE
The dog genome: survey sequencing and comparative analysis

JOURNAL
Science 301 (5641), 1898-1903 (2003)

PUBMED
22875432

COMMENT
14512627

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Email: ekirknes@tigr.org
Class: shotgun.

FEATURES

source

Location/Qualifiers
1. .468
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/notes="Site 1: BstXI; Libraries were prepared from peripheral blood"

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Query Match 35.4%; Score 17; DB 9; Length 468;
Best Local Similarity 100.0%; Pred. No. 42; Mismatches 0; Indels 0; Gaps 0;
Matches 17; Conservative 0

QY 4 GAGACGGTTCGAGGC 20
|||||
Db 329 GAGACGGTTCGAGGC 345

RESULT 20

CE724068

LOCUS

DEFINITION tigr-gss-dog-17000315207540 Dog Library Canis familiaris genomic, genomic survey sequence.

ACCESSION CE724068

VERSION CE724068.1

KEYWORDS GI:37064093

SOURCE GSS.

ORGANISM Canis familiaris (dog)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

AUTHORS Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.

TITLE The dog genome: survey sequencing and comparative analysis

JOURNAL Science 301 (5641), 1898-1903 (2003)

MEDLINE 22875432

PUBMED 14512627

COMMENT Contact: Kirkness EF
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Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.

FEATURES

source

Location/Qualifiers
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/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/notes="Site 1: BstXI; Libraries were prepared from peripheral blood"

ORIGIN

Query Match 35.4%; Score 17; DB 9; Length 471;
Best Local Similarity 100.0%; Pred. No. 42; Mismatches 0; Indels 0; Gaps 0;
Matches 17; Conservative 0

QY 4 GAGACGGTTCGAGGC 20
|||||
Db 211 GAGACGGTTCGAGGC 227

RESULT 21

CE788674/c

LOCUS

DEFINITION tigr-gss-dog-1700031779733 Dog Library Canis familiaris genomic, genomic survey sequence.

ACCESSION CE788674

VERSION CE788674.1

KEYWORDS GI:37129437

SOURCE GSS.

ORGANISM Canis familiaris (dog)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

AUTHORS Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.

TITLE The dog genome: survey sequencing and comparative analysis

JOURNAL Science 301 (5641), 1898-1903 (2003)

MEDLINE 22875432

PUBMED 14512627

COMMENT Contact: Kirkness EF
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Tel: 301-838-0200
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Email: ekirknes@tigr.org
Class: shotgun.

FEATURES

source

Location/Qualifiers
1. .498
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/notes="Site 1: BstXI; Libraries were prepared from peripheral blood"

ORIGIN

Query Match 35.4%; Score 17; DB 9; Length 498;
Best Local Similarity 100.0%; Pred. No. 42; Mismatches 0; Indels 0; Gaps 0;
Matches 17; Conservative 0

QY 4 GAGACGGTTCGAGGC 20
|||||
Db 135 GAGACGGTTCGAGGC 119

RESULT 22

CE679750/c

LOCUS

DEFINITION tigr-gss-dog-17000314411471 Dog Library Canis familiaris genomic, genomic survey sequence.

ACCESSION CE679750

VERSION CE679750.1

KEYWORDS GI:36998750

SOURCE GSS.

ORGANISM Canis familiaris (dog)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

AUTHORS Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.

TITLE The dog genome: survey sequencing and comparative analysis

JOURNAL Science 301 (5641), 1898-1903 (2003)

MEDLINE 22875432

PUBMED 14512627

COMMENT Contact: Kirkness EF
The Institute for Genomic Research
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Tel: 301-838-0200

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FEATURES
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    Location/Qualifiers
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        /mol_type="genomic DNA"
        /strain="Standard Poodle"
        /db_xref="taxon:9615"
        /clone_lib="Dog Library"
        /note="Site 1: BstXI; Libraries were prepared from
        peripheral blood"
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  Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY      4 GAGACGGTTCGAGGCG 20
          |||||
  Db      253 GAGACGGTTCGAGGCG 237

RESULT 23
CE411475/c
LOCUS
DEFINITION
  tigr-gss-dog-17000362273066 Dog Library Canis familiaris genomic,
  genomic survey sequence.
CE411475
VERSION
  CE411475.1 GI:36668289
KEYWORDS
  GSS.
SOURCE
  Canis familiaris (dog)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
  1 (bases 1 to 566)
  Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
  Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
  Venter,J.C.
  The dog genome: survey sequencing and comparative analysis
  Science 301 (5641), 1898-1903 (2003)
  14512627
  PubMed
  Contact: Kirkness EF
  The Institute for Genomic Research
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  Rockville, MD 20850, USA
  Tel: 301-838-0200
  Fax: 301-838-0208
  Email: ekirknes@tigr.org
  Class: shotgun.
  Location/Qualifiers
    1..556
      /organism="Canis familiaris"
      /mol_type="genomic DNA"
      /strain="Standard Poodle"
      /db_xref="taxon:9615"
      /clone_lib="Dog Library"
      /note="Site 1: BstXI; Libraries were prepared from
      peripheral blood"
ORIGIN
  Query Match      35.4%; Score 17; DB 9; Length 556;
  Best Local Similarity 100.0%; Pred. No. 43;
  Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY      4 GAGACGGTTCGAGGCG 20
          |||||
  Db      113 GAGACGGTTCGAGGCG 97

RESULT 24
CE274341/c
LOCUS
DEFINITION
  tigr-gss-dog-17000333595430 Dog Library Canis familiaris genomic,
  genomic survey sequence.
CE274341
VERSION
  CE274341.1 GI:36012978
KEYWORDS
  GSS.
SOURCE
  Canis familiaris (dog)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
  1 (bases 1 to 565)
  Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
  Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
  Venter,J.C.
  The dog genome: survey sequencing and comparative analysis
  Science 301 (5641), 1898-1903 (2003)
  14512627
  PubMed
  Contact: Kirkness EF
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  Rockville, MD 20850, USA
  Tel: 301-838-0200
  Fax: 301-838-0208
  Email: ekirknes@tigr.org
  Class: shotgun.
  Location/Qualifiers
    1..565
      /organism="Canis familiaris"
      /mol_type="genomic DNA"
      /strain="Standard Poodle"
      /db_xref="taxon:9615"
      /clone_lib="Dog Library"
      /note="Site 1: BstXI; Libraries were prepared from
      peripheral blood"
ORIGIN
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  Best Local Similarity 100.0%; Pred. No. 43;
  Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY      4 GAGACGGTTCGAGGCG 20
          |||||
  Db      113 GAGACGGTTCGAGGCG 97

RESULT 25
CE671584/c
LOCUS
DEFINITION
  tigr-gss-dog-17000313756475 Dog Library Canis familiaris genomic,
  genomic survey sequence.
CE671584
VERSION
  CE671584.1 GI:36990584
KEYWORDS
  GSS.
SOURCE
  Canis familiaris (dog)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
  1 (bases 1 to 566)
  Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
  Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
  Venter,J.C.
  The dog genome: survey sequencing and comparative analysis
  Science 301 (5641), 1898-1903 (2003)
  14512627
  PubMed
  Contact: Kirkness EF
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  Rockville, MD 20850, USA
  Tel: 301-838-0200
  Fax: 301-838-0208
  Email: ekirknes@tigr.org
  Class: shotgun.
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/note="Site 1: BtXI; Libraries were prepared from
peripheral blood"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAGACGGTTCGAGGGC 20
|||||
Db 432 GAGACGGTTCGAGGGC 448

RESULT 29
CA229401
LOCUS CA229401 600 bp mRNA linear EST 25-SEP-2003
DEFINITION SCAGFL3025C06.9 Saccharum officinarum FL3 Saccharum officinarum
cDNA clone SCAGFL3025C06 5', mRNA sequence.
ACCESSION CA229401
VERSION CA229401
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
complex.
REFERENCE 1 (bases 1 to 600)
AUTHORS Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
TITLE The libraries that made SUCEST
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bccccenter.fcav.unesp.br
Plate: 025 row: C column: 06
Seq primer: T7 Promoter Primer.
Location/Qualifiers
1. .600
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/lab_host="DH10B"
/clone_lib="Saccharum officinarum FL3"
/note="Organ: Base of developing inflorescence (5cm-long);
Vector: pSport1; Site 1: SalI; Site 2: NotI; An
unidirectional cDNA library generated from [base of
developing inflorescence (5cm-long)]. cDNA was prepared
from polyA+ mRNA using SuperScript Plasmid System Kit
(Invitrogen). The double-strand cDNAs were fractionated
in a sepharose CL-2B 40cm-columns and fragments sizing
between 0.8 and 1.5 Kb were directionally cloned into the
vector. Details of each source of RNA and library
construction can be obtained at
http://sucust.lad.ic.unicamp.br/public"

ORIGIN
Query Match 35.4%; Score 17; DB 6; Length 600;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 18 GGCTTACATGGATCACT 34
|||||
Db 142 GGCTTACATGGATCACT 158

RESULT 30
CE237342/c
LOCUS CE237342 605 bp DNA linear GSS 25-SEP-2003
DEFINITION tigr-gss-dog-1700033398507 Dog Library Canis familiaris genomic,
genomic survey sequence.
ACCESSION CE237342
VERSION CE237342.1 GI:35393100
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 605)
AUTHORS Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
MEDLINE 22875432
PUBMED 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
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Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
Location/Qualifiers
1. 605
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BtXI; Libraries were prepared from
peripheral blood"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAGACGGTTCGAGGGC 20
|||||
Db 345 GAGACGGTTCGAGGGC 329

RESULT 31
CE069149
LOCUS CE069149 612 bp DNA linear GSS 24-SEP-2003
DEFINITION tigr-gss-dog-17000322919379 Dog Library Canis familiaris genomic,
genomic survey sequence.
ACCESSION CE069149
VERSION CE069149.1 GI:35129037
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 612)
AUTHORS Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
MEDLINE 22875432

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14512627
PUBMED
COMMENT
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Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.

FEATURES
source
1..612
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"

ORIGIN
Query Match 35.4%; Score 17; DB 9; Length 612;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGACGGTTCTGAGGCG 20
|||||
Db 346 GAGACGGTTCTGAGGCG 362

RESULT 32
CE183667/c
LOCUS
DEFINITION
tigr-gss-dog-17000326827776 Dog Library Canis familiaris genomic,
genomic survey sequence.
CE183667 GI:35336135
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Canis familiaris (dog)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
AUTHORS
Kirkness,E.F., Batna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
22875432
PUBMED
COMMENT
Contact: Kirkness EF
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Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.

FEATURES
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/organism="Canis familiaris"
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/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"

ORIGIN
Query Match 35.4%; Score 17; DB 9; Length 612;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGACGGTTCTGAGGCG 20
|||||
Db 346 GAGACGGTTCTGAGGCG 362

RESULT 33
CE346969/c
LOCUS
DEFINITION
tigr-gss-dog-17000334140128 Dog Library Canis familiaris genomic,
genomic survey sequence.
CE346969 GI:36177228
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Canis familiaris (dog)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
AUTHORS
Kirkness,E.F., Batna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
22875432
PUBMED
COMMENT
Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.

FEATURES
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/organism="Canis familiaris"
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/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"

ORIGIN
Query Match 35.4%; Score 17; DB 9; Length 627;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGACGGTTCTGAGGCG 20
|||||
Db 220 GAGACGGTTCTGAGGCG 204

RESULT 34
CE689678
LOCUS
DEFINITION
tigr-gss-dog-17000368561594 Dog Library Canis familiaris genomic,
genomic survey sequence.
CE689678 GI:37008748
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Canis familiaris (dog)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
AUTHORS
Kirkness,E.F., Batna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
22875432
PUBMED
COMMENT
Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.

FEATURES
source
1..612
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"

ORIGIN
Query Match 35.4%; Score 17; DB 9; Length 612;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGACGGTTCTGAGGCG 20
|||||
Db 346 GAGACGGTTCTGAGGCG 362

```

The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.

FEATURES

source
1. .649
Location/Qualifiers
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/notes="Site 1: BstXI; Libraries were prepared from
peripheral blood"

ORIGIN

Query Match 35.4%; Score 17; DB 9; Length 649;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGACGGTTCGAGGC 20
|||||
Db 405 GAGACGGTTCGAGGC 421

RESULT 35

AW422619

LOCUS

DEFINITION
AW422619 660 bp mRNA linear EST 09-FEB-2000
IMAGE:2640515 5' similar to SW:BTEL_HUMAN Q13886 TRANSCRIPTION
FACTOR BTEB1 ; mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

DEFINITION
AW422619.1 GI:6950551
EST.
Danio rerio (zebrafish)

REFERENCE

AUTHORS

Sugano, S., Kawakami, K., Johnson, S., Li, F., Marra, M., Eddy, S.,
Hillier, L., Clifton, S., Allen, M., Gibbons, M., Jost, S., Kucaba, T.,
Martin, J., Pape, D., Stepien, M., Underwood, K., Theising, B.,
Ritter, E., Bowers, Y., Wyllie, T., Waterston, R. and Wilson, R.
WashU Zebrafish EST Project 1999
Unpublished (1999)

TITLE

JOURNAL

COMMENT

Contact: S.L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu
Library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami DNA
Sequencing by: Washington University Genome Sequencing Center
Seq primer: T3 ET from Amersham
High quality sequence stop: 455.

FEATURES

source

1. .660
Location/Qualifiers
/organism="Danio rerio"
/mol_type="mRNA"
/strain="AB"
/db_xref="taxon:7955"
/clone_lib="IMAGE:2640515"
/sex="mixed (one male and one female, including
unfertilized eggs)"
/dev_stage="adult"

/lab_host="DH10B (phage resistant)"

/clone_lib="Sugano Kawakami zebrafish DRA"

/notes="Vector: PME188-FL3; Site_1: DraIII (CACTGTGTC);

Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed

with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTT];

double-stranded cDNA was ligated to a DraIII adaptor
[TGTGGCTACTGG], digested and cloned into distinct DraIII
sites of the pME188-FL3 vector (5' site CACTGTGTC, 3' site
CACCATGTG). XhoI should be used to isolate the cDNA
insert. Size selection was performed to exclude fragments
<1.5kb. Library constructed by Dr. Sumio Sugano
(University of Tokyo Institute of Medical Science) and
kindly donated by Dr. Koichi Kawakami. Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGG and 3' end
primer CGACCTGCAGCTCGACACA. "

ORIGIN

Query Match 35.4%; Score 17; DB 2; Length 660;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 ATGGATCACTTCGAGC 41
|||||

Db 226 ATGGATCACTTCGAGC 242
|||||

RESULT 36

CE844747

LOCUS

DEFINITION
CE844747 668 bp DNA linear GSS 01-OCT-2003
tigr-gss-dog-17000332719174 Dog Library Canis familiaris genomic,
genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

DEFINITION
CE844747.1 GI:37207016
GSS.
Canis familiaris (dog)

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
22875432
14512627
Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.

FEATURES

source

1. .668
Location/Qualifiers
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"

ORIGIN

Query Match 35.4%; Score 17; DB 9; Length 668;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGACGGTTCGAGGC 20
|||||

Db 428 GAGACGGTTCGAGGC 444
|||||

RESULT 37

BH014887/c

LOCUS

DEFINITION

BH014887 672 bp DNA linear GSS 18-MAY-2001
TDGBR95TH cTOG Lycopersicon esculentum genomic clone cTOG11P22,

```

genomic survey sequence.
BH014887
VERSION BH014887.1 GI:14145925
KEYWORDS GSS.
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE 1 (bases 1 to 672)
AUTHORS van der Hoeven,R., Sun,H., Cho,J., Utterback,T., Ronning,C. and
Tanksley,S.
TITLE Tomato Demethylated Genomic DNA Sequences
JOURNAL Unpublished (2001)
COMMENT Contact: CUGI
Clemson University
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
tomato demethylated genomic DNA
Seq primer: M13F-R
Class: shotgun.
Location/Qualifiers
source 1..672
/organism="Lycopersicon esculentum"
/mol_type="genomic DNA"
/cultivar="E6203"
/db_xref="taxon:4081"
/clone="cTOG11P22"
/tissue_type="young leaves"
/dev_stage="12-14 weeks post harvest"
/lab_host="E.coli JM109"
/clone_lib="cTOG"
/notes="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; This library was made from short EcoRI digested
fragments of the genome of Lycopersicon esculentum ligated
into pBS (SK-). The fragments were cloned into the
methylation restrictive E.coli strain JM109 with the
purpose of enriching the library for non-methylated DNA
fragments. This procedure may enrich the pool of cloned
fragments in JM109 cells for sequences representing
expressed genes. Average insert size 1.27 Kb."

ORIGIN
Query Match 35.4%; Score 17; DB 8; Length 672;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 GGGCTTACATGGATCAC 33
|||||
DB 248 GGGCTTACATGGATCAC 232

RESULT 38
BH012308
LOCUS TDGM74TH cTOG Lycopersicon esculentum genomic clone cTOG2N4,
genomic survey sequence.
DEFINITION BH012308.1 GI:14142497
ACCESSION GSS.
VERSION BH012308
KEYWORDS Lycopersicon esculentum (tomato)
SOURCE Lycopersicon esculentum
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE 1 (bases 1 to 673)
AUTHORS van der Hoeven,R., Sun,H., Cho,J., Utterback,T., Ronning,C. and
Tanksley,S.
TITLE Tomato Demethylated Genomic DNA Sequences
JOURNAL Unpublished (2001)
COMMENT Contact: CUGI
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
tomato demethylated genomic DNA
Insert Length: 1270 Std Error: 0.00
Seq primer: M13F-R
Class: shotgun.
Location/Qualifiers
source 1..673
/organism="Lycopersicon esculentum"
/mol_type="genomic DNA"
/cultivar="E6203"
/db_xref="taxon:4081"
/clone="cTOG32J24"
/tissue_type="young leaves"
/dev_stage="12-14 weeks post harvest"

```

```

Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
tomato demethylated genomic DNA
Seq primer: M13F-R
Class: shotgun.
Location/Qualifiers
source 1..673
/organism="Lycopersicon esculentum"
/mol_type="genomic DNA"
/cultivar="E6203"
/db_xref="taxon:4081"
/clone="cTOG2N4"
/tissue_type="young leaves"
/dev_stage="12-14 weeks post harvest"
/lab_host="E.coli JM109"
/clone_lib="cTOG"
/notes="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; This library was made from short EcoRI digested
fragments of the genome of Lycopersicon esculentum ligated
into pBS (SK-). The fragments were cloned into the
methylation restrictive E.coli strain JM109 with the
purpose of enriching the library for non-methylated DNA
fragments. This procedure may enrich the pool of cloned
fragments in JM109 cells for sequences representing
expressed genes. Average insert size 1.27 Kb."

ORIGIN
Query Match 35.4%; Score 17; DB 8; Length 673;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 GGGCTTACATGGATCAC 33
|||||
DB 420 GGGCTTACATGGATCAC 436

RESULT 39
BH145540
LOCUS TDGEX60TH cTOG Lycopersicon esculentum genomic clone cTOG32J24,
genomic survey sequence.
DEFINITION BH145540.1 GI:15201636
ACCESSION GSS.
VERSION BH145540
KEYWORDS Lycopersicon esculentum (tomato)
SOURCE Lycopersicon esculentum
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE 1 (bases 1 to 673)
AUTHORS van der Hoeven,R., Sun,H., Cho,J., Utterback,T., Ronning,C. and
Tanksley,S.
TITLE Tomato Demethylated Genomic DNA Sequences
JOURNAL Unpublished (2001)
COMMENT Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
tomato demethylated genomic DNA
Insert Length: 1270 Std Error: 0.00
Seq primer: M13F-R
Class: shotgun.
Location/Qualifiers
source 1..673
/organism="Lycopersicon esculentum"
/mol_type="genomic DNA"
/cultivar="E6203"
/db_xref="taxon:4081"
/clone="cTOG32J24"
/tissue_type="young leaves"
/dev_stage="12-14 weeks post harvest"

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/lab host="E.coli JM109"
 /clone lib="ctcg"
 /note="Vector: pbluescript SK(-); Site 1: EcoRI; Site 2:
 XhoI; this library was made from short EcoRI digested
 fragments of the genome of Lycopersicon esculentum ligated
 into pBS (SK-). The fragments were cloned into the
 methylation restrictive E.coli strain JM109 with the
 purpose of enriching the library for non-methylated DNA
 fragments. This procedure may enrich the pool of cloned
 fragments in JM109 cells for sequences representing
 expressed genes. Average insert size 1.27 kb."

ORIGIN

Query Match 35.4%; Score 17; DB 8; Length 673;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 GGGCTTACATGATCAC 33
 Db 419 GGGCTTACATGATCAC 435

RESULT 40

CE552243/c
 LOCUS

DEFINITION tigr-gss-dog-17000312313299 Dog Library Canis familiaris genomic,
 genomic survey sequence.

ACCESSION CE552243

VERSION CE552243.1 GI:36869024

KEYWORDS GSS.

SOURCE Canis familiaris (dog)

ORGANISM Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE

AUTHORS

1 (bases 1 to 689)
 Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
 Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
 Venter,J.C.

TITLE

The dog genome: survey sequencing and comparative analysis

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Kirkness EF
 The Institute for Genomic Research
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
 Rockville, MD 20850, USA
 Tel: 301-838-0200
 Fax: 301-838-0208
 Email: ekirknes@tigr.org
 Class: shotgun.

FEATURES

source

Location/Qualifiers
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 /mol_type="genomic DNA"
 /strain="Standard Poodle"
 /db_xref="taxon:9615"
 /clone_lib="Dog Library"
 /notes="Site 1: BstXI; Libraries were prepared from
 peripheral blood"

ORIGIN

Query Match 35.4%; Score 17; DB 9; Length 689;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAGACGGTCTGAGGCG 20
 Db 360 GAGACGGTCTGAGGCG 344

RESULT 41

CE667057/c

LOCUS

CE667057 709 bp DNA linear GSS 29-SEP-2003

DEFINITION

tigr-gss-dog-17000313695737 Dog Library Canis familiaris genomic,
 genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Canis familiaris (dog)
 Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE

AUTHORS

1 (bases 1 to 709)
 Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
 Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
 Venter,J.C.

TITLE

The dog genome: survey sequencing and comparative analysis

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Kirkness EF
 The Institute for Genomic Research
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
 Rockville, MD 20850, USA
 Tel: 301-838-0200
 Fax: 301-838-0208
 Email: ekirknes@tigr.org
 Class: shotgun.

FEATURES

source

Location/Qualifiers
 1..709
 /organism="Canis familiaris"
 /mol_type="genomic DNA"
 /strain="Standard Poodle"
 /db_xref="taxon:9615"
 /clone_lib="Dog Library"
 /note="Site 1: BstXI; Libraries were prepared from
 peripheral blood"

ORIGIN

Query Match 35.4%; Score 17; DB 9; Length 709;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAGACGGTCTGAGGCG 20

Db 330 GAGACGGTCTGAGGCG 314

RESULT 42

CE322509/c

LOCUS

DEFINITION

tigr-gss-dog-17000360493114 Dog Library Canis familiaris genomic,
 genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Canis familiaris (dog)
 Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE

AUTHORS

1 (bases 1 to 712)
 Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
 Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
 Venter,J.C.

TITLE

The dog genome: survey sequencing and comparative analysis

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Kirkness EF
 The Institute for Genomic Research
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
 Rockville, MD 20850, USA
 Tel: 301-838-0200
 Fax: 301-838-0208
 Email: ekirknes@tigr.org
 Class: shotgun.

FEATURES	source	Location/Qualifiers	1. .712 /organism="Canis familiaris" /mol_type="genomic DNA" /strain="Standard Poodle" /db_xref="taxon:9615" /clone_lib="Dog Library" /note="Site_1: BstXI; Libraries were prepared from peripheral blood"
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Qy	4	GAGACGGTTCTGAGGCG 20 	
Db	314	GAGACGGTTCTGAGGCG 298	
RESULT 43			
AG300452			
LOCUS			
DEFINITION		AG300452 716 bp DNA linear GSS 02-JUN-2004	
ACCESSION		Mus musculus molossinus DNA, clone:MSMg01-079F15.TJ, genomic survey	
VERSION		sequence.	
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS		Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.	
TITLE		BAC end Sequences of Library MSMg01	
JOURNAL		Unpublished	
AUTHORS			
TITLE			
JOURNAL			
COMMENT		1-7-22 Suehiro-choi,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@sec.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170) Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institute, Bio Resource Center. The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199 e-mail: abe@rtc.riken.jp PRIMERS Sequencing : TJ Library : pBACe3.6 Vector : pBACe3.6 R.Site 1 : EcoRI R.Site 2 : EcoRI.	
FEATURES	source	Location/Qualifiers 1. .716 /organism="Mus musculus molossinus" /mol_type="genomic DNA" /sub_species="molossinus" /db_xref="taxon:57486" /clone="MSMg01-079F15.TJ" /sex="male" /tissue_type="mixture of kidney and spleen" /clone_lib="MSMg01 Mouse Male BAC Library"	
ORIGIN		Query Match 35.4%; Score 17; DB 9; Length 716; Best Local Similarity 100.0%; Pred. No. 43; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	4	GAGACGGTTCTGAGGCG 20 	
Db	314	GAGACGGTTCTGAGGCG 298	
RESULT 43			
AG300452			
LOCUS			
DEFINITION		AG300452 716 bp DNA linear GSS 02-JUN-2004	
ACCESSION		Mus musculus molossinus DNA, clone:MSMg01-079F15.TJ, genomic survey	
VERSION		sequence.	
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS		Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.	
TITLE		BAC end Sequences of Library MSMg01	
JOURNAL		Unpublished	
AUTHORS			
TITLE			
JOURNAL			
COMMENT		1-7-22 Suehiro-choi,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@sec.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170) Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institute, Bio Resource Center. The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199 e-mail: abe@rtc.riken.jp PRIMERS Sequencing : TJ Library : pBACe3.6 Vector : pBACe3.6 R.Site 1 : EcoRI R.Site 2 : EcoRI.	
FEATURES	source	Location/Qualifiers 1. .716 /organism="Mus musculus molossinus" /mol_type="genomic DNA" /sub_species="molossinus" /db_xref="taxon:57486" /clone="MSMg01-079F15.TJ" /sex="male" /tissue_type="mixture of kidney and spleen" /clone_lib="MSMg01 Mouse Male BAC Library"	
ORIGIN		Query Match 35.4%; Score 17; DB 9; Length 716; Best Local Similarity 100.0%; Pred. No. 43; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	4	GAGACGGTTCTGAGGCG 20 	
Db	314	GAGACGGTTCTGAGGCG 298	
RESULT 43			
AG300452			
LOCUS			
DEFINITION		AG300452 716 bp DNA linear GSS 02-JUN-2004	
ACCESSION		Mus musculus molossinus DNA, clone:MSMg01-079F15.TJ, genomic survey	
VERSION		sequence.	
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS		Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.	
TITLE		BAC end Sequences of Library MSMg01	
JOURNAL		Unpublished	
AUTHORS			
TITLE			
JOURNAL			
COMMENT		1-7-22 Suehiro-choi,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@sec.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170) Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institute, Bio Resource Center. The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199 e-mail: abe@rtc.riken.jp PRIMERS Sequencing : TJ Library : pBACe3.6 Vector : pBACe3.6 R.Site 1 : EcoRI R.Site 2 : EcoRI.	
FEATURES	source	Location/Qualifiers 1. .716 /organism="Mus musculus molossinus" /mol_type="genomic DNA" /sub_species="molossinus" /db_xref="taxon:57486" /clone="MSMg01-079F15.TJ" /sex="male" /tissue_type="mixture of kidney and spleen" /clone_lib="MSMg01 Mouse Male BAC Library"	
ORIGIN		Query Match 35.4%; Score 17; DB 9; Length 716; Best Local Similarity 100.0%; Pred. No. 43; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	4	GAGACGGTTCTGAGGCG 20 	
Db	314	GAGACGGTTCTGAGGCG 298	
RESULT 43			
AG300452			
LOCUS			
DEFINITION		AG300452 716 bp DNA linear GSS 02-JUN-2004	
ACCESSION		Mus musculus molossinus DNA, clone:MSMg01-079F15.TJ, genomic survey	
VERSION		sequence.	
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS		Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.	
TITLE		BAC end Sequences of Library MSMg01	
JOURNAL		Unpublished	
AUTHORS			
TITLE			
JOURNAL			
COMMENT		1-7-22 Suehiro-choi,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@sec.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170) Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institute, Bio Resource Center. The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199 e-mail: abe@rtc.riken.jp PRIMERS Sequencing : TJ Library : pBACe3.6 Vector : pBACe3.6 R.Site 1 : EcoRI R.Site 2 : EcoRI.	
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 sequence.
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 VERSION BU466018.1 GI:25959595
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 1 (bases 1 to 816)
 REFERENCE Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
 Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
 A Comprehensive Collection of Chicken cDNAs
 Curr. Biol. 12 (22), 1965-1969 (2002)
 22335534
 MEDLINE PUBMED
 COMMENT 12445392
 CONTACT: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology
 (UMIST)
 PO Box 88, Manchester, M60 1QD, UK
 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.

FEATURES
 source
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 /dev_stage="adult"
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 /clone_lib="CSEQBN20"

NOTE: Vector: pBluescript II KS(+); Site_1: EcoRI;
 Site_2: NotI; This normalized library was constructed from
 1 million independent clones. cDNA synthesis was initiated
 using an oligo(dT) primer, using methylated C in the first
 strand synthesis reaction. Following this first strand
 reaction, double-stranded cDNA was blunted, ligated to
 NotI adapters, digested with EcoRI, size-selected, and
 cloned into the NotI and EcoRI compatible sites of a
 custom modified MCS of the pBluescript (KS+) vector. The
 library was normalized in 2 rounds using conditions
 adapted from Soares et al., PNAS (1994) 91: 9228-9232 and
 Bonaldo et al., Genome Research 6 (1996): 791, except that
 a significantly longer reannealing hybridization was
 used."

ORIGIN

Query Match 35.4%; Score 17; DB 5; Length 816;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TTCTGAGGGCTTACATG 27
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 DB 551 TTCTGAGGGCTTACATG 535

RESULT 46
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 5', mRNA sequence.
 ACCESSION CF549567
 VERSION CF549567.1 GI:34886399
 KEYWORDS EST.
 SOURCE Danio rerio (zebrafish)

ORGANISM

Danio rerio
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Danio.
 1 (bases 1 to 816)
 REFERENCE NIH-MGC http://mgi.nci.nih.gov/.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL
 COMMENT Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgabs-remail.nih.gov
 Tissue Procurement: John Ngai, Univ of CA, Berkeley
 cDNA Library Prepared by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
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 High quality sequence stop: 706.

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ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 ATGGATCACTTCGCAGC 41
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 DB 307 ATGGATCACTTCGCAGC 323

RESULT 47

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 sequence.
 ACCESSION BU467348
 VERSION BU467348.1 GI:25960925
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 1 (bases 1 to 821)
 REFERENCE Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
 Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
 A Comprehensive Collection of Chicken cDNAs
 Curr. Biol. 12 (22), 1965-1969 (2002)
 22335534
 MEDLINE PUBMED
 COMMENT 12445392

Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology
 (UMIST)
 PO Box 88, Manchester, M60 1QD, UK
 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.
 Location/Qualifiers

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ORIGIN
Query Match 35.4%; Score 17; DB 5; Length 821;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TTCTGAGGGCTTACATG 27
|||||
Db 555 TTCTGAGGGCTTACATG 539

RESULT 48
BU467944/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
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/sex="Male and female"

FEATURES
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/sex="Male and female"

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/tissue_type="Chondrocytes isolated from growth plate cartilage"
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ORIGIN
Query Match 35.4%; Score 17; DB 5; Length 825;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 555 TTCTGAGGGCTTACATG 540

RESULT 49
CR241446
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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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/db_xref="taxon:10090"
/clone="MHPN290f03"
/clone_lib="MHPN"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 63 TGAGGGCTTACATGGAT 79

RESULT 50
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LOCUS
DEFINITION
ACCESSION

CN511377
AGENCOURT_22408468 NIH_ZGC_9 Danio rerio cDNA clone IMAGE:7275760
5', mRNA sequence.
CN511377

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VERSION CN511377.1 GI:46824001
 KEYWORDS EST.
 SOURCE Danio rerio (zebrafish)
 ORGANISM Danio rerio
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Danio.
 1 (bases 1 to 896)
 NIH-MGC <http://mgi.nci.nih.gov/>
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Chi-Bin Chien
 cDNA Library Preparation: Dr. Sumio Sugano
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LAM5266 row: n column: 14
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 High quality sequence stop: 738.
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 [GCGGCTGAAGACGGCTATGTGGCTTTTTTTTTTTTTTTT];
 double-stranded cDNA was ligated to a DralII adaptor
 [GGCCUACUGG], digested and directionally cloned into
 distinct DralII sites of the pME18S-FL3. Library was size
 selected for 1.0 kb, with an average insert size of ~1.2kb,
 and is not amplified. Library constructed by Yutaka Suzuki
 (University of Tokyo Institute of Medical Science). Custom
 primers recommended for sequencing: 5' end primer
 5'-GGATGTTGCTTTACTTCTA-3' and 3' end primer
 5'-CGACCTGCAGTCGACACA-3'. Note: This is a Zebrafish Gene
 Collection (ZGC) library"

ORIGIN

Query Match 35.4%; Score 17; DB 7; Length 896;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 |||||
 Db 592 ATGGATCACTTCGCAGC 576

Search completed: March 25, 2005, 09:07:03
 Job time : 1975.92 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 25, 2005, 07:32:14 ; Search time 83.2405 Seconds
(without alignments)
943.546 Million cell updates/sec

Title: US-10-688-489-73

Perfect score: 48

Sequence: 1 tccgagacgttctgagggc.....atcacttcgcagctttgttc 48

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 81813359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : Issued Patents NA.*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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C 4	15	31.2	601	4	US-09-949-016-88595
C 5	15	31.2	726	4	US-09-252-991A-6538
C 6	15	31.2	1027	2	US-08-867-087B-54
C 7	15	31.2	1521	4	US-09-252-991A-6495
C 8	15	31.2	5319	2	US-08-861-464-7
C 9	15	31.2	5319	2	US-08-396-001-7
C 10	15	31.2	5319	3	US-09-323-433A-7
C 11	15	31.2	5319	4	US-09-826-752-7
C 12	15	31.2	73853	4	US-09-949-016-12029
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C 95	13	27.1	20	2	US-08-854-727-29	Sequence 29, Appl
C 96	13	27.1	20	2	US-08-663-230-13	Sequence 13, Appl
C 97	13	27.1	20	3	US-09-038-637-9	Sequence 9, Appl
C 98	13	27.1	20	3	US-09-038-637-41	Sequence 41, Appl
C 99	13	27.1	20	3	US-08-968-733-9	Sequence 9, Appl
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101	13	27.1	20	4	US-09-164-764-9	Sequence 9, Appli	174	13	27.1	862	3	US-09-221-017B-245	Sequence 245, App
102	13	27.1	20	4	US-09-164-764-29	Sequence 29, Appli	c 175	13	27.1	868	1	US-07-885-970A-16	Sequence 16, Appl
103	13	27.1	20	4	US-08-734-011-1	Sequence 1, Appli	c 176	13	27.1	868	1	US-08-298-687A-16	Sequence 16, Appl
104	13	27.1	20	4	US-09-948-909-9	Sequence 9, Appli	c 177	13	27.1	868	1	US-08-530-797-17	Sequence 17, Appl
105	13	27.1	20	4	US-09-948-909-41	Sequence 41, Appli	c 178	13	27.1	868	1	US-08-298-829-16	Sequence 16, Appl
106	13	27.1	20	5	PCT-US95-11233-9	Sequence 9, Appli	c 179	13	27.1	868	2	US-08-787-335-17	Sequence 17, Appl
107	13	27.1	20	5	PCT-US95-11233-29	Sequence 29, Appli	c 180	13	27.1	882	4	US-09-270-767-25620	Sequence 25620, A
108	13	27.1	32	3	US-07-751-891B-22	Sequence 22, Appli	181	13	27.1	993	4	US-09-671-317-3	Sequence 3, Appli
109	13	27.1	149	4	US-09-270-767-26785	Sequence 26785, A	182	13	27.1	999	4	US-09-671-317-2	Sequence 2, Appli
110	13	27.1	186	4	US-09-328-352-1954	Sequence 1954, Ap	183	13	27.1	1101	1	US-08-525-505A-1	Sequence 1, Appli
111	13	27.1	231	4	US-09-489-039A-4117	Sequence 4117, Ap	c 184	13	27.1	1145	3	US-09-227-794-1	Sequence 1, Appli
112	13	27.1	300	4	US-09-489-039A-299	Sequence 299, App	c 185	13	27.1	1176	4	US-09-252-991A-1650	Sequence 1, Appli
113	13	27.1	304	4	US-09-313-294A-6596	Sequence 6596, Ap	c 186	13	27.1	1184	4	US-09-270-767-11242	Sequence 11242, A
114	13	27.1	313	4	US-09-513-999C-13692	Sequence 13692, A	c 187	13	27.1	1286	4	US-09-252-991A-1524	Sequence 1524, Ap
115	13	27.1	315	4	US-09-893-737-63	Sequence 63, Appli	c 188	13	27.1	1315	4	US-09-949-016-2088	Sequence 2088, Ap
116	13	27.1	363	4	US-09-513-999C-12251	Sequence 12251, A	c 189	13	27.1	1324	2	US-08-330-272-1	Sequence 1, Appli
117	13	27.1	393	4	US-09-711-164-149	Sequence 149, App	c 190	13	27.1	1324	5	PCT-US95-13663-1	Sequence 1, Appli
118	13	27.1	393	4	US-09-492-709A-158	Sequence 158, App	c 191	13	27.1	1368	4	US-09-620-312D-871	Sequence 871, App
119	13	27.1	399	4	US-09-328-352-2131	Sequence 2131, App	c 192	13	27.1	1374	4	US-09-328-352-690	Sequence 690, App
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121	13	27.1	404	4	US-09-640-211A-1983	Sequence 1983, Ap	c 194	13	27.1	1581	4	US-09-949-016-243	Sequence 243, App
122	13	27.1	440	4	US-09-621-976-1208	Sequence 1208, Ap	c 195	13	27.1	1581	4	US-09-949-016-243	Sequence 243, App
123	13	27.1	457	4	US-09-621-976-1208	Sequence 1208, Ap	c 196	13	27.1	1581	4	US-09-949-016-243	Sequence 243, App
124	13	27.1	471	4	US-09-902-540-9068	Sequence 13809, A	c 197	13	27.1	1611	4	US-09-808-701A-13	Sequence 1165, Ap
125	13	27.1	480	4	US-09-902-540-9068	Sequence 13809, A	c 198	13	27.1	1611	4	US-09-808-701A-13	Sequence 1165, Ap
126	13	27.1	486	4	US-09-621-976-1208	Sequence 1571, Ap	c 199	13	27.1	1697	4	US-09-270-767-10255	Sequence 10255, A
127	13	27.1	487	4	US-09-621-976-1208	Sequence 1209, Ap	c 200	13	27.1	1760	4	US-09-495-050A-139	Sequence 139, App
128	13	27.1	503	4	US-09-621-976-1208	Sequence 10616, A	c 201	13	27.1	1769	1	US-07-792-865D-3	Sequence 3, Appli
129	13	27.1	516	4	US-09-489-039A-5292	Sequence 5292, Ap	c 202	13	27.1	1842	4	US-09-607-248B-2	Sequence 2, Appli
130	13	27.1	519	4	US-09-489-039A-5292	Sequence 17968, A	c 203	13	27.1	1920	3	US-08-817-913-17	Sequence 17, Appl
131	13	27.1	534	3	US-09-134-001C-1645	Sequence 1645, Ap	c 204	13	27.1	1980	4	US-08-248-796A-6828	Sequence 6828, Ap
132	13	27.1	582	4	US-09-252-991A-1450	Sequence 1450, Ap	c 205	13	27.1	2100	4	US-09-919-039A-139	Sequence 139, App
133	13	27.1	601	4	US-09-949-016-22999	Sequence 22999, A	c 206	13	27.1	2115	1	US-08-285-641-19	Sequence 19, Appl
134	13	27.1	601	4	US-09-949-016-22999	Sequence 37837, A	c 207	13	27.1	2142	4	US-09-774-528-100	Sequence 100, App
135	13	27.1	601	4	US-09-949-016-22999	Sequence 37837, A	c 208	13	27.1	2163	4	US-09-774-528-99	Sequence 99, Appl
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137	13	27.1	601	4	US-09-949-016-22999	Sequence 41206, A	c 210	13	27.1	2272	4	US-09-949-016-5499	Sequence 5499, Ap
138	13	27.1	601	4	US-09-949-016-22999	Sequence 42170, A	c 211	13	27.1	2272	4	US-09-949-016-5500	Sequence 5500, Ap
139	13	27.1	601	4	US-09-949-016-22999	Sequence 42170, A	c 212	13	27.1	2283	4	US-09-248-796A-4902	Sequence 4902, Ap
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141	13	27.1	601	4	US-09-949-016-22999	Sequence 43515, A	c 214	13	27.1	2460	4	US-09-489-039A-4934	Sequence 4934, Ap
142	13	27.1	601	4	US-09-949-016-22999	Sequence 43744, A	c 215	13	27.1	2460	4	US-09-634-238-4	Sequence 4, Appli
143	13	27.1	601	4	US-09-949-016-22999	Sequence 51717, A	c 216	13	27.1	2658	4	US-09-107-532A-1450	Sequence 1450, Ap
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145	13	27.1	601	4	US-09-949-016-22999	Sequence 76610, A	c 218	13	27.1	2799	3	US-09-536-224-5	Sequence 5, Appli
146	13	27.1	601	4	US-09-949-016-22999	Sequence 76611, A	c 219	13	27.1	2989	6	5378464-1	Patent No. 5378464
147	13	27.1	601	4	US-09-949-016-22999	Sequence 81510, A	c 220	13	27.1	2989	6	5378464-1	Patent No. 5378464
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151	13	27.1	601	4	US-09-949-016-22999	Sequence 88307, A	c 224	13	27.1	3132	4	US-09-252-991A-14540	Sequence 14540, A
152	13	27.1	601	4	US-09-949-016-22999	Sequence 88308, A	c 225	13	27.1	3142	1	US-08-110-158-3	Sequence 3, Appli
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156	13	27.1	601	4	US-09-949-016-22999	Sequence 129085, A	c 229	13	27.1	3198	4	US-09-949-016-4400	Sequence 4400, Ap
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158	13	27.1	601	4	US-09-949-016-22999	Sequence 157731, A	c 231	13	27.1	3400	4	US-09-793-372-1	Sequence 1, Appli
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161	13	27.1	601	4	US-09-949-016-22999	Sequence 171867, A	c 234	13	27.1	3495	4	US-09-976-594-470	Sequence 470, App
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163	13	27.1	601	4	US-09-949-016-22999	Sequence 195080, A	c 236	13	27.1	3559	2	US-08-211-312-1	Sequence 1, Appli
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165	13	27.1	601	4	US-09-949-016-22999	Sequence 201646, A	c 238	13	27.1	3559	3	US-08-472-285-1	Sequence 1, Appli
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168	13	27.1	666	4	US-09-107-433-1248	Sequence 15, Appli	c 241	13	27.1	3715	3	US-09-041-886-10	Sequence 10, Appl
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C 252	13	27.1	4922	5	PCT-US95-13663-5	Sequence 5, Appli	C 325	13	27.1	45323	4	US-09-949-016-16142	Sequence 16142, A
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C 254	13	27.1	5201	4	US-09-640-882-2	Sequence 2, Appli	C 327	13	27.1	59479	4	US-09-949-016-16910	Sequence 16910, A
C 255	13	27.1	5201	4	US-09-640-882-3	Sequence 3, Appli	C 328	13	27.1	65745	4	US-09-949-016-12591	Sequence 12591, A
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C 257	13	27.1	5670	4	US-09-630-931A-14	Sequence 14, Appli	C 330	13	27.1	65524	4	US-09-949-001-32	Sequence 32, Appli
C 258	13	27.1	5677	1	US-07-623-953A-11	Sequence 11, Appli	C 331	13	27.1	65525	4	US-09-949-001-38	Sequence 38, Appli
C 259	13	27.1	5826	4	US-09-630-931A-11	Sequence 11, Appli	C 332	13	27.1	80632	4	US-09-949-016-12951	Sequence 12951, A
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C 261	13	27.1	5838	2	US-08-850-880-3	Sequence 3, Appli	C 334	13	27.1	86213	4	US-09-949-016-17241	Sequence 17241, A
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C 263	13	27.1	5838	2	US-09-272-432A-3	Sequence 3, Appli	C 336	13	27.1	88490	4	US-09-949-016-17243	Sequence 17243, A
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C 265	13	27.1	6071	4	US-09-630-931A-12	Sequence 12, Appli	C 338	13	27.1	88992	4	US-09-949-016-14222	Sequence 14222, A
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C 267	13	27.1	6363	2	US-08-929-967-6	Sequence 6, Appli	C 340	13	27.1	100863	4	US-09-949-016-14389	Sequence 14389, A
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C 306	13	27.1	27617	4	US-09-949-016-17040	Sequence 17040, A	C 379	13	27.1	828152	4	US-09-949-016-12777	Sequence 12777, A
C 307	13	27.1	29905	4	US-09-949-016-16788	Sequence 16788, A	C 380	13	27.1	4403765	3	US-09-103-840A-2	Sequence 2, Appli
C 308	13	27.1	30310	4	US-09-657-346A-96	Sequence 96, Appli	C 381	13	27.1	4411529	3	US-09-103-840A-1	Sequence 1, Appli
C 309	13	27.1	31144	4	US-09-949-016-15993	Sequence 15993, A	C 382	12	25.0	20	4	US-09-193-881-22	Sequence 22, Appli
C 310	13	27.1	33519	4	US-09-949-016-17165	Sequence 17165, A	C 383	12	25.0	22	4	US-08-857-636-19	Sequence 19, Appli
C 311	13	27.1	34628	4	US-09-949-016-12304	Sequence 12304, A	C 384	12	25.0	22	4	US-09-332-5228-65	Sequence 65, Appli
C 312	13	27.1	34628	4	US-09-949-016-12629	Sequence 12629, A	C 385	12	25.0	25	4	US-09-396-196G-58911	Sequence 58911, A
C 313	13	27.1	34658	4	US-09-949-016-12829	Sequence 12829, A	C 386	12	25.0	25	4	US-09-396-196G-122549	Sequence 122549, A
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C 316	13	27.1	40130	4	US-09-964-469-3	Sequence 3, Appli	C 389	12	25.0	30	3	US-08-891-292A-76	Sequence 76, Appli
C 317	13	27.1	41125	4	US-09-949-016-17275	Sequence 17275, A	C 390	12	25.0	30	4	US-09-927-737C-76	Sequence 76, Appli
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C 319	13	27.1	41941	4	US-09-949-016-17380	Sequence 17380, A	C 392	12	25.0	37	5	PCT-US95-02861-4	Sequence 4, Appli

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394 12 25.0 41 5 PCT-US96-10905-34 Sequence 34, Appl
395 12 25.0 45 3 US-09-446-504-42 Sequence 42, Appl
396 12 25.0 45 3 US-09-712-266-42 Sequence 42, Appl
397 12 25.0 45 3 US-09-091-889A-6 Sequence 6, Appl
398 12 25.0 47 4 US-09-671-317-495 Sequence 495, App
399 12 25.0 50 4 US-09-554-329-61 Sequence 61, Appl
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404 12 25.0 63 5 PCT-US93-08364-94 Sequence 94, Appl
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406 12 25.0 124 4 US-08-781-386A-1451 Sequence 1451, App
407 12 25.0 143 3 US-08-469-318-181 Sequence 181, App
408 12 25.0 143 3 US-08-468-609A-181 Sequence 181, App
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410 12 25.0 143 3 US-08-762-227A-181 Sequence 181, App
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415 12 25.0 180 3 US-08-469-318-182 Sequence 182, App
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420 12 25.0 212 3 US-09-008-892-8 Sequence 8, Appl
421 12 25.0 216 4 US-09-107-532A-729 Sequence 729, App
422 12 25.0 242 1 US-08-464-164-3 Sequence 3, Appl
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429 12 25.0 270 4 US-09-313-294A-1213 Sequence 1213, App
430 12 25.0 274 4 US-09-313-294A-3649 Sequence 3649, App
431 12 25.0 279 4 US-09-313-294A-5090 Sequence 5090, App
432 12 25.0 285 4 US-09-489-039A-1749 Sequence 1749, App
433 12 25.0 285 4 US-09-621-976-17225 Sequence 17225, A
434 12 25.0 288 4 US-09-252-991A-15424 Sequence 15424, A
435 12 25.0 292 4 US-09-497-855A-33 Sequence 33, Appl
436 12 25.0 292 4 US-09-513-999C-8327 Sequence 8327, App
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439 12 25.0 312 4 US-09-513-999C-4377 Sequence 4377, A
440 12 25.0 325 4 US-09-722-377-56 Sequence 56, Appl
441 12 25.0 338 3 US-08-928-881-27 Sequence 27, Appl
442 12 25.0 338 3 US-09-543-921-27 Sequence 27, Appl
443 12 25.0 338 4 US-09-491-759-27 Sequence 27, Appl
444 12 25.0 339 4 US-09-270-767-8172 Sequence 8172, App
445 12 25.0 339 4 US-09-270-767-23454 Sequence 23454, A
446 12 25.0 344 4 US-09-651-169A-39 Sequence 39, Appl
447 12 25.0 351 4 US-09-513-999C-97 Sequence 97, Appl
448 12 25.0 357 3 US-09-712-016-69 Sequence 69, Appl
449 12 25.0 357 4 US-08-956-171E-4249 Sequence 4249, App
450 12 25.0 357 4 US-08-781-986A-4249 Sequence 4249, App
451 12 25.0 364 4 US-09-902-540-2117 Sequence 2117, App
452 12 25.0 372 4 US-09-640-211A-343 Sequence 343, App
453 12 25.0 389 4 US-09-621-976-14888 Sequence 14888, A
454 12 25.0 390 2 US-08-494-907-19 Sequence 19, Appl
455 12 25.0 390 5 PCT-US96-10986-19 Sequence 19, Appl
456 12 25.0 400 4 US-09-722-377-55 Sequence 55, Appl
457 12 25.0 413 4 US-09-949-016-65058 Sequence 65058, A
458 12 25.0 416 4 US-09-902-540-1614 Sequence 1614, App
459 12 25.0 417 4 US-09-107-532A-3252 Sequence 3252, App
460 12 25.0 417 4 US-09-489-039A-5287 Sequence 5287, App
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462 12 25.0 421 4 US-09-270-767-11842 Sequence 11842, A
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491 12 25.0 505 4 US-09-270-767-20502 Sequence 20502, A
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493 12 25.0 519 4 US-09-248-796A-7154 Sequence 7154, App
494 12 25.0 520 4 US-09-621-976-12177 Sequence 12177, App
495 12 25.0 527 4 US-09-702-705-1 Sequence 1, Appl
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499 12 25.0 527 4 US-09-589-184-1 Sequence 1, Appl
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ALIGNMENTS

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RESULT 1
US-09-949-016-67727/c
; Sequence 67727, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67727
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-67727
Query Match 31.2%; Score 15; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 22 TACATGATCATTTC 36

Db 601 TACATGATCATTTC 587


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RESULT 2
US-09-949-016-88593
; Sequence 88593, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88593
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-88593

Query Match          31.2%; Score 15; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 TTACATGGATCACTT 35
Db 36 TTACATGGATCACTT 50

RESULT 3
US-09-949-016-88594
; Sequence 88594, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88594
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-88594

Query Match          31.2%; Score 15; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 TTACATGGATCACTT 35
Db 38 TTACATGGATCACTT 52

RESULT 4
US-09-949-016-88595
; Sequence 88595, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88595
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-88595

Query Match          31.2%; Score 15; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 TTACATGGATCACTT 35
Db 562 CATGGATCACTTCGC 548

RESULT 5
US-09-252-991A-6538/c
; Sequence 6538, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6538
; LENGTH: 726
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6538

Query Match          31.2%; Score 15; DB 4; Length 726;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 CATGGATCACTTCGC 38
Db 562 CATGGATCACTTCGC 548

RESULT 6
US-08-867-087B-54
; Sequence 54, Application US/08867087B
; Patent No. 5990386
; GENERAL INFORMATION:
; APPLICANT: An, Gynheung
; TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT
; AND APICAL DOMINANCE IN PLANTS
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
; Winston, LLP
```

STREET: One World Trade Center
STREET: 121 S.W. Salmon Street
STREET: Suite 1600
CITY: Portland
STATE: Oregon
COUNTRY: United States of America
ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,087B
FILING DATE: June 2, 1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/323,449
FILING DATE: October 14, 1994
APPLICATION NUMBER: U.S. 08/485,981
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Alan. E.
REGISTRATION NUMBER: 35,123
REFERENCE/DOCKET NUMBER: 4630-47071
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 base pairs
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
US-08-867-087B-54

Query Match 31.2%; Score 15; DB 2; Length 1027;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GCTTACATGATCAC 33
Db 776 GCTTACATGATCAC 790

RESULT 7
US-09-252-991A-6495
Sequence 6495, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 6495
LENGTH: 1521
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6495

Query Match 31.2%; Score 15; DB 4; Length 1521;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 CATGGATCACTTCGC 38
Db 776 GCTTACATGATCAC 790

Db 1008 CATGGATCACTTCGC 1022

RESULT 8
US-08-861-464-7
Sequence 7, Application US/08861464
Patent No. 5874210
GENERAL INFORMATION:
APPLICANT: Guarente, Leonard P.
APPLICANT: Austriaco Jr., Nicanor
APPLICANT: Kennedy, Brian
TITLE OF INVENTION: Genes Determining Cellular Senescence
TITLE OF INVENTION: in Yeast
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/861,464
FILING DATE: 22-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/396,001
FILING DATE: 28-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09351
FILING DATE: 15-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/107,408
FILING DATE: 16-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-6408A2Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 5319 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 57..3614
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 57..3614
US-08-861-464-7

Query Match 31.2%; Score 15; DB 2; Length 5319;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGTTCGAGGCTTA 23
Db 1008 GGTTCGAGGCTTA 1022

RESULT 9
US-08-396-001-7
Sequence 7, Application US/08396001

; Patent No. 5919618
; GENERAL INFORMATION:
; APPLICANT: Guarente, Leonard P.
; APPLICANT: Austriaco Jr., Nicanor
; APPLICANT: Claus, James
; APPLICANT: Cole, Francesca
; APPLICANT: Kennedy, Brian
; TITLE OF INVENTION: Genes Determining Cellular Senescence in
; TITLE OF INVENTION: Yeast
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/396,001
; FILING DATE: 28-FEB-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: MIT-6408A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5319 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 57..3614
; US-08-396-001-7

Query Match 31.2%; Score 15; DB 2; Length 5319;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGTCTGAGGGCTTA 23
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Db 1008 GGTCTGAGGGCTTA 1022

RESULT 10
US-09-323-433A-7
; Sequence 7, Application US/09323433A
; Patent No. 6218512
; GENERAL INFORMATION:
; APPLICANT: Guarente, Leonard P.
; APPLICANT: Austriaco Jr., Nicanor
; APPLICANT: Claus, James J.
; APPLICANT: Cole, Francesca
; APPLICANT: Kennedy, Brian
; TITLE OF INVENTION: GENES DETERMINING CELLULAR SENESCENCE IN
; TITLE OF INVENTION: YEAST
; FILE REFERENCE: 0050.1491-003
; CURRENT APPLICATION NUMBER: US/09/323,433A
; CURRENT FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: US 08/396,001
; PRIOR FILING DATE: 1995-02-28
; PRIOR APPLICATION NUMBER: PCT/US94/09351
; PRIOR FILING DATE: 1994-08-15

; PRIOR APPLICATION NUMBER: US 08/107,408
; PRIOR FILING DATE: 1993-08-16
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 5319
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (57)...(3614)
; OTHER INFORMATION: D43951
; US-09-323-433A-7

Query Match 31.2%; Score 15; DB 3; Length 5319;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGTCTGAGGGCTTA 23
|||||
Db 1008 GGTCTGAGGGCTTA 1022

RESULT 11
US-09-826-752-7
; Sequence 7, Application US/09826752
; Patent No. 6787300
; GENERAL INFORMATION:
; APPLICANT: Guarente, Leonard P.
; APPLICANT: Austriaco Jr., Nicanor
; APPLICANT: Claus, James J.
; APPLICANT: Cole, Francesca
; APPLICANT: Kennedy, Brian
; TITLE OF INVENTION: GENES DETERMINING CELLULAR SENESCENCE IN
; TITLE OF INVENTION: YEAST
; FILE REFERENCE: 0050.1491-005
; CURRENT APPLICATION NUMBER: US/09/826,752
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 08/396,001
; PRIOR FILING DATE: 1995-02-28
; PRIOR APPLICATION NUMBER: PCT/US94/09351
; PRIOR FILING DATE: 1994-08-15
; PRIOR APPLICATION NUMBER: US 08/107,408
; PRIOR FILING DATE: 1993-08-16
; PRIOR APPLICATION NUMBER: US 09/323,433
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 5319
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (57)...(3614)
; OTHER INFORMATION: D43951
; US-09-826-752-7

Query Match 31.2%; Score 15; DB 4; Length 5319;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGTCTGAGGGCTTA 23
|||||
Db 1008 GGTCTGAGGGCTTA 1022

RESULT 12
US-09-949-016-12029/c
; Sequence 12029, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.

```
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12029
; LENGTH: 73853
; TYPE: DNA
; ORGANISM: Human
;
US-09-949-016-12029

Query Match      31.2%; Score 15; DB 4; Length 73853;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CGGTTCTGAGGGCTT 22
      |||||
Db      1324 CGGTTCTGAGGGCTT 1310

RESULT 13
US-09-949-016-13597/c
; Sequence 13597, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13597
; LENGTH: 98439
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(98439)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13597
```

```
Query Match      31.2%; Score 15; DB 4; Length 98439;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 GGTTCGAGGGCTTA 23
      |||||
Db      5385 GGTTCGAGGGCTTA 5371
```

```
RESULT 14
US-09-949-016-13730
; Sequence 13730, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
```

```
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13730
; LENGTH: 163181
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(163181)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13730
```

```
Query Match      31.2%; Score 15; DB 4; Length 163181;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      22 TACATGGATCACTTC 36
      |||||
Db      111655 TACATGGATCACTTC 111669
```

```
RESULT 15
US-09-949-016-11968/c
; Sequence 11968, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11968
; LENGTH: 174259
; TYPE: DNA
; ORGANISM: Human
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11968
```

```
Query Match      31.2%; Score 15; DB 4; Length 174259;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      21 TTACATGGATCACTT 35
      |||||
Db      36881 TTACATGGATCACTT 36867
```

```
RESULT 16
US-09-949-016-14259/c
; Sequence 14259, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14259
; LENGTH: 174259
; TYPE: DNA
; ORGANISM: Human
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14259
```

FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14259
LENGTH: 174262
TYPE: DNA
ORGANISM: Human
US-09-949-016-14259

Query Match 31.2%; Score 15; DB 4; Length 174262;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 TTACATGGATCACTT 35
DB 36881 TTACATGGATCACTT 36867

RESULT 17
US-09-513-999C-17495/c
Sequence 17495, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 17495
LENGTH: 110
TYPE: DNA
ORGANISM: Homo sapiens
US-09-513-999C-17495

Query Match 29.2%; Score 14; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGGTTCTGAGGCT 21
DB 108 CGGTTCTGAGGCT 95

RESULT 18
US-09-513-999C-18518/c
Sequence 18518, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 18518
LENGTH: 110
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 7
OTHER INFORMATION: s-g or c
US-09-513-999C-18518

Query Match 29.2%; Score 14; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGGTTCTGAGGCT 21
DB 108 CGGTTCTGAGGCT 95

RESULT 19
US-09-016-434-461
Sequence 461, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 461:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PROSNOT16
CLONE: 2231705
US-09-016-434-461

Query Match 29.2%; Score 14; DB 4; Length 255;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY      23 ACATGGATCACTTC 36
      |||||||
Db      154 ACATGGATCACTTC 167

RESULT 20
US-09-270-767-5714
; Sequence 5714, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5714
; LENGTH: 453
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-5714

Query Match      29.2%; Score 14; DB 4; Length 453;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      19 GCTTACATGGATCA 32
      |||||||
Db      347 GCTTACATGGATCA 360

RESULT 21
US-09-270-767-20996
; Sequence 20996, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20996
; LENGTH: 453
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-20996

Query Match      29.2%; Score 14; DB 4; Length 453;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      19 GCTTACATGGATCA 32
      |||||||
Db      347 GCTTACATGGATCA 360

RESULT 22
US-09-016-84794
; Sequence 84794, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; SOFTWARE: FastSeq for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 207012
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
```

```
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84794
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-84794

Query Match      29.2%; Score 14; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      35 TCGCAGCTTTGTTTC 48
      |||||||
Db      466 TCGCAGCTTTGTTTC 479

RESULT 23
US-09-949-016-94216/c
; Sequence 94216, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 94216
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-94216

Query Match      29.2%; Score 14; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 GGTTCGAGGGCTT 22
      |||||||
Db      117 GGTTCGAGGGCTT 104

RESULT 24
US-09-949-016-124634/c
; Sequence 124634, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; SOFTWARE: FastSeq for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 207012
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
```

; SEQ ID NO 124634
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-124634

Query Match 29.2%; Score 14; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 TACATGGATCACTT 35
DB 213 TACATGGATCACTT 200

RESULT 25
US-09-949-016-130860
; Sequence 130860, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 130860
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-130860

Query Match 29.2%; Score 14; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGTCTCTGAGGGCTT 22
DB 135 GGTCTCTGAGGGCTT 148

RESULT 26
US-09-949-016-161379/c
; Sequence 161379, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 161379
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-161379

Query Match 29.2%; Score 14; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GAGGGCTTACATGG 28
DB 452 GAGGGCTTACATGG 439

RESULT 27
US-09-949-016-172387/c
; Sequence 172387, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 172387
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-172387

Query Match 29.2%; Score 14; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 ACATGGATCACTTC 36
DB 129 ACATGGATCACTTC 116

RESULT 28
US-09-489-039A-975/c
; Sequence 975, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 975
; LENGTH: 624
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-975

Query Match 29.2%; Score 14; DB 4; Length 624;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 GGATCACTTCGCAG 40
DB 172 GGATCACTTCGCAG 159

```
RESULT 29
US-09-489-039A-6225/c
; Sequence 6225, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 6225
; LENGTH: 831
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-6225
Query Match      29.2%; Score 14; DB 4; Length 831;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TTCTGAGGGCTTAC 24
Db 609 TTCTGAGGGCTTAC 596

RESULT 30
US-09-489-039A-3317/c
; Sequence 3317, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 3317
; LENGTH: 909
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-3317
Query Match      29.2%; Score 14; DB 4; Length 909;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TTCTGAGGGCTTAC 24
Db 609 TTCTGAGGGCTTAC 596

RESULT 31
US-09-807-757C-5
; Sequence 5, Application US/09807757C
; Patent No. 6825035
; GENERAL INFORMATION:
; APPLICANT: Owens, Gary K.
; APPLICANT: Mack, Christopher
; APPLICANT: Blank, Randall
; APPLICANT: University of Virginia Patent Foundation
; TITLE OF INVENTION: Compositions and Methods for Modulating Expression
; FILE REFERENCE: 021258-000500US
; CURRENT APPLICATION NUMBER: US/09/807,757C
; CURRENT FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: US 60/105,330
```

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; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: WO PCT/US99/24972
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1074
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: smooth muscle alpha-actin (SM alpha-A) gene
; OTHER INFORMATION: 5' promoter region
US-09-807-757C-5
Query Match      29.2%; Score 14; DB 4; Length 1074;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTTCTGAGGGCTTA 23
Db 825 GTTCTGAGGGCTTA 838

RESULT 32
US-09-369-247-23/c
; Sequence 23, Application US/09369247
; Patent No. 6569992
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 44 Human Secreted Proteins
; FILE REFERENCE: P2024P1
; CURRENT APPLICATION NUMBER: US/09/369,247
; CURRENT FILING DATE: 1999-08-05
; EARLIER APPLICATION NUMBER: 60/074,118
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,157
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,137
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,341
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,141
; EARLIER FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 1492
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-369-247-23
Query Match      29.2%; Score 14; DB 4; Length 1492;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGGTTCTGAGGGCT 21
Db 907 CGGTTCTGAGGGCT 894

RESULT 33
US-09-248-796A-2667/c
; Sequence 2667, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
```


; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 2667
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-2667

Query Match 29.2%; Score 14; DB 4; Length 1620;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GCTTACATCGATCA 32
|||||
DB 1399 GCTTACATCGATCA 1386

RESULT 34
US-09-489-039A-5962/c
; Sequence 5962, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 5962
; LENGTH: 1635
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1556)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-489-039A-5962

Query Match 29.2%; Score 14; DB 4; Length 1635;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 GGATCACTTCGCAG 40
|||||
DB 550 GGATCACTTCGCAG 537

RESULT 35
US-09-134-001C-157/c
; Sequence 157, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 157
; LENGTH: 1824
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-157

Query Match 29.2%; Score 14; DB 3; Length 1824;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 TTCGACGCTTTGTT 47
|||||
DB 1763 TTCGACGCTTTGTT 1750

RESULT 36
US-09-949-016-1271
; Sequence 1271, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1271
; LENGTH: 1990
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1271

Query Match 29.2%; Score 14; DB 4; Length 1990;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 ACATGGATCACTTC 36
|||||
DB 841 ACATGGATCACTTC 854

RESULT 37
US-09-221-017B-885
; Sequence 885, Application US/09221017B
; Patent No. 6444799
; GENERAL INFORMATION:
; APPLICANT: Ross, Bruce C.
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
; NUMBER OF SEQUENCES: 1120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/221,017B
; FILING DATE: 23-DEC-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP1182
; FILING DATE: 31-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP1546
; FILING DATE: 30-JAN-1998

```

; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PP2911
; FILING DATE: 09-APR-1998
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU98/01023
; FILING DATE: 10-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: MONROY, Gladys H
; REGISTRATION NUMBER: 32,430
; REFERENCE/DOCKET NUMBER: 27340-20021.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 885:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2165 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: UNKNOWN
; ORIGINAL SOURCE:
; ORGANISM: PORPHYROMONAS GINGIVALIS
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..2165
US-09-221-017B-885

Query Match 29.2%; Score 14; DB 3; Length 2165;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 ACATGGATCACTTC 36
Db 109 ACATGGATCACTTC 122

RESULT 38
US-09-923-684-2
; Sequence 2, Application US/09923684
; Patent No. 6780642
; GENERAL INFORMATION:
; APPLICANT: Narayanan, Ramaswamy
; TITLE OF INVENTION: ASSOCIATION OF SIM2 WITH CANCER
; FILE REFERENCE: 6818-24
; CURRENT APPLICATION NUMBER: US/09/923,684
; CURRENT FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 2859
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-923-684-2

Query Match 29.2%; Score 14; DB 4; Length 2859;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 ATCACTTCGCAGCT 42
Db 189 ATCACTTCGCAGCT 202

RESULT 39
US-09-949-016-3231/c
; Sequence 3231, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PP2911
; FILING DATE: 09-APR-1998
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU98/01023
; FILING DATE: 10-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: MONROY, Gladys H
; REGISTRATION NUMBER: 32,430
; REFERENCE/DOCKET NUMBER: 27340-20021.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 885:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2165 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: UNKNOWN
; ORIGINAL SOURCE:
; ORGANISM: PORPHYROMONAS GINGIVALIS
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..2165
US-09-221-017B-885

Query Match 29.2%; Score 14; DB 3; Length 2165;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 ACATGGATCACTTC 36
Db 109 ACATGGATCACTTC 122

RESULT 38
US-09-923-684-2
; Sequence 2, Application US/09923684
; Patent No. 6780642
; GENERAL INFORMATION:
; APPLICANT: Narayanan, Ramaswamy
; TITLE OF INVENTION: ASSOCIATION OF SIM2 WITH CANCER
; FILE REFERENCE: 6818-24
; CURRENT APPLICATION NUMBER: US/09/923,684
; CURRENT FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 2859
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-923-684-2

Query Match 29.2%; Score 14; DB 4; Length 2859;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 ATCACTTCGCAGCT 42
Db 189 ATCACTTCGCAGCT 202

RESULT 39
US-09-949-016-3231/c
; Sequence 3231, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PP2911
; FILING DATE: 09-APR-1998
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU98/01023
; FILING DATE: 10-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: MONROY, Gladys H
; REGISTRATION NUMBER: 32,430
; REFERENCE/DOCKET NUMBER: 27340-20021.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 885:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2165 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: UNKNOWN
; ORIGINAL SOURCE:
; ORGANISM: PORPHYROMONAS GINGIVALIS
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..2165
US-09-221-017B-885

Query Match 29.2%; Score 14; DB 3; Length 2165;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 ACATGGATCACTTC 36
Db 109 ACATGGATCACTTC 122

RESULT 38
US-09-923-684-2
; Sequence 2, Application US/09923684
; Patent No. 6780642
; GENERAL INFORMATION:
; APPLICANT: Narayanan, Ramaswamy
; TITLE OF INVENTION: ASSOCIATION OF SIM2 WITH CANCER
; FILE REFERENCE: 6818-24
; CURRENT APPLICATION NUMBER: US/09/923,684
; CURRENT FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 3920
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-923-684-1

Query Match 29.2%; Score 14; DB 4; Length 3920;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 ATCACTTCGCAGCT 42
Db 189 ATCACTTCGCAGCT 202

RESULT 41
US-08-630-915A-33/c
; Sequence 33, Application US/08630915A
; Patent No. 6309820
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: HOFFMAN, No. 6309820h
; APPLICANT: KAY, Brian K.
; APPLICANT: FOWLES, Dana M.
; APPLICANT: McCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; NUMBER OF INVENTION: USING SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York

```

; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,915A
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4091 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-630-915A-33

Query Match 29.2%; Score 14; DB 3; Length 4091;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGGTTCTGAGGCT 21
|||||
Db 3288 CGGTTCTGAGGCT 3275

RESULT 42
US-09-879-957-33/c
; Sequence 33, Application US/09879957
; Patent No. 6709821
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; HOFFMAN, No. 6709821h
; KAY, Brian K.
; FOWLKES, Dana M.
; MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; USING SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/879,957
; FILING DATE: 13-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,915
; FILING DATE: 03-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872

; REFERENCE/DOCKET NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4091 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-879-957-33

Query Match 29.2%; Score 14; DB 4; Length 4091;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGGTTCTGAGGCT 21
|||||
Db 3288 CGGTTCTGAGGCT 3275

RESULT 43
US-09-289-368-1/c
; Sequence 1, Application US/09289368
; Patent No. 5998148
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROTUBULE-ASSOCIATED PROTEIN 4 EXPRESSION
; FILE REFERENCE: RTS-0051
; CURRENT APPLICATION NUMBER: US/09/289,368
; CURRENT FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 1
; LENGTH: 5022
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: {91}..(3549)
US-09-289-368-1

Query Match 29.2%; Score 14; DB 2; Length 5022;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TGAGGGCTTACATG 27
|||||
Db 4755 TGAGGGCTTACATG 4742

RESULT 44
US-09-949-016-14973/c
; Sequence 14973, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 14973
; LENGTH: 7620
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-14973

Query Match      29.2%; Score 14; DB 4; Length 7620;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 TTCTGAGGGCTTAC 24
Db      4816 TTCTGAGGGCTTAC 4803

RESULT 45
US-09-949-016-17224/c
; Sequence 17224, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17224
; LENGTH: 8580
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-17224

Query Match      29.2%; Score 14; DB 4; Length 8580;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 GGTCTGAGGGCTT 22
Db      7909 GGTCTGAGGGCTT 7896

RESULT 46
US-09-147-119-5
; Sequence 5, Application US/09147119
; Patent No. 6338844
; GENERAL INFORMATION:
; APPLICANT: KURTH, Ruth
; APPLICANT: BAIER, Michael
; APPLICANT: BANNERT, No. 6338844bert
; APPLICANT: METZNER, Karin
; APPLICANT: WERNER, Albrecht
; TITLE OF INVENTION: GENOMIC NUCLEIC ACIDS, cDNA AND mRNA WHICH
; CODE FOR POLYPEPTIDES WITH IL-16 ACTIVITY, PROCESS FOR THE
; PRODUCTION THEREOF AND THEIR USE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
; STREET: 655 Fifteenth St., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/147,119
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP97/01753
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 196 14 099.4
; FILING DATE: 10-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Wong, King L.
; REGISTRATION NUMBER: 37,500
; REFERENCE/DOCKET NUMBER: P1614-8068
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-5000
; TELEFAX: (202) 638-4810
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9096 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1..338
; FEATURE:
; NAME/KEY: intron
; LOCATION: 339..663
; FEATURE:
; NAME/KEY: exon
; LOCATION: 664..832
; FEATURE:
; NAME/KEY: intron
; LOCATION: 833..2870
; FEATURE:
; NAME/KEY: exon
; LOCATION: 2871..2972
; FEATURE:
; NAME/KEY: intron
; LOCATION: 2973..5224
; FEATURE:
; NAME/KEY: exon
; LOCATION: 5225..5483
; FEATURE:
; NAME/KEY: intron
; LOCATION: 5484..5737
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; Sequence 14295, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
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; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14295

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; Sequence 13013, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
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; PRIOR FILING DATE: 2000-09-08
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; ORGANISM: Human
US-09-949-016-13013

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RESULT 49
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; Sequence 1, Application US/09147119

; Patent No. 6338844
; GENERAL INFORMATION:
; APPLICANT: KURTH, Ruth
; APPLICANT: BAIER, Michael
; APPLICANT: BANNERT, No. 6338844bert
; APPLICANT: METZNER, Karin
; APPLICANT: WERNER, Albrecht
; TITLE OF INVENTION: GENOMIC NUCLEIC ACIDS, CDNA AND mRNA WHICH
; CODE FOR POLYPEPTIDES WITH IL-16 ACTIVITY, PROCESS FOR THE
; PRODUCTION THEREOF AND THEIR USE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
; STREET: 655 Fifteenth St., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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; FILING DATE: HEREWITH
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP97/01753
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 196 14 099.4
; FILING DATE: 10-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Wong, King L.
; REGISTRATION NUMBER: 37,500
; REFERENCE/DOCKET NUMBER: P1614-8068
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-5000
; TELEFAX: (202) 638-4810
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15936 base pairs
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; Sequence 23 Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
;           Gil H. Choi
;           Patrick S. Dillon
;           Craig A. Rosen
;           Steven C. Barash
;           Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
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; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
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; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17310 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-08-956-171E-23

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SUMMARIES

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124	15	31.2	5359	14	US-10-197-666A-139	Sequence 139, App	c 197	14	29.2	981	17	US-10-282-122A-8172	Sequence 8172, Ap
125	15	31.2	5361	17	US-10-379-632-76	Sequence 76, Appl	c 198	14	29.2	992	17	US-10-424-599-22495	Sequence 22495, A
126	15	31.2	5366	17	US-10-379-632-46	Sequence 46, Appl	c 199	14	29.2	1049	17	US-10-282-122A-36482	Sequence 36482, A
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132	15	31.2	5463	17	US-10-379-632-48	Sequence 48, Appl	c 205	14	29.2	1242	17	US-10-282-122A-39677	Sequence 39677, A
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134	15	31.2	5494	17	US-10-379-632-45	Sequence 45, Appl	c 207	14	29.2	1492	14	US-10-062-548-23	Sequence 23, Appl
135	15	31.2	5494	13	US-10-027-632-174763	Sequence 174763, A	c 208	14	29.2	1492	19	US-10-918-446-23	Sequence 23, Appl
136	15	31.2	5494	17	US-10-027-632-174763	Sequence 174763, A	c 209	14	29.2	1508	17	US-10-108-260A-967	Sequence 967, App
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145	14	29.2	5519	9	US-09-969-373-314	Sequence 314, App	c 218	14	29.2	2174	13	US-10-027-632-103226	Sequence 103226, A
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c 237	14	29.2	3303	18	US-10-741-601-266	Sequence 266, App	c 310	13	27.1	20	9	US-09-863-806-9	Sequence 9, Appli
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c 246	14	29.2	3621	14	US-10-198-846-10650	Sequence 10650, A	c 319	13	27.1	25	15	US-10-098-263B-113700	Sequence 41, Appl
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C 401	13	27.1	272	18	US-10-357-930-60637	Sequence 60637, A	C 474	13	27.1	385	9	US-09-954-456-1889	Sequence 430, App
C 402	13	27.1	277	18	US-10-357-930-60414	Sequence 60414, A	C 475	13	27.1	385	9	US-09-880-107-493	Sequence 1889, Ap
C 403	13	27.1	278	18	US-10-357-930-60499	Sequence 60499, A	C 476	13	27.1	385	18	US-10-425-115-8868	Sequence 493, App
C 404	13	27.1	281	18	US-10-357-930-60585	Sequence 60585, A	C 477	13	27.1	386	17	US-10-242-535A-57365	Sequence 8868, Ap
C 405	13	27.1	282	18	US-10-357-930-60551	Sequence 60551, A	C 478	13	27.1	386	17	US-10-085-783A-57365	Sequence 57365, A
C 406	13	27.1	286	18	US-10-357-930-60582	Sequence 60582, A	C 479	13	27.1	389	18	US-10-357-930-10193	Sequence 10193, A
C 407	13	27.1	288	18	US-10-430-201-167	Sequence 167, App	C 480	13	27.1	390	17	US-10-282-122A-37381	Sequence 37381, A
C 408	13	27.1	288	18	US-10-430-201-167	Sequence 167, App	C 481	13	27.1	390	17	US-10-282-122A-37381	Sequence 37381, A
C 409	13	27.1	289	18	US-10-357-930-60690	Sequence 60690, A	C 482	13	27.1	393	9	US-09-741-669-101	Sequence 101, App
C 410	13	27.1	289	17	US-10-424-599-128296	Sequence 128296, A	C 483	13	27.1	393	9	US-09-912-020-158	Sequence 158, App
C 411	13	27.1	291	18	US-10-357-930-60444	Sequence 60444, A	C 484	13	27.1	393	9	US-09-815-242-6248	Sequence 6248, Ap
C 412	13	27.1	291	18	US-10-357-930-60635	Sequence 60635, A	C 485	13	27.1	393	9	US-09-815-242-10006	Sequence 10006, A
C 413	13	27.1	293	17	US-10-282-122A-2305	Sequence 2305, Ap	C 486	13	27.1	393	16	US-10-287-274-149	Sequence 149, App
C 414	13	27.1	295	18	US-10-357-930-60537	Sequence 60537, A	C 487	13	27.1	393	17	US-10-282-122A-6761	Sequence 6761, Ap
C 415	13	27.1	295	18	US-10-357-930-60601	Sequence 60601, A	C 488	13	27.1	393	17	US-10-282-122A-39540	Sequence 39540, A
C 416	13	27.1	296	17	US-10-424-599-108494	Sequence 108494, A	C 489	13	27.1	393	18	US-10-771-241-158	Sequence 158, App
C 417	13	27.1	299	18	US-10-357-930-60576	Sequence 60576, A	C 490	13	27.1	394	18	US-10-357-930-1024	Sequence 1024, Ap
C 418	13	27.1	300	17	US-10-242-535A-19210	Sequence 19210, A	C 491	13	27.1	395	18	US-10-425-115-142258	Sequence 142258, A
C 419	13	27.1	300	17	US-10-085-783A-19210	Sequence 19210, A	C 492	13	27.1	397	9	US-09-960-352-2124	Sequence 2124, Ap
C 420	13	27.1	301	18	US-10-357-930-60532	Sequence 60532, A	C 493	13	27.1	398	18	US-10-674-124A-23252	Sequence 23252, A
C 421	13	27.1	302	18	US-10-357-930-60400	Sequence 60400, A	C 494	13	27.1	398	19	US-10-696-639-634	Sequence 634, App
C 422	13	27.1	303	18	US-10-357-930-60634	Sequence 60634, A	C 495	13	27.1	399	11	US-09-864-408A-3731	Sequence 3731, Ap
C 423	13	27.1	304	17	US-10-282-122A-3360	Sequence 3360, Ap	C 496	13	27.1	400	17	US-10-242-535A-8411	Sequence 8411, Ap
C 424	13	27.1	307	18	US-10-357-930-60493	Sequence 60493, A	C 497	13	27.1	400	17	US-10-085-783A-8411	Sequence 8411, Ap
C 425	13	27.1	307	18	US-10-357-930-60436	Sequence 60436, A	C 498	13	27.1	401	18	US-10-357-930-31391	Sequence 31391, A
C 426	13	27.1	308	18	US-10-357-930-60617	Sequence 60617, A	C 499	13	27.1	404	18	US-10-856-499-1983	Sequence 1983, Ap
C 427	13	27.1	310	17	US-10-242-535A-47698	Sequence 47698, A	C 500	13	27.1	405	10	US-09-814-353-15583	Sequence 15583, A
C 428	13	27.1	310	17	US-10-085-783A-47698	Sequence 47698, A							
C 429	13	27.1	311	18	US-10-357-930-60456	Sequence 60456, A							
C 430	13	27.1	312	17	US-10-424-599-70508	Sequence 70508, A							
C 431	13	27.1	315	9	US-09-893-737-63	Sequence 63, Appl							
C 432	13	27.1	318	18	US-10-357-930-60482	Sequence 60482, A							
C 433	13	27.1	320	18	US-10-357-930-60652	Sequence 60652, A							
C 434	13	27.1	321	17	US-10-282-122A-2152	Sequence 2152, Ap							
C 435	13	27.1	321	17	US-10-282-122A-2717	Sequence 2717, Ap							
C 436	13	27.1	321	18	US-10-021-323-1943	Sequence 1943, Ap							
C 437	13	27.1	324	17	US-10-424-599-110582	Sequence 110582, A							
C 438	13	27.1	324	18	US-10-357-930-60543	Sequence 60543, A							
C 439	13	27.1	324	18	US-10-357-930-60604	Sequence 60604, A							
C 440	13	27.1	327	17	US-10-282-122A-21245	Sequence 21245, A							
C 441	13	27.1	330	10	US-09-814-353-3891	Sequence 3891, Ap							
C 442	13	27.1	330	10	US-09-814-353-10159	Sequence 10159, A							
C 443	13	27.1	331	18	US-10-674-124A-21341	Sequence 21341, A							
C 444	13	27.1	332	9	US-09-974-300-3609	Sequence 3609, Ap							
C 445	13	27.1	332	17	US-10-424-599-132445	Sequence 132445, A							
C 446	13	27.1	333	18	US-10-425-115-64762	Sequence 64762, A							
C 447	13	27.1	337	18	US-10-425-115-1482	Sequence 1482, Ap							
C 448	13	27.1	339	9	US-09-783-590-10122	Sequence 10122, A							
C 449	13	27.1	339	17	US-10-424-599-78272	Sequence 78272, A							

ALIGNMENTS

RESULT 1

US-10-688-489-73
; Sequence 73, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE OF INVENTION: West Nile Virus
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16

; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 73
; LENGTH: 48
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-73

Query Match 100.0%; Score 48; DB 18; Length 48;
Best Local Similarity 100.0%; Pred. No. 5.3e-19;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCTGAGGGCTTACATGGATCACTTCGACGTTTGTC 48
|||||
Db 1 TCCGAGACGGTCTCTGAGGGCTTACATGGATCACTTCGACGTTTGTC 48
|||||

RESULT 2

US-10-688-489-72
; Sequence 72, Application US/10688489
; Publication No. US20040259108A1

GENERAL INFORMATION:

; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; TITLE OF INVENTION: West Nile Virus
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 72
; LENGTH: 70
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-72

Query Match 100.0%; Score 48; DB 18; Length 70;
Best Local Similarity 100.0%; Pred. No. 5.2e-19;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCTGAGGGCTTACATGGATCACTTCGACGTTTGTC 48
|||||
Db 1 TCCGAGACGGTCTCTGAGGGCTTACATGGATCACTTCGACGTTTGTC 48
|||||

RESULT 3

US-10-815-480-71/c
; Sequence 71, Application US/10815480
; Publication No. US20040229261A1

GENERAL INFORMATION:

; APPLICANT: Young, Karen K. Y.
; APPLICANT: Roche Molecular Systems, Inc.
; TITLE OF INVENTION: Compositions and Methods for Detecting Certain
; TITLE OF INVENTION: Flaviviruses, Including Members of the Japanese
; TITLE OF INVENTION: Encephalitis Virus Serogroup
; FILE REFERENCE: 022101-000230US
; CURRENT APPLICATION NUMBER: US/10/815,480
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US 60/459,491

; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/552,454
; PRIOR FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: US 60/555,530
; PRIOR FILING DATE: 2004-03-22
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 71
; LENGTH: 98
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: region of
; OTHER INFORMATION: conserved sequence in 3' untranslated region of
; OTHER INFORMATION: the genome of flavivirus AF196835
US-10-815-480-71

Query Match 79.2%; Score 38; DB 18; Length 98;
Best Local Similarity 100.0%; Pred. No. 6.1e-13;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCTGAGGGCTTACATGGATCACTTCGC 38
|||||
Db 68 TCCGAGACGGTCTCTGAGGGCTTACATGGATCACTTCGC 31
|||||

RESULT 4

US-10-361-002-5/c
; Sequence 5, Application US/10361002
; Publication No. US20040170954A1

GENERAL INFORMATION:

; APPLICANT: Clearant, Inc.
; APPLICANT: McKenney, Keith
; APPLICANT: Gillmeister, Lidja
; APPLICANT: Marlowe, Kristina
; APPLICANT: Armistead, David
; TITLE OF INVENTION: Pathogen Inactivation Assay
; FILE REFERENCE: CI-0043
; CURRENT APPLICATION NUMBER: US/10/361,002
; CURRENT FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 10945
; TYPE: DNA
; ORGANISM: West Nile virus
US-10-361-002-5

Query Match 79.2%; Score 38; DB 18; Length 10945;
Best Local Similarity 100.0%; Pred. No. 5.1e-13;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCTGAGGGCTTACATGGATCACTTCGC 38
|||||
Db 10587 TCCGAGACGGTCTCTGAGGGCTTACATGGATCACTTCGC 10550
|||||

RESULT 5

US-10-361-004-5/c
; Sequence 5, Application US/10361004
; Publication No. US20040170981A1

GENERAL INFORMATION:

; APPLICANT: Clearant, Inc.
; APPLICANT: McKenney, Keith
; APPLICANT: Gillmeister, Lidja
; APPLICANT: Marlowe, Kristina
; APPLICANT: Armistead, David
; TITLE OF INVENTION: Real-time Polymerase Chain Reaction Using Large Target Amplicons
; FILE REFERENCE: CI-0042
; CURRENT APPLICATION NUMBER: US/10/361,004
; CURRENT FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.2

<pre>; SEQ ID NO 5 ; LENGTH: 10945 ; TYPE: DNA ; ORGANISM: West Nile virus US-10-361-004-5 Query Match 79.2%; Score 38; DB 18; Length 10945; Best Local Similarity 100.0%; Pred. No. 5.1e-13; Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 TCCGAGACGGTTCTGAGGCGTTACATGGATCACTTCGC 38 Db 10587 TCCGAGACGGTTCTGAGGCGTTACATGGATCACTTCGC 10550</pre>	<pre>RESULT 6 US-10-699-550-1/c ; Sequence 1, Application US/10699550 ; Publication No. US20040197769A1 ; GENERAL INFORMATION: ; APPLICANT: WONG, SUSAN J. ; TITLE OF INVENTION: DIAGNOSTIC TEST FOR WEST NILE VIRUS ; FILE REFERENCE: 454311-2232.1 ; CURRENT APPLICATION NUMBER: US/10/699,550 ; PRIOR FILING DATE: 2003-10-31 ; PRIOR APPLICATION NUMBER: 60/476,513 ; PRIOR FILING DATE: 2003-06-06 ; PRIOR APPLICATION NUMBER: 60/422,755 ; PRIOR FILING DATE: 2002-10-31 ; PRIOR APPLICATION NUMBER: PCT/US02/09036 ; PRIOR FILING DATE: 2002-03-11 ; PRIOR APPLICATION NUMBER: 60/402,860 ; PRIOR FILING DATE: 2002-08-08 ; PRIOR APPLICATION NUMBER: 60/281,947 ; PRIOR FILING DATE: 2001-04-05 ; PRIOR APPLICATION NUMBER: 60/275,025 ; PRIOR FILING DATE: 2001-03-12 ; NUMBER OF SEQ ID NOS: 20 ; SOFTWARE: PatentIn Ver. 3.2 ; SEQ ID NO 1 ; LENGTH: 10975 ; TYPE: DNA ; ORGANISM: West Nile virus US-10-699-550-1</pre>	<pre>Query Match 79.2%; Score 38; DB 18; Length 10975; Best Local Similarity 100.0%; Pred. No. 5.1e-13; Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 TCCGAGACGGTTCTGAGGCGTTACATGGATCACTTCGC 38 Db 10611 TCCGAGACGGTTCTGAGGCGTTACATGGATCACTTCGC 10574</pre>	<pre>RESULT 7 US-10-699-550-2/c ; Sequence 2, Application US/10699550 ; Publication No. US20040197769A1 ; GENERAL INFORMATION: ; APPLICANT: WONG, SUSAN J. ; TITLE OF INVENTION: DIAGNOSTIC TEST FOR WEST NILE VIRUS ; FILE REFERENCE: 454311-2232.1 ; CURRENT APPLICATION NUMBER: US/10/699,550 ; PRIOR FILING DATE: 2003-10-31 ; PRIOR APPLICATION NUMBER: 60/476,513 ; PRIOR FILING DATE: 2003-06-06 ; PRIOR APPLICATION NUMBER: 60/422,755 ; PRIOR FILING DATE: 2002-10-31 ; PRIOR APPLICATION NUMBER: PCT/US02/09036 ; PRIOR FILING DATE: 2002-03-11 ; PRIOR APPLICATION NUMBER: 60/402,860</pre>
<pre>; PRIOR FILING DATE: 2002-08-08 ; PRIOR APPLICATION NUMBER: 60/281,947 ; PRIOR FILING DATE: 2001-04-05 ; PRIOR APPLICATION NUMBER: 60/275,025 ; PRIOR FILING DATE: 2001-03-12 ; NUMBER OF SEQ ID NOS: 20 ; SOFTWARE: PatentIn Ver. 3.2 ; SEQ ID NO 2 ; LENGTH: 11029 ; TYPE: DNA ; ORGANISM: West Nile virus US-10-699-550-2 Query Match 79.2%; Score 38; DB 18; Length 11029; Best Local Similarity 100.0%; Pred. No. 5.1e-13; Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 TCCGAGACGGTTCTGAGGCGTTACATGGATCACTTCGC 38 Db 10629 TCCGAGACGGTTCTGAGGCGTTACATGGATCACTTCGC 10592</pre>	<pre>RESULT 8 US-10-679-520A-66/c ; Sequence 66, Application US/10679520A ; Publication No. US20050031641A1 ; GENERAL INFORMATION: ; APPLICANT: LOOSMORE, SHEENA MAY ; APPLICANT: AUDONNET, JEAN-CHRISTOPHE FRANCIS ; APPLICANT: MINKE, JULES MAERTEN ; TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST WEST NILE VIRUS ; FILE REFERENCE: 574313-3161.4 ; CURRENT APPLICATION NUMBER: US/10/679,520A ; CURRENT FILING DATE: 2003-10-06 ; PRIOR APPLICATION NUMBER: 10/374,953 ; PRIOR FILING DATE: 2003-02-26 ; PRIOR APPLICATION NUMBER: 10/116,298 ; PRIOR FILING DATE: 2002-04-04 ; PRIOR APPLICATION NUMBER: 60/281,923 ; PRIOR FILING DATE: 2001-04-06 ; PRIOR APPLICATION NUMBER: PCT/FR02/01200 ; PRIOR FILING DATE: 2002-04-05 ; PRIOR APPLICATION NUMBER: FR 01/04737 ; PRIOR FILING DATE: 2001-04-06 ; NUMBER OF SEQ ID NOS: 85 ; SOFTWARE: PatentIn Ver. 3.2 ; SEQ ID NO 66 ; LENGTH: 11029 ; TYPE: DNA ; ORGANISM: West Nile virus ; FEATURE: ; NAME/KEY: CDS ; LOCATION: (97)..(10395) US-10-679-520A-66</pre>	<pre>Query Match 79.2%; Score 38; DB 19; Length 11029; Best Local Similarity 100.0%; Pred. No. 5.1e-13; Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 TCCGAGACGGTTCTGAGGCGTTACATGGATCACTTCGC 38 Db 10629 TCCGAGACGGTTCTGAGGCGTTACATGGATCACTTCGC 10592</pre>	<pre>RESULT 9 US-10-706-892-1/c ; Sequence 1, Application US/10706892 ; Publication No. US20050058987A1 ; GENERAL INFORMATION: ; APPLICANT: SHI, PEI-YONG ; TITLE OF INVENTION: SCREENING FOR WEST NILE VIRUS ANTIVIRAL THERAPY ; FILE REFERENCE: 454311-2231.1 ; CURRENT APPLICATION NUMBER: US/10/706,892</pre>

```
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/427,117
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 11029
; TYPE: DNA
; ORGANISM: West Nile virus
US-10-706-892-1

Query Match      79.2%; Score 38; DB 19; Length 11029;
Best Local Similarity 100.0%; Pred. No. 5.1e-13;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTGAGGGCTTACATGATCACTTCGC 38
Db 10629 TCCGAGACGGTCTGAGGGCTTACATGATCACTTCGC 10592

RESULT 10
US-10-688-489-101/c
; Sequence 101, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 101
; LENGTH: 87
; TYPE: DNA
; ORGANISM: West Nile virus
US-10-688-489-101

Query Match      68.8%; Score 33; DB 18; Length 87;
Best Local Similarity 100.0%; Pred. No. 6.8e-10;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GACGGTCTGAGGGCTTACATGATCACTTCGC 38
Db 87 GACGGTCTGAGGGCTTACATGATCACTTCGC 55

RESULT 11
US-10-688-489-74
; Sequence 74, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16

; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 24
; TYPE: DNA
; ORGANISM: West Nile virus
US-10-688-489-75

Query Match      50.0%; Score 24; DB 18; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTGAGGGCTTAC 24
Db 1 TCCGAGACGGTCTGAGGGCTTAC 24

RESULT 12
US-10-688-489-75
; Sequence 75, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 75
; LENGTH: 24
; TYPE: DNA
; ORGANISM: West Nile virus
US-10-688-489-75

Query Match      50.0%; Score 24; DB 18; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTGAGGGCTTAC 24
Db 1 TCCGAGACGGTCTGAGGGCTTAC 24

RESULT 13
US-10-815-480-1/c
; Sequence 1, Application US/10815480
; Publication No. US20040229261A1
; GENERAL INFORMATION:
; APPLICANT: Young, Karen K. Y.
; APPLICANT: Roche Molecular Systems, Inc.
; TITLE OF INVENTION: Compositions and Methods for Detecting Certain
; TITLE OF INVENTION: Flaviviruses, Including Members of the Japanese
; TITLE OF INVENTION: Encephalitis Virus Serogroup
; FILE REFERENCE: 022101-000230US
; CURRENT APPLICATION NUMBER: US/10/815,480
```

; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US 60/459,491
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/552,454
; PRIOR FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: US 60/555,530
; PRIOR FILING DATE: 2004-03-22
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: region of
; OTHER INFORMATION: conserved sequence in 3' untranslated region of
; OTHER INFORMATION: the genomes of flaviviruses
US-10-815-480-1

Query Match 50.0%; Score 24; DB 18; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTTCGAGGGCTTAC 24
Db 24 TCCGAGACGGTTCGAGGGCTTAC 1

RESULT 14
US-10-815-480-2
; Sequence 2, Application US/10815480
; Publication No. US20040229261A1
; GENERAL INFORMATION:
; APPLICANT: Young, Karen K. Y.
; APPLICANT: Roche Molecular Systems, Inc.
; TITLE OF INVENTION: Compositions and Methods for Detecting Certain
; TITLE OF INVENTION: Flaviviruses, Including Members of the Japanese
; TITLE OF INVENTION: Encephalitis Virus Serogroup
; FILE REFERENCE: 022101-000230US
; CURRENT APPLICATION NUMBER: US/10/815,480
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US 60/459,491
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/552,454
; PRIOR FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: US 60/555,530
; PRIOR FILING DATE: 2004-03-22
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: complement to
; OTHER INFORMATION: SEQ ID NO:1
US-10-815-480-2

Query Match 50.0%; Score 24; DB 18; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTTCGAGGGCTTAC 24
Db 2 TCCGAGACGGTTCGAGGGCTTAC 25

RESULT 15
US-10-815-480-7/c
; Sequence 7, Application US/10815480
; Publication No. US20040229261A1
; GENERAL INFORMATION:
; APPLICANT: Young, Karen K. Y.

; APPLICANT: Roche Molecular Systems, Inc.
; TITLE OF INVENTION: Compositions and Methods for Detecting Certain
; TITLE OF INVENTION: Flaviviruses, Including Members of the Japanese
; TITLE OF INVENTION: Encephalitis Virus Serogroup
; FILE REFERENCE: 022101-000230US
; CURRENT APPLICATION NUMBER: US/10/815,480
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US 60/459,491
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/552,454
; PRIOR FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: US 60/555,530
; PRIOR FILING DATE: 2004-03-22
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Koutango virus
; OTHER INFORMATION: Primer 1
US-10-815-480-7

Query Match 50.0%; Score 24; DB 18; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTTCGAGGGCTTAC 24
Db 24 TCCGAGACGGTTCGAGGGCTTAC 1

RESULT 16
US-10-815-480-8/c
; Sequence 8, Application US/10815480
; Publication No. US20040229261A1
; GENERAL INFORMATION:
; APPLICANT: Young, Karen K. Y.
; APPLICANT: Roche Molecular Systems, Inc.
; TITLE OF INVENTION: Compositions and Methods for Detecting Certain
; TITLE OF INVENTION: Flaviviruses, Including Members of the Japanese
; TITLE OF INVENTION: Encephalitis Virus Serogroup
; FILE REFERENCE: 022101-000230US
; CURRENT APPLICATION NUMBER: US/10/815,480
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US 60/459,491
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/552,454
; PRIOR FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: US 60/555,530
; PRIOR FILING DATE: 2004-03-22
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Example Primer
; OTHER INFORMATION: 1
US-10-815-480-8

Query Match 50.0%; Score 24; DB 18; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTTCGAGGGCTTAC 24
Db 24 TCCGAGACGGTTCGAGGGCTTAC 1

RESULT 17

US-10-688-489-84
 ; Sequence 84, Application US/10688489
 ; Publication No. US20040259108A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Linnen, Jeffrey M.
 ; APPLICANT: Pollner, Reinhold B.
 ; APPLICANT: Wu, Wen
 ; APPLICANT: Dennis, Geoffrey G.
 ; APPLICANT: Darby, Paul M.
 ; TITLE OF INVENTION: Compositions and Methods for Detecting
 ; FILE OF INVENTION: West Nile Virus
 ; FILE REFERENCE: GP140-04.UT
 ; CURRENT APPLICATION NUMBER: US/10/688,489
 ; CURRENT FILING DATE: 2003-10-16
 ; PRIOR APPLICATION NUMBER: 60/418,891
 ; PRIOR FILING DATE: 2002-10-16
 ; PRIOR APPLICATION NUMBER: 60/429,006
 ; PRIOR FILING DATE: 2002-11-25
 ; PRIOR APPLICATION NUMBER: 60/449,810
 ; PRIOR FILING DATE: 2003-02-24
 ; NUMBER OF SEQ ID NOS: 196
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 84
 ; LENGTH: 51
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)..(27)
 ; OTHER INFORMATION: T7 promoter sequence
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (28)..(51)
 ; OTHER INFORMATION: WNV-complementary sequence
 US-10-688-489-84

Query Match 50.0%; Score 24; DB 18; Length 51;
 Best Local Similarity 100.0%; Pred. No. 0.0002;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTGAGGCTTAC 24
 Db 28 TCCGAGACGGTCTGAGGCTTAC 51

RESULT 18
 US-10-688-489-76
 ; Sequence 76, Application US/10688489
 ; Publication No. US20040259108A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Linnen, Jeffrey M.
 ; APPLICANT: Pollner, Reinhold B.
 ; APPLICANT: Wu, Wen
 ; APPLICANT: Dennis, Geoffrey G.
 ; APPLICANT: Darby, Paul M.
 ; TITLE OF INVENTION: Compositions and Methods for Detecting
 ; FILE OF INVENTION: West Nile Virus
 ; FILE REFERENCE: GP140-04.UT
 ; CURRENT APPLICATION NUMBER: US/10/688,489
 ; CURRENT FILING DATE: 2003-10-16
 ; PRIOR APPLICATION NUMBER: 60/418,891
 ; PRIOR FILING DATE: 2002-10-16
 ; PRIOR APPLICATION NUMBER: 60/429,006
 ; PRIOR FILING DATE: 2002-11-25
 ; PRIOR APPLICATION NUMBER: 60/449,810
 ; PRIOR FILING DATE: 2003-02-24
 ; NUMBER OF SEQ ID NOS: 196
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 76
 ; LENGTH: 23
 ; TYPE: DNA
 ; ORGANISM: West Nile Virus
 US-10-688-489-76

Query Match 47.9%; Score 23; DB 18; Length 23;
 Best Local Similarity 100.0%; Pred. No. 0.00086;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTGAGGCTTA 23
 Db 1 TCCGAGACGGTCTGAGGCTTA 23

RESULT 19
 US-10-688-489-149
 ; Sequence 149, Application US/10688489
 ; Publication No. US20040259108A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Linnen, Jeffrey M.
 ; APPLICANT: Pollner, Reinhold B.
 ; APPLICANT: Wu, Wen
 ; APPLICANT: Dennis, Geoffrey G.
 ; APPLICANT: Darby, Paul M.
 ; TITLE OF INVENTION: Compositions and Methods for Detecting
 ; FILE OF INVENTION: West Nile Virus
 ; FILE REFERENCE: GP140-04.UT
 ; CURRENT APPLICATION NUMBER: US/10/688,489
 ; CURRENT FILING DATE: 2003-10-16
 ; PRIOR APPLICATION NUMBER: 60/418,891
 ; PRIOR FILING DATE: 2002-10-16
 ; PRIOR APPLICATION NUMBER: 60/429,006
 ; PRIOR FILING DATE: 2002-11-25
 ; PRIOR APPLICATION NUMBER: 60/449,810
 ; PRIOR FILING DATE: 2003-02-24
 ; NUMBER OF SEQ ID NOS: 196
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 149
 ; LENGTH: 23
 ; TYPE: RNA
 ; ORGANISM: West Nile Virus
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)..(23)
 ; OTHER INFORMATION: 2'-OME nucleotide analogs
 US-10-688-489-149

Query Match 47.9%; Score 23; DB 18; Length 23;
 Best Local Similarity 73.9%; Pred. No. 0.00086;
 Matches 17; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGACGGTCTGAGGCTTACAT 26
 Db 1 GAGACGGTCTGAGGCTTACAU 23

RESULT 20
 US-10-688-489-85
 ; Sequence 85, Application US/10688489
 ; Publication No. US20040259108A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Linnen, Jeffrey M.
 ; APPLICANT: Pollner, Reinhold B.
 ; APPLICANT: Wu, Wen
 ; APPLICANT: Dennis, Geoffrey G.
 ; APPLICANT: Darby, Paul M.
 ; TITLE OF INVENTION: Compositions and Methods for Detecting
 ; FILE OF INVENTION: West Nile Virus
 ; FILE REFERENCE: GP140-04.UT
 ; CURRENT APPLICATION NUMBER: US/10/688,489
 ; CURRENT FILING DATE: 2003-10-16
 ; PRIOR APPLICATION NUMBER: 60/418,891
 ; PRIOR FILING DATE: 2002-10-16
 ; PRIOR APPLICATION NUMBER: 60/429,006
 ; PRIOR FILING DATE: 2002-11-25
 ; PRIOR APPLICATION NUMBER: 60/449,810
 ; PRIOR FILING DATE: 2003-02-24

```
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 85
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(27)
; OTHER INFORMATION: T7 promoter sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (28)...(50)
; OTHER INFORMATION: WNV-complementary sequence
US-10-688-489-85

Query Match      47.9%; Score 23; DB 18; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.00083;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCGAGGGCTTA 23
   |||||
Db 28 TCCGAGACGGTCTCGAGGGCTTA 50

RESULT 21
US-10-688-489-77
; Sequence 77, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT FILING DATE: 2003-10-16
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 77
; LENGTH: 22
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-77

Query Match      45.8%; Score 22; DB 18; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCGAGGGCTT 22
   |||||
Db 1 TCCGAGACGGTCTCGAGGGCTT 22

RESULT 22
US-10-688-489-86
; Sequence 86, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT FILING DATE: 2003-10-16
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 86
; LENGTH: 36
; TYPE: RNA
; ORGANISM: West Nile Virus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(36)
; OTHER INFORMATION: 2'-OME nucleotide analogs
US-10-688-489-195

Query Match      43.8%; Score 21; DB 18; Length 36;
Best Local Similarity 61.9%; Pred. No. 0.014;
Matches 13; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
```

```
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 86
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(27)
; OTHER INFORMATION: T7 promoter sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (28)...(49)
; OTHER INFORMATION: WNV-complementary sequence
US-10-688-489-86
```

```
Query Match      45.8%; Score 22; DB 18; Length 49;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 TCCGAGACGGTCTCGAGGGCTT 22
   |||||
Db 28 TCCGAGACGGTCTCGAGGGCTT 49
```

```
RESULT 23
US-10-688-489-195
; Sequence 195, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 195
; LENGTH: 36
; TYPE: RNA
; ORGANISM: West Nile Virus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(36)
; OTHER INFORMATION: 2'-OME nucleotide analogs
US-10-688-489-195
```

```
Query Match      43.8%; Score 21; DB 18; Length 36;
Best Local Similarity 61.9%; Pred. No. 0.014;
Matches 13; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
```


QY 28 GATCACTTCGACGCTTGTTC 48
||:||||:||||:||||:||||:
Db 1 GAUCACUUGCGAGCUUUGUC 21

RESULT 24
US-10-706-892-2/c
; Sequence 2, Application US/10706892
; Publication No. US20050058987A1
; GENERAL INFORMATION:
; APPLICANT: SHI, PEI-YONG
; TITLE OF INVENTION: SCREENING FOR WEST NILE VIRUS ANTIVIRAL THERAPY
; FILE REFERENCE: 454311-2231.1
; CURRENT APPLICATION NUMBER: US/10/706,892
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/427,117
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 2
; LENGTH: 11029
; TYPE: DNA
; ORGANISM: West Nile virus
US-10-706-892-2

Query Match 43.8%; Score 21; DB 19; Length 11029;
Best Local Similarity 100.0%; Pred. No. 0.011; 0; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Gaps 0;

QY 18 GCCTTACATGGATCACTTCGC 38
|||||
Db 10612 GCCTTACATGGATCACTTCGC 10592

RESULT 25
US-10-688-489-116/c
; Sequence 116, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Wu, Wen
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 116
; LENGTH: 19
; TYPE: DNA
; ORGANISM: West Nile Virus
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)-(19)
; OTHER INFORMATION: 2'-OME nucleotide analogs
US-10-688-489-116

Query Match 39.6%; Score 19; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GACGGTTCGAGGCTTAC 24
|||||

Db 19 GACGGTTCGAGGCTTAC 1

RESULT 26
US-10-688-489-114/c
; Sequence 114, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 114
; LENGTH: 20
; TYPE: DNA
; ORGANISM: West Nile Virus
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)-(20)
; OTHER INFORMATION: 2'-OME nucleotide analogs
US-10-688-489-114

Query Match 37.5%; Score 18; DB 18; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 CACTTCGACGCTTGTTC 48
|||||
Db 20 CACTTCGACGCTTGTTC 3

RESULT 27
US-10-688-489-196
; Sequence 196, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 196
; LENGTH: 23
; TYPE: RNA
; ORGANISM: West Nile Virus
; FEATURE:

```
; NAME/KEY: misc feature
; LOCATION: (1)...(23)
; OTHER INFORMATION: 2'-OME nucleotide analogs
US-10-688-489-196

Query Match      33.3%; Score 16; DB 18; Length 23;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 23 ACATGGATCACTTCG 38
    |||:|||||:|||||
Db 1 ACAUGGAUCACUUCG 16

RESULT 28
US-09-987-899-5166
; Sequence 5166, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 5166
; LENGTH: 160
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700265822H1
US-09-987-899-5166

Query Match      33.3%; Score 16; DB 11; Length 160;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 TACATGGATCACTTCG 37
    |||:|||||:|||||
Db 65 TACATGGATCACTTCG 80

RESULT 29
US-09-987-899-5163
; Sequence 5163, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 5163
; LENGTH: 240
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700265822H1
US-09-987-899-5163

Query Match      33.3%; Score 16; DB 16; Length 240;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 TACATGGATCACTTCG 37
    |||:|||||:|||||
Db 43 TACATGGATCACTTCG 58

RESULT 30
US-09-987-899-5161
; Sequence 5161, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 5161
; LENGTH: 256
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700029043H1
US-09-987-899-5161

Query Match      33.3%; Score 16; DB 11; Length 256;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 TACATGGATCACTTCG 37
    |||:|||||:|||||
Db 8 TACATGGATCACTTCG 23

RESULT 31
US-09-987-899-5159
; Sequence 5159, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 5159
; LENGTH: 274
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700029043H1
US-09-987-899-5159
```

OTHER INFORMATION: Clone ID: 700574357H2
US-09-987-899-5159

Query Match 33.3%; Score 16; DB 11; Length 274;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 TACATGGATCACTTCG 37
|||||
DB 95 TACATGGATCACTTCG 110
|||||

RESULT 32

US-09-987-899-5162
; Sequence 5162, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; TITLE OF INVENTION: With the Carbon Assimilation Pathway
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 5162
; LENGTH: 279
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700553323H1
US-09-987-899-5162

Query Match 33.3%; Score 16; DB 11; Length 279;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 TACATGGATCACTTCG 37
|||||
DB 56 TACATGGATCACTTCG 71
|||||

RESULT 33

US-09-987-899-5157
; Sequence 5157, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; TITLE OF INVENTION: With the Carbon Assimilation Pathway
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 5157
; LENGTH: 313
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700077313H1

US-09-987-899-5157

Query Match 33.3%; Score 16; DB 11; Length 313;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 TACATGGATCACTTCG 37
|||||
DB 134 TACATGGATCACTTCG 149
|||||

RESULT 34

US-09-770-445-56
; Sequence 56, Application US/09770445
; Patent No. US2002023281A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Krickler, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; TITLE OF INVENTION: thaliana
; FILE REFERENCE: 2023US (PARA-012PRV)
; CURRENT APPLICATION NUMBER: US/09/770,445
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/178,472
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 1168
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(1168)
; OTHER INFORMATION: n = A,T,C or G
US-09-770-445-56

Query Match 33.3%; Score 16; DB 9; Length 1168;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GCTTACATGGATCACT 34
|||||
DB 248 GCTTACATGGATCACT 263
|||||

RESULT 35

US-10-425-114-31937
; Sequence 31937, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E

```
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53313)B
; CURRENT FILING DATE: 2003-04-28
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 31937
; LENGTH: 1233
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73237H05_FLI
US-10-425-114-31937

Query Match      33.3%; Score 16; DB 17; Length 1233;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 TACATGGATCACTTCG 37
Db 58 TACATGGATCACTTCG 73

RESULT 36
US-10-024-130A-1/c
; Sequence 1, Application US/100241130A
; Publication No. US20030157593A1
; GENERAL INFORMATION:
; APPLICANT: Stevens, Donna
; APPLICANT: Wang, Michelle
; APPLICANT: Rice, John
; APPLICANT: Lanning, Beth
; APPLICANT: Broadwell, David
; APPLICANT: Glasbrook, No. US20030157593A1man
; APPLICANT: Sevala, Veeresh
; APPLICANT: Crawford, John
; APPLICANT: Stewart, Sandy
; TITLE OF INVENTION: METHODS FOR DETERMINING SQUALENE
; TITLE OF INVENTION: SYNTHASE ACTIVITY
; FILE REFERENCE: 2148US
; CURRENT APPLICATION NUMBER: US/10/024,130A
; CURRENT FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-024-130A-1

Query Match      33.3%; Score 16; DB 16; Length 1599;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 GCTTACATGGATCACT 34
Db 1361 GCTTACATGGATCACT 1346

RESULT 37
US-10-425-114-33763
; Sequence 33763, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
```

```
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 33763
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLM017168D04_FLI
US-10-425-114-33763

Query Match      33.3%; Score 16; DB 17; Length 2000;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 TACATGGATCACTTCG 37
Db 834 TACATGGATCACTTCG 849

RESULT 38
US-10-425-114-1427
; Sequence 1427, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 1427
; LENGTH: 2401
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700152625_FLI
US-10-425-114-1427

Query Match      33.3%; Score 16; DB 17; Length 2401;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 TACATGGATCACTTCG 37
Db 1226 TACATGGATCACTTCG 1241

RESULT 39
US-10-437-963-42274
; Sequence 42274, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Li, Ping
; APPLICANT: Barbazuk, Brad
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
```

; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 42274
; LENGTH: 2973
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_45542C.1
US-10-437-963-42274

Query Match 33.3%; Score 16; DB 18; Length 2973;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 TACATGGATCACTTCG 37
|||
DB 2051 TACATGGATCACTTCG 2066

RESULT 40
US-10-425-114-4145
; Sequence 4145, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 4145
; LENGTH: 2989
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700349524_FLI
US-10-425-114-4145

Query Match 33.3%; Score 16; DB 17; Length 2989;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 TACATGGATCACTTCG 37
|||
DB 1850 TACATGGATCACTTCG 1865

RESULT 41
US-10-425-114-1470
; Sequence 1470, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 1470
; LENGTH: 3244
; TYPE: DNA
; ORGANISM: Zea mays

; FEATURE:
; OTHER INFORMATION: Clone ID: 700154435_FLI
US-10-425-114-1470

Query Match 33.3%; Score 16; DB 17; Length 3244;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 TACATGGATCACTTCG 37
|||
DB 2109 TACATGGATCACTTCG 2124

RESULT 42
US-10-425-115-182436
; Sequence 182436, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 182436
; LENGTH: 3563
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)...(3563)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_97964C.1
US-10-425-115-182436

Query Match 33.3%; Score 16; DB 18; Length 3563;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 TACATGGATCACTTCG 37
|||
DB 2146 TACATGGATCACTTCG 2161

RESULT 43
US-10-437-963-42273
; Sequence 42273, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 42273
; LENGTH: 3858
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_45541C.1
US-10-437-963-42273

Query Match 33.3%; Score 16; DB 18; Length 3858;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 TACATGATCACTTCG 37
|||||
Db 2145 TACATGATCACTTCG 2160

RESULT 44
US-10-087-192-1129/c
; Sequence 1129, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1129
; LENGTH: 57561
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(57561)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-1129

Query Match 33.3%; Score 16; DB 13; Length 57561;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CTATCATGATCACTT 35
|||||
Db 258 CTATCATGATCACTT 243

RESULT 45
US-10-388-838-55
; Sequence 55, Application US/10388838
; Publication No. US20040180344A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
; FILE REFERENCE: 529452001600
; CURRENT APPLICATION NUMBER: US/10/388,838
; CURRENT FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 94781
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(94781)
; OTHER INFORMATION: n = A,T,C or G
US-10-388-838-55

Query Match 33.3%; Score 16; DB 18; Length 94781;

Best Local Similarity 100.0%; Pred. No. 11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GGCTTACATGATCAC 33
|||||
Db 72560 GGCTTACATGATCAC 72575

RESULT 46
US-10-688-489-115/c
; Sequence 115, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; TITLE OF INVENTION: West Nile Virus
; FILE REFERENCE: GPI40-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 20
; TYPE: DNA
; ORGANISM: West Nile Virus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(20)
; OTHER INFORMATION: 2'-OME nucleotide analogs
US-10-688-489-115

Query Match 31.2%; Score 15; DB 18; Length 20;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 CATGATCACTTCGC 38
|||||
Db 20 CATGATCACTTCGC 6

RESULT 47
US-10-688-489-103/c
; Sequence 103, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; TITLE OF INVENTION: West Nile Virus
; FILE REFERENCE: GPI40-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
US-10-688-489-103/c

```

; SEQ ID NO 103
; LENGTH: 52
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-103

Query Match      31.2%; Score 15; DB 18; Length 52;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 CATGGATCACTTCGC 38
Db 52 CATGGATCACTTCGC 38

RESULT 48
US-10-688-489-102/c
; Sequence 102, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; TITLE OF INVENTION: West Nile Virus
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 102
; LENGTH: 69
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-102

Query Match      31.2%; Score 15; DB 18; Length 69;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 CATGGATCACTTCGC 38
Db 69 CATGGATCACTTCGC 55

RESULT 49
US-09-987-899-5802/c
; Sequence 5802, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; TITLE OF INVENTION: With the Carbon Assimilation Pathway
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 5802
; LENGTH: 104
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700100451H1
US-09-987-899-5820/c
; Sequence 5820, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; TITLE OF INVENTION: With the Carbon Assimilation Pathway
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 5820
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700100451H1
US-09-987-899-5820

Query Match      31.2%; Score 15; DB 11; Length 306;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 GGATCACTTCGCAGC 41
Db 104 GGATCACTTCGCAGC 90

Search completed: March 25, 2005, 11:08:02
Job time : 329.291 secs

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OM nucleic - nucleic search, using sw model

Run on: March 25, 2005, 07:23:09 ; Search time 610.582 Seconds
(without alignments)
2460.130 Million cell updates/sec

Title: US-10-688-489-59
Perfect score: 31
Sequence: 1 tcgcacacggaagttgagtagacgtgctg 31

Scoring table: OLIGO_NUC
Gapop_60.0 , Gapext 60.0
Searched: 4708233 seqs, 24227607955 residues
Word size : 0
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Listing first 500 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sta:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	458	14	AF458356 Kunjin vi
2	31	100.0	462	14	AF458350 West Nile
3	31	100.0	463	14	AF458343 West Nile
4	31	100.0	463	14	AF458344 West Nile
5	31	100.0	463	14	AF458347 West Nile
6	31	100.0	463	14	AF458348 West Nile
7	31	100.0	463	14	AF458355 West Nile
8	31	100.0	545	14	AF297850 Kunjin vi
9	31	100.0	585	14	AF297840 Kunjin vi
10	31	100.0	593	14	AF297847 Kunjin vi
11	31	100.0	593	14	AF297852 Kunjin vi
12	31	100.0	594	14	AF297853 Kunjin vi
13	31	100.0	600	14	AF297846 Kunjin vi
14	31	100.0	616	14	AF297845 Kunjin vi
15	31	100.0	644	14	AF297848 Kunjin vi
16	31	100.0	657	14	AF297849 Kunjin vi
17	31	100.0	659	14	AF196536 West Nile
18	31	100.0	669	14	AF196541 West Nile
19	31	100.0	670	14	AF196542 West Nile

20	31	100.0	1524	14	AF017254
21	31	100.0	10842	14	AY278442 West Nile
22	31	100.0	10845	14	AY277252 West Nile
23	31	100.0	10972	14	AF317203 West Nile
24	31	100.0	10984	14	AY262283 West Nile
25	31	100.0	10989	14	AY268132 West Nile
26	31	100.0	11029	14	AF260968 West Nile
27	31	100.0	11029	14	AF260969 West Nile
28	31	100.0	11029	14	AF404757 West Nile
29	30	96.8	456	14	AF458351 Kunjin vi
30	30	96.8	463	14	AF458360 West Nile
31	30	96.8	463	14	AF458361 West Nile
32	30	96.8	542	14	AF297854 Kunjin vi
33	30	96.8	587	14	KUNNSGGA
34	30	96.8	587	14	KUNNSGAB
35	30	96.8	601	14	AF297844 Kunjin vi
36	30	96.8	607	14	AF297841 Kunjin vi
37	30	96.8	609	14	AF297856 Kunjin vi
38	30	96.8	620	14	AF297859 Kunjin vi
39	30	96.8	622	14	AF297842 Kunjin vi
40	30	96.8	623	14	AF297843 Kunjin vi
41	30	96.8	627	14	KUNNONCODB
42	30	96.8	633	14	AF297858 Kunjin vi
43	30	96.8	645	14	AY187012 West Nile
44	30	96.8	645	14	AY187013 West Nile
45	30	96.8	645	14	AY187014 West Nile
46	30	96.8	645	14	AY187015 West Nile
47	30	96.8	652	14	AF297855 Kunjin vi
48	30	96.8	10945	14	AF202541 West Nile
49	30	96.8	10975	14	AF208518 West Nile
50	30	96.8	10989	14	AY268133 West Nile
51	30	96.8	10988	14	AY278441 West Nile
52	30	96.8	11022	14	AY274504 Kunjin vi
53	30	96.8	11022	14	AY274505 Kunjin vi
54	30	96.8	11029	6	AX576542 Sequence
55	30	96.8	11029	6	AX577796 Sequence
56	30	96.8	11029	14	AB185914 West Nile
57	30	96.8	11029	14	AB185915 West Nile
58	30	96.8	11029	14	AB185916 West Nile
59	30	96.8	11029	14	AB185917 West Nile
60	30	96.8	11029	14	AF196835 West Nile
61	30	96.8	11029	14	AF260967 West Nile
62	30	96.8	11029	14	AF404753 West Nile
63	30	96.8	11029	14	AF404754 West Nile
64	30	96.8	11029	14	AF404755 West Nile
65	30	96.8	11029	14	AF404756 West Nile
66	30	96.8	11029	14	AF481864 West Nile
67	30	96.8	11029	14	AF533540 West Nile
68	30	96.8	11029	14	AY289214 West Nile
69	29	93.5	464	14	AY590190 West Nile
70	29	93.5	464	14	AY590191 West Nile
71	29	93.5	464	14	AY590192 West Nile
72	29	93.5	464	14	AY590193 West Nile
73	29	93.5	464	14	AY590194 West Nile
74	29	93.5	464	14	AY590195 West Nile
75	29	93.5	464	14	AY590196 West Nile
76	29	93.5	464	14	AY590197 West Nile
77	29	93.5	464	14	AY590198 West Nile
78	29	93.5	464	14	AY590199 West Nile
79	29	93.5	464	14	AY590200 West Nile
80	29	93.5	464	14	AY590201 West Nile
81	29	93.5	464	14	AY590202 West Nile
82	29	93.5	464	14	AY590203 West Nile
83	29	93.5	464	14	AY590204 West Nile
84	29	93.5	464	14	AY590205 West Nile
85	29	93.5	464	14	AY590206 West Nile
86	29	93.5	464	14	AY590207 West Nile
87	29	93.5	464	14	AY590208 West Nile
88	29	93.5	464	14	AY590209 West Nile
89	28	90.3	395	14	AF458358 West Nile
90	28	90.3	481	14	AF458359 West Nile
91	28	90.3	483	14	AF458345 West Nile
92	28	90.3	483	14	AF458357 West Nile

93	28	90.3	484	14	AF458354	AF458354 West Nile	166	15	48.4	3528	10	MUSJAK3A	L40172 Mus musculus
94	28	90.3	497	14	AF458346	AF458346 West Nile	167	15	48.4	3723	10	MUSPTYKIN	L32955 Mouse prote
95	28	90.3	591	14	AF196533	AF196533 West Nile	168	15	48.4	4016	10	MUSJAK3H	L33768 Mus musculus
96	28	90.3	593	14	AF196535	AF196535 West Nile v	169	15	48.4	4638	1	AB011811	AB011811 Chromatiu
97	28	90.3	677	14	AF196535	AF196535 West Nile	170	15	48.4	6794	1	AE005671	AE005671 Escherich
98	28	90.3	687	14	AF196539	AF196539 West Nile	171	15	48.4	6947	1	AB003398	AB003398 Shewanell
99	28	90.3	917	14	AF208017	AF208017 West Nile	172	15	48.4	10129	1	AE006751	AE006751 Sulfolobu
100	28	90.3	10962	14	WNFGC	M12294 West Nile v	173	15	48.4	10863	1	AE005678	AE005678 Caulobact
101	28	90.3	11057	14	AF688948	AF688948 West Nile	174	15	48.4	15829	10	MMU71201	U71201 Mus musculus
102	28	90.3	11064	14	AY453412	AY453412 Usutu vir	175	15	48.4	31414	3	U41557	U41557 Caenorhabdi
103	28	90.3	11066	14	AY453411	AY453411 Usutu vir	176	15	48.4	32320	3	CBF13H10	Z68748 Caenorhabdi
104	27	87.1	583	14	AF297857	AF297857 Kunjin vi	177	15	48.4	39330	2	AC137816	AC137816 Homo sapi
105	20	64.5	11028	14	AF490240	AF490240 West Nile	178	15	48.4	42095	2	DMC103E12	AL132651 Drosophil
106	18	58.1	451	14	AF458352	AF458352 West Nile	179	15	48.4	57213	2	AC104415	AC104415 Mus muscu
107	18	58.1	481	14	AF458349	AF458349 West Nile	180	15	48.4	76052	2	AC151322	AC151322 Xenopus t
108	18	58.1	604	14	KUNNS5	L49311 Kunjin viru	181	15	48.4	91654	9	AL357118	AL357118 Human DNA
109	18	58.1	644	14	AF196538	AF196538 West Nile	182	15	48.4	92911	2	AC020218	AC020218 Drosophil
110	18	58.1	648	14	AF196540	AF196540 West Nile	183	15	48.4	103061	2	AC151680	AC151680 Gallus ga
111	17	54.8	35652	2	AC017428	AC017428 Drosophil	184	15	48.4	110000	2	AC108998	Continuation (3 of
112	17	54.8	52872	6	CQ576911	AC007532 Drosophil	185	15	48.4	110000	2	AP006499	Continuation (7 of
113	17	54.8	171105	3	AC007532	AC007532 Drosophil	186	15	48.4	110000	2	EX927234	Continuation (3 of
114	17	54.8	181009	3	AC007535	AE003603 Drosophil	187	15	48.4	110000	8	CR382137	CR382137 Debaryomy
115	17	54.8	295289	3	AE003603	AF306514 Japanese	188	15	48.4	110000	8	CR382138	Continuation (2 of
116	16	51.6	463	14	AF278556	AF278556 Japanese	189	15	48.4	114946	2	AC151691	AC151691 Gallus ga
117	16	51.6	572	14	AF306514	AX663976 Sequence	190	15	48.4	115603	2	AC069498	AC069498 Mus muscu
118	16	51.6	1323	6	AX663976	AB041543 Mus muscu	191	15	48.4	128469	2	AC020029	AC020029 Drosophil
119	16	51.6	3691	10	AB041543	BC66816 Mus muscu	192	15	48.4	134728	8	AC090683	AC090683 Oryza sat
120	16	51.6	3986	10	BC66816	AK128931 Mus muscu	193	15	48.4	135825	10	AL645760	AL645760 Mouse DNA
121	16	51.6	4000	10	AK128931	AK128931 Mus muscu	194	15	48.4	137081	8	AP003866	AP003866 Oryza sat
122	16	51.6	5753	10	AK173281	AK173281 Mus muscu	195	15	48.4	137132	9	AC136628	AC136628 Homo sapi
123	16	51.6	10664	14	KUNCG	D00246 Kunjin viru	196	15	48.4	139182	9	AC109917	AC109917 Bos tauru
124	16	51.6	10741	14	AY277251	D027251 West Nile	197	15	48.4	140306	9	HS1068F16	AL023913 Human DNA
125	16	51.6	10963	14	AF045551	AF045551 Japanese	198	15	48.4	146154	2	AF004400	AP004400 Oryza sat
126	16	51.6	10963	14	AF316157	AY316157 Japanese	199	15	48.4	147702	2	AC109918	AC109918 Bos tauru
127	16	51.6	10965	14	AB051292	AB051292 Japanese	200	15	48.4	148852	9	AC005878	AC005878 citb 255
128	16	51.6	18385	1	MAD7PMCO	BX649604 Methylocl	201	15	48.4	149615	2	CR388383	CR388383 Danilo rer
129	16	51.6	31068	6	CQ612365	CQ612365 Sequence	202	15	48.4	150313	9	AC137672	AC137672 Homo sapi
130	16	51.6	61969	2	AC014103	AC014103 Drosophil	203	15	48.4	152383	9	H5F18108	AP005468 Oryza sat
131	16	51.6	63314	2	AC017803	AC017803 Drosophil	204	15	48.4	153894	8	AP005468	AP005468 Oryza sat
132	16	51.6	110000	1	CR000516	Continuation (15 o	205	15	48.4	158312	2	AC083922	AC083922 Homo sapi
133	16	51.6	110000	2	CR000516	Continuation (2 of	206	15	48.4	160770	9	AC010336	AC010336 Homo sapi
134	16	51.6	124372	10	AC012104	AC012104 Mus muscu	207	15	48.4	163998	9	AC022166	AC022166 Homo sapi
135	16	51.6	13985	5	AC009232	AC009232 Homo sapi	208	15	48.4	165002	2	AL355814	AL355814 Homo sapi
136	16	51.6	150975	5	BX088694	BX088694 Zebrafish	209	15	48.4	167065	2	AC150567	AC150567 Bos tauru
137	16	51.6	158646	9	AC142307	AC142307 Pan trogl	210	15	48.4	168764	1	AP002569	AP002569 Escherich
138	16	51.6	163933	5	AL929559	AL929559 Zebrafish	211	15	48.4	169557	3	AC104287	AC104287 Drosophil
139	16	51.6	163970	3	AC010580	AC010580 Drosophil	212	15	48.4	169623	10	AC131581	AC131581 Mus muscu
140	16	51.6	169271	3	AC009916	AC009916 Drosophil	213	15	48.4	172061	3	AC092203	AC092203 Drosophil
141	16	51.6	169902	3	AC008209	AC008209 Drosophil	214	15	48.4	173603	10	AC132222	AC132222 Mus muscu
142	16	51.6	176317	2	AL670857	AL670857 Mus muscu	215	15	48.4	176769	5	BX539308	BX539308 Zebrafish
143	16	51.6	186802	5	BX908803	BX908803 Zebrafish	216	15	48.4	177622	2	AC023559	AC023559 Homo sapi
144	16	51.6	189862	2	AC108317	AC108317 Rattus no	217	15	48.4	177641	10	AC146296	AC146296 Mus muscu
145	16	51.6	215711	3	AC008205	AC008205 Drosophil	218	15	48.4	177862	9	AC084782	AC084782 Homo sapi
146	16	51.6	226793	3	AE003753	AE003753 Drosophil	219	15	48.4	177911	1	AB017206	AB017206 Lactobaci
147	16	51.6	228433	3	AE003749	AE003749 Drosophil	220	15	48.4	178501	2	AL392165	AL392165 Homo sapi
148	16	51.6	231807	5	BE000529	BE000529 Zebrafish	221	15	48.4	180571	9	AC113425	AC113425 Homo sapi
149	16	51.6	233428	2	AC011064	AC011064 Drosophil	222	15	48.4	183043	6	AX926717	AX926717 Sequence
150	16	51.6	237686	2	AC129817	AC129817 Rattus no	223	15	48.4	183095	8	AP005186	AP005186 Oryza sat
151	16	51.6	269675	2	AC094496	AC094496 Rattus no	224	15	48.4	185580	2	AC123732	AC123732 Mus muscu
152	16	51.6	299450	1	BX248338	BX248338 Mycobacte	225	15	48.4	185867	10	AL606744	AL606744 Mouse DNA
153	16	51.6	307327	1	BX842856	BX842856 Bdellovib	226	15	48.4	185953	2	AC136593	AC136593 Homo sapi
154	16	51.6	348264	1	AR246572	AR246572 Mycobacte	227	15	48.4	189186	2	AC115861	AC115861 Mus muscu
155	15	48.4	436	6	AR305566	AR305566 Sequence	228	15	48.4	189308	9	AC068726	AC068726 Homo sapi
156	15	48.4	600	8	BT008964	BT008964 Tricicum	229	15	48.4	190628	2	AC024700	AC024700 Homo sapi
157	15	48.4	606	6	AR305576	AR305576 Sequence	230	15	48.4	192199	2	AC139312	AC139312 Bos tauru
158	15	48.4	616	6	AR305576	AR305576 Sequence	231	15	48.4	195696	10	AC125058	AC125058 Mus muscu
159	15	48.4	600	8	BT008964	BT008964 Tricicum	232	15	48.4	200393	2	AC150994	AC150994 Bos tauru
160	15	48.4	616	6	AR305576	AR305576 Sequence	233	15	48.4	201720	10	AL670778	AL670778 Mouse DNA
161	15	48.4	780	8	CNS01BVP	AL114749 Botrytis	234	15	48.4	204513	2	AC150900	AC150900 Mus muscu
162	15	48.4	1863	6	BD162638	BD162638 Novel pol	235	15	48.4	205725	10	AC122928	AC122928 Mus muscu
163	15	48.4	1863	6	AX120521	AX120521 Sequence	236	15	48.4	206167	2	AC113586	AC113586 Mus muscu
164	15	48.4	1969	6	AX773825	AX773825 Sequence	237	15	48.4	207298	2	AC136631	AC136631 Homo sapi
165	15	48.4	2399	8	PHCHIA	X14589 Petunia CHI	238	15	48.4	207890	2	AC102521	AC102521 Mus muscu

c 239	15	48.4	214508	2	AC103532	AC103532 Rattus no	312	14	45.2	522	12	AY202600	AY202600 Arabidops
c 240	15	48.4	215391	2	AC120168	Rattus muscu	c 313	14	45.2	536	6	AR426219	AR426219 Sequence
c 241	15	48.4	216912	2	AC114349	Rattus no	c 314	14	45.2	536	6	AX986913	AX986913 Sequence
c 242	15	48.4	217459	2	AC138998	Homo sapi	c 315	14	45.2	536	6	BD121772	BD121772 EST and e
c 243	15	48.4	217585	2	AC123225	Rattus no	c 316	14	45.2	562	14	FVNS55GAH	L48980 Koutango vi
c 244	15	48.4	218208	2	AC073700	Rattus muscu	c 317	14	45.2	564	6	AX896241	AX896241 Sequence
c 245	15	48.4	220632	2	AC136596	Homo sapi	c 318	14	45.2	564	6	BD031774	BD031774 Sequence
c 246	15	48.4	223274	2	AC112443	Rattus no	c 319	14	45.2	579	6	AR414185	AR414185 Sequence
c 247	15	48.4	223374	2	AC073750	Rattus no	c 320	14	45.2	579	6	AX971019	AX971019 Sequence
c 248	15	48.4	224040	2	AC107566	Rattus no	c 321	14	45.2	579	6	BD109738	BD109738 EST and e
c 249	15	48.4	224499	14	AF482758	Compox vi	c 322	14	45.2	696	11	BV076460	BV076460 S212P6548
c 250	15	48.4	224721	2	AC139632	Bos tauru	c 323	14	45.2	822	11	BV016791	BV016791 S212P6528
c 251	15	48.4	224821	2	AC096276	Rattus no	c 324	14	45.2	884	8	AY202271	AY202271 Arabidops
c 252	15	48.4	224859	2	AC073800	Rattus muscu	c 325	14	45.2	941	6	CQ818142	CQ818142 Sequence
c 253	15	48.4	227299	10	AC138722	AC138722 Mus muscu	c 326	14	45.2	977	8	BT014412	BT014412 Lycopersi
c 254	15	48.4	228851	10	AC123616	AC123616 Mus muscu	c 327	14	45.2	1047	5	AY225729	AY225729 Micropter
c 255	15	48.4	230200	2	AC129375	Rattus no	c 328	14	45.2	1047	5	AY225730	AY225730 Micropter
c 256	15	48.4	230236	10	AC093366	AC093366 Mus muscu	c 329	14	45.2	1047	5	AY225731	AY225731 Micropter
c 257	15	48.4	231096	2	AC125549	AC125549 Rattus no	c 330	14	45.2	1047	5	AY225732	AY225732 Micropter
c 258	15	48.4	232737	3	AE003660	AE003660 Drosophil	c 331	14	45.2	1047	5	AY225733	AY225733 Micropter
c 259	15	48.4	234160	2	AC103270	AC103270 Rattus no	c 332	14	45.2	1047	5	AY225734	AY225734 Micropter
c 260	15	48.4	235958	2	AC115507	AC115507 Rattus no	c 333	14	45.2	1100	10	AF290194	AF290194 Rattus no
c 261	15	48.4	237222	2	AC121742	AC121742 Rattus no	c 334	14	45.2	1138	8	AK104811	AK104811 Oryza sat
c 262	15	48.4	247577	2	AC106930	AC106930 Rattus no	c 335	14	45.2	1144	8	AK066070	AK066070 Oryza sat
c 263	15	48.4	248475	2	AC094641	AC094641 Rattus no	c 336	14	45.2	1162	8	AK108584	AK108584 Oryza sat
c 264	15	48.4	253169	2	AC094461	AC094461 Rattus no	c 337	14	45.2	1225	9	HS329217	HS329217 Homo sapi
c 265	15	48.4	269195	2	AC111879	AC111879 Rattus no	c 338	14	45.2	1257	5	DREVK2	X99290 D.erio Evx
c 266	15	48.4	277935	2	AC132671	AC132671 Rattus no	c 339	14	45.2	1278	5	XLJ010161	U10161 Xenopus lae
c 267	15	48.4	300350	1	AP006574	AP006574 Gloebact	c 340	14	45.2	1320	12	AF265109	AF265109 Synthetic
c 268	15	48.4	306598	3	AB003419	AB003419 Drosophil	c 341	14	45.2	1330	5	BC049528	BC049528 Danio rer
c 269	15	48.4	318862	1	AP005275	AP005275 Rattus no	c 342	14	45.2	1360	12	AF265113	AF265113 Synthetic
c 270	15	48.4	328050	2	AP005275	AP005275 Coryneb	c 343	14	45.2	1362	12	AF265114	AF265114 Synthetic
c 271	15	48.4	340000	9	HS21C046	AL163246 Homo sapi	c 344	14	45.2	1363	12	AF265112	AF265112 Synthetic
c 272	15	48.4	349174	1	AB063522	Wiggleswo	c 345	14	45.2	1377	8	AK108672	AK108672 Oryza sat
c 273	15	48.4	349887	1	BX927149	BX927149 Coryneb	c 346	14	45.2	1451	1	AY697896	AY697896 Unculture
c 274	15	48.4	349980	6	AX127144	AX127144 Sequence	c 347	14	45.2	1473	8	AY692997	AY692997 Saccharom
c 275	14	45.2	127	6	CQ430592	CQ430592 Sequence	c 348	14	45.2	1569	8	AK106909	AK106909 Oryza sat
c 276	14	45.2	120	6	AX245342	AX245342 Sequence	c 349	14	45.2	1676	8	AF445196	AF445196 Musa acum
c 277	14	45.2	251	6	BD077014	BD077014 5' EST of	c 350	14	45.2	1738	9	HS984G1A	AL450346 Novel hum
c 278	14	45.2	223	6	AX426218	AX426218 Sequence	c 351	14	45.2	1841	14	AJ781402	AJ781402 Cherry ch
c 279	14	45.2	223	6	AX986912	AX986912 Sequence	c 352	14	45.2	1844	9	HSCOMT1	Z26490 H.sapiens c
c 280	14	45.2	223	6	BD121771	BD121771 EST and e	c 353	14	45.2	1854	6	AX834969	AX834969 Sequence
c 281	14	45.2	231	6	CQ421725	CQ421725 Sequence	c 354	14	45.2	1854	9	AX097708	AX097708 Homo sapi
c 282	14	45.2	236	6	BD204219	BD204219 5' EST and	c 355	14	45.2	1865	9	HUMCOMT	L43122 Homo sapien
c 283	14	45.2	348	14	HCU56588	U56588 Hepatitis C	c 356	14	45.2	1931	8	AB019694	AB019694 Homo sapi
c 284	14	45.2	348	14	HCU56589	U56589 Hepatitis C	c 357	14	45.2	1938	8	AK109643	AK109643 Oryza sat
c 285	14	45.2	348	14	HCU56590	U56590 Hepatitis C	c 358	14	45.2	1944	10	WINKERA	V00830 Mouse mRNA
c 286	14	45.2	348	14	HCU56594	U56594 Hepatitis C	c 359	14	45.2	1950	9	AF171054	AF171054 Homo sapi
c 287	14	45.2	348	14	HCU56595	U56595 Hepatitis C	c 360	14	45.2	1955	6	AX195192	AX195192 Sequence
c 288	14	45.2	348	14	HCU56601	U56601 Hepatitis C	c 361	14	45.2	1960	9	AF044212	AF044212 Homo sapi
c 289	14	45.2	370	6	CQ477062	CQ477062 Sequence	c 362	14	45.2	2010	6	CQ602835	CQ602835 Sequence
c 290	14	45.2	390	6	CQ709746	CQ709746 Sequence	c 363	14	45.2	2084	11	BV177077	BV177077 sqm92606
c 291	14	45.2	400	6	BD076285	BD076285 5' EST of	c 364	14	45.2	2084	11	BV177509	BV177509 sqm95100
c 292	14	45.2	406	9	AF086763	AF086763 Homo sapi	c 365	14	45.2	2084	11	BV179316	BV179316 sqm10484
c 293	14	45.2	409	6	CQ729638	CQ729638 Sequence	c 366	14	45.2	2099	1	PAFGK979	X98465 Pseudomonas
c 294	14	45.2	419	6	AR177398	AR177398 Sequence	c 367	14	45.2	2113	6	CQ716679	CQ716679 Sequence
c 295	14	45.2	419	6	BD132537	BD132537 Secrete	c 368	14	45.2	2165	3	AF145658	AF145658 Drosophil
c 296	14	45.2	419	6	BD131472	BD131472 CDNA enco	c 369	14	45.2	2180	9	AF106697	AF106697 Homo sapi
c 297	14	45.2	425	6	AR177379	AR177379 Sequence	c 370	14	45.2	2184	9	BC035394	BC035394 Homo sapi
c 298	14	45.2	425	6	BD131453	BD131453 CDNA enco	c 371	14	45.2	2187	6	BC020723	AR207293 Sequence
c 299	14	45.2	427	6	CQ506978	CQ506978 Sequence	c 372	14	45.2	2194	8	SPIC70A	L26243 Spiniacia ol
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c 301	14	45.2	440	6	AX986914	AX986914 Sequence	c 374	14	45.2	2391	8	AK073061	AK073061 Oryza sat
c 302	14	45.2	440	6	BD121773	BD121773 EST and e	c 375	14	45.2	2498	8	AK109111	AK109111 Oryza sat
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c 304	14	45.2	443	6	AR509523	AR509523 Sequence	c 377	14	45.2	2561	8	SCYBR283C	Z36152 S.cerevisia
c 305	14	45.2	468	14	AY514902	AY514902 Fowl aden	c 378	14	45.2	2571	3	AY051852	AY051852 Drosophil
c 306	14	45.2	468	6	AR425864	AR425864 Sequence	c 379	14	45.2	2573	3	DMU36584	U36584 Drosophila
c 307	14	45.2	468	6	AX986558	AX986558 Sequence	c 380	14	45.2	2699	8	SCU05336	U05336 Saccharomyc
c 308	14	45.2	468	6	BD121417	BD121417 EST and e	c 381	14	45.2	2761	14	AB028604	AB028604 Tobacco 1
c 309	14	45.2	495	14	MVNS5GAD	L48975 Murray Vall	c 382	14	45.2	2761	14	AB079689	AB079689 Tobacco 1
c 310	14	45.2	501	14	MVNS5GAC	L48974 Murray Vall	c 383	14	45.2	2764	14	AB055008	AB055008 Tobacco 1
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387	14	45.2	2922	8	PSELIP	X05979 Pea ELIP ge	C 460	14	45.2	63658	2	AC018188	AC018188 Drosophil
388	14	45.2	2929	14	FAD554049	AJ554049 Fowl aden	C 461	14	45.2	64382	2	AC100251	AC100251 Mus muscu
389	14	45.2	2952	3	AK027212	AK027212 Homo sapi	C 462	14	45.2	64827	8	AB016873	AB016873 Arabidops
390	14	45.2	3071	3	DRODERA	L47260 Drosophila	C 463	14	45.2	65608	2	AC132197	AC132197 Homo sapi
391	14	45.2	3085	6	CQ594678	CQ594678 Sequence	C 464	14	45.2	66188	9	AL391136	AL391136 Human DNA
392	14	45.2	3130	9	AF201385	AF201385 Homo sapi	C 465	14	45.2	68362	2	AC012648	AC012648 Drosophil
393	14	45.2	3130	9	AF201385	AF201385 Homo sapi	C 466	14	45.2	68362	2	AC012648	AC012648 Drosophil
394	14	45.2	3300	14	FAD431719	AJ431719 Fowl aden	C 467	14	45.2	70475	8	AB018112	AB018112 Arabidops
395	14	45.2	3315	14	FAU26221	U26221 Fowl adenov	C 468	14	45.2	73294	8	AC027231	AC027231 Homo sapi
396	14	45.2	3334	5	BC057443	BC057443 Danio rer	C 469	14	45.2	74301	2	AC137736	AC137736 Homo sapi
397	14	45.2	3858	6	CQ590225	CQ590225 Sequence	C 470	14	45.2	74723	8	EX842633	EX842633 Neurospor
398	14	45.2	4349	8	AF034618	AF034618 Spinacia	C 471	14	45.2	75326	2	AC026999	AC026999 Homo sapi
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400	14	45.2	4477	3	DROTPM	M27659 D. melanog	C 473	14	45.2	76485	3	AC024211	AC024211 Caenorhab
401	14	45.2	4488	6	CQ595125	CQ595125 Sequence	C 474	14	45.2	76485	3	AC024872	AC024872 Caenorhab
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403	14	45.2	4720	8	AF515628	AF515628 Emericell	C 476	14	45.2	78419	3	AC004639	AC004639 Drosophil
404	14	45.2	5177	3	BT001531	BT001531 Drosophil	C 477	14	45.2	80141	9	HSEWSGAR	Y07848 Homo sapien
405	14	45.2	5186	6	CQ590012	CQ590012 Sequence	C 478	14	45.2	80141	9	HSEWSGAR	Y07848 Homo sapien
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408	14	45.2	6361	10	AY014962	AY014962 Mus muscu	C 481	14	45.2	81347	8	AB015478	AB015478 Arabidops
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412	14	45.2	8046	6	CQ595124	CQ595124 Sequence	C 485	14	45.2	82964	9	AL604028	AL604028 Human DNA
413	14	45.2	10091	1	AF135398	AF135398 Thermus b	C 486	14	45.2	83078	8	AF072897	AF072897 Arabidops
414	14	45.2	10413	1	AE004865	AE004865 Pseudomon	C 487	14	45.2	83373	8	AB017064	AB017064 Arabidops
415	14	45.2	11404	1	AE003934	AE003934 Xylella f	C 488	14	45.2	84761	9	AC093648	AC093648 Homo sapi
416	14	45.2	11541	8	AF233343	AF233343 Candida g	C 489	14	45.2	84761	9	AC093648	AC093648 Homo sapi
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420	14	45.2	13373	10	AB191468	AB191468 Mus muscu	C 493	14	45.2	93427	9	AL591076	AL591076 Human DNA
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423	14	45.2	16697	1	AF057696	AF057696 Haemophil	C 496	14	45.2	93695	2	ATF2009	AL021749 Arabidops
424	14	45.2	18796	6	CQ363729	CQ363729 Sequence	C 497	14	45.2	95597	2	AC014022	AC014022 Drosophil
425	14	45.2	20261	6	CQ594677	CQ594677 Sequence	C 498	14	45.2	95643	8	F6N15	AF069299 Arabidops
426	14	45.2	23738	3	CEP08H9	Z77657 Caenorhabdi	C 499	14	45.2	95961	2	AC017329	AC017329 Drosophil
427	14	45.2	24595	1	ATACH5	X00493 Agrobacteri	C 500	14	45.2	98224	2	AC148450	AC148450 Xenopus t
428	14	45.2	24595	6	E00404	E00404 Ti plasmid							AL645736 Mouse DNA
429	14	45.2	24595	6	E00546	E00546 DNA fragmen							
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433	14	45.2	26356	3	AF077538	AF077538 Caenorhab							
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436	14	45.2	32421	8	SCDPB3	X76053 S.cerevisia							
437	14	45.2	32463	8	CNS080C9W	AL772418 Oryza sat							
438	14	45.2	32668	9	MPU575934	AJ575934 Micromono							
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442	14	45.2	36123	3	AC093553	AC093553 Leishmani							
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454	14	45.2	45256	9	AC000090	AC000090 Homo sapi							
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457	14	45.2	51531	2	AC017444	AC017444 Drosophil							
458	14	45.2	57050	7	AY129333	AY129333 Mycobacte							

ALIGNMENTS

RESULT 1	AF458356	Kunjin virus strain K6453 nonstructural protein 5 gene, partial cds.	458 bp	RNA	linear	VRL 18-JUN-2003
LOCUS	AF458356					
DEFINITION	AF458356.1	GI:21636491				
ACCESSION	AF458356					
VERSION	AF458356.1	GI:21636491				
KEYWORDS						
SOURCE						
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Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCCACCGGAAGTTGAGTAGACGGTGCTG 31
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Db 293 TCCGCCACCGGAAGTTGAGTAGACGGTGCTG 323

RESULT 2
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LOCUS            West Nile virus strain And-27875 nonstructural protein 5 gene,
DEFINITION      partial cds.
ACCESSION       AF458350
VERSION         AF458350.1 GI:21636479
KEYWORDS
SOURCE          West Nile virus (WNV)
ORGANISM        West Nile virus
                Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
                Flavivirus; Japanese encephalitis virus group.
REFERENCE       1 (bases 1 to 462)
AUTHORS         Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
TITLE           Mouse neuroinvasive phenotype of West Nile virus strains varies
                depending upon virus genotype
JOURNAL         Virology 296 (1), 17-23 (2002)
MEDLINE        22033887
PUBMED         12036314
REFERENCE       2 (bases 1 to 462)
AUTHORS         Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE           Direct Submission
JOURNAL         Submitted (14-DEC-2001) Department of Pathology and WHO
                Collaborating Center for Tropical Diseases, The University of Texas
                Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA

FEATURES
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Query Match          100.0%; Score 31; DB 14; Length 462;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AF458350          462 bp RNA linear VRL 18-JUN-2003
LOCUS            West Nile virus strain And-27875 nonstructural protein 5 gene,
DEFINITION      partial cds.
ACCESSION       AF458350
VERSION         AF458350.1 GI:21636479
KEYWORDS
SOURCE          West Nile virus (WNV)
ORGANISM        West Nile virus
                Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
                Flavivirus; Japanese encephalitis virus group.
REFERENCE       1 (bases 1 to 462)
AUTHORS         Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
TITLE           Mouse neuroinvasive phenotype of West Nile virus strains varies
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JOURNAL         Virology 296 (1), 17-23 (2002)
MEDLINE        22033887
PUBMED         12036314
REFERENCE       2 (bases 1 to 462)
AUTHORS         Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE           Direct Submission
JOURNAL         Submitted (14-DEC-2001) Department of Pathology and WHO
                Collaborating Center for Tropical Diseases, The University of Texas
                Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA

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RESULT 3
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LOCUS            West Nile virus strain ArB310/67 nonstructural protein 5 gene,
DEFINITION      partial cds.
ACCESSION       AF458343
VERSION         AF458343.1 GI:21636465
KEYWORDS
SOURCE          West Nile virus (WNV)
ORGANISM        West Nile virus
                Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
                Flavivirus; Japanese encephalitis virus group.
REFERENCE       1 (bases 1 to 463)
AUTHORS         Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
TITLE           Mouse neuroinvasive phenotype of West Nile virus strains varies
                depending upon virus genotype
JOURNAL         Virology 296 (1), 17-23 (2002)
MEDLINE        22033887
PUBMED         12036314
REFERENCE       2 (bases 1 to 463)
AUTHORS         Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE           Direct Submission
JOURNAL         Submitted (14-DEC-2001) Department of Pathology and WHO
                Collaborating Center for Tropical Diseases, The University of Texas
                Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA

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Db 298 TCCGCCACCGGAAGTTGAGTAGACGGTGCTG 328

RESULT 4
AF458344          463 bp RNA linear VRL 18-JUN-2003
LOCUS            West Nile virus strain 68856 nonstructural protein 5 gene, partial
DEFINITION      cds.
ACCESSION       AF458344
VERSION         AF458344.1 GI:21636467
KEYWORDS
SOURCE          West Nile virus (WNV)
ORGANISM        West Nile virus
                Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
                Flavivirus; Japanese encephalitis virus group.
REFERENCE       1 (bases 1 to 463)
AUTHORS         Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
TITLE           Mouse neuroinvasive phenotype of West Nile virus strains varies

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depending upon virus genotype
Virology 296 (1), 17-23 (2002)
MEDLINE
PUBMED
12036314
REFERENCE
2 (bases 1 to 463)
Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
Direct Submission
Submitted (14-DEC-2001) Department of Pathology and WHO
Collaborating Center for Tropical Diseases, The University of Texas
Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
JOURNAL
Location/Qualifiers
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ACCESSION
AF458347
VERSION
AF458347.1 GI:21636473
KEYWORDS
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ORGANISM
West Nile virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
1 (bases 1 to 463)
Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.
Mouse neuroinvasive phenotype of West Nile virus strains varies
depending upon virus genotype
Virology 296 (1), 17-23 (2002)
MEDLINE
PUBMED
12036314
REFERENCE
2 (bases 1 to 463)
Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
Direct Submission
Submitted (14-DEC-2001) Department of Pathology and WHO
Collaborating Center for Tropical Diseases, The University of Texas
Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
JOURNAL
Location/Qualifiers
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Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 298 TCCGCCACCGGAAGTTGAGTAGACGGTGCTG 328
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LOCUS
DEFINITION
West Nile virus strain IbAn7019 nonstructural protein 5 gene,
partial cds.
ACCESSION
AF458348
VERSION
AF458348.1 GI:21636475
KEYWORDS
West Nile virus (WNV)
ORGANISM
West Nile virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
1 (bases 1 to 463)
Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.
Mouse neuroinvasive phenotype of West Nile virus strains varies
depending upon virus genotype
Virology 296 (1), 17-23 (2002)
MEDLINE
PUBMED
12036314
REFERENCE
2 (bases 1 to 463)
Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
Direct Submission
Submitted (14-DEC-2001) Department of Pathology and WHO
Collaborating Center for Tropical Diseases, The University of Texas
Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
JOURNAL
Location/Qualifiers
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RESULT 7
AF458355
LOCUS
DEFINITION
West Nile virus strain Egypt101 nonstructural protein 5 gene,
partial cds.

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ACCESSION AF458355.1 GI:21636489
VERSION
KEYWORDS
SOURCE West Nile virus (WNV)
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 463)
AUTHORS Beasley,D.W., Li,L., Suderman,M.T. and Barrett,A.D.
TITLE Mouse neuroinvasive phenotype of West Nile virus strains varies
depending upon virus genotype
JOURNAL Virology 296 (1), 17-23 (2002)
MEDLINE 22033887
PUBMED 12036314
REFERENCE 2 (bases 1 to 463)
AUTHORS Beasley,D.W.C., Li,L., Suderman,M.T. and Barrett,A.D.T.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-2001) Department of Pathology and WHO
Collaborating Center for Tropical Diseases, The University of Texas
Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
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Db 298 TCGCCACCGGAAGTTGAGTAGACGCTGCTG 328
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LOCUS Kunjin virus isolate K6590 nonstructural protein 5 gene, partial
DEFINITION
ACCESSION AF297850
VERSION AF297850.1 GI:11991990
KEYWORDS Kunjin virus
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 545)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE The relationships between West Nile and Kunjin viruses
Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE 21469816
PUBMED 11585535
REFERENCE 2 (bases 1 to 545)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE Definitive studies of the relationships between West Nile and
Kunjin viruses
Unpublished
JOURNAL
REFERENCE 3 (bases 1 to 585)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE Direct Submission
JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University
of Queensland, St Lucia, QLD 4072, Australia
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LOCUS
DEFINITION
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ACCESSION
AF297847
VERSION
AF297847.1 GI:11991984
KEYWORDS
Kunjin virus
SOURCE
Kunjin virus
ORGANISM
Kunjin virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
1 (bases 1 to 593)
AUTHORS
Scherrret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE
The relationships between West Nile and Kunjin viruses
JOURNAL
Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE
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PUBMED
11585535
REFERENCE
2 (bases 1 to 593)
AUTHORS
Scherrret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE
Definitive studies of the relationships between West Nile and
Kunjin viruses
JOURNAL
Unpublished
REFERENCE
3 (bases 1 to 593)
AUTHORS
Scherrret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE
Direct Submission
JOURNAL
Submitted (22-AUG-2000) Microbiology and Parasitology, University
of Queensland, St Lucia, QLD 4072, Australia
LOCATION/Qualifiers
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Db 366 TCCGCCACCGGAAGTTGAGTAGACGGTGCTG 396

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LOCUS
DEFINITION
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cds.
ACCESSION
AF297852
VERSION
AF297852.1 GI:11991994
KEYWORDS
Kunjin virus
SOURCE
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ORGANISM
Kunjin virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
1 (bases 1 to 594)
AUTHORS
Scherrret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE
The relationships between West Nile and Kunjin viruses
JOURNAL
Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE
21469816
PUBMED
11585535
REFERENCE
2 (bases 1 to 594)
AUTHORS
Scherrret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE
Definitive studies of the relationships between West Nile and
Kunjin viruses
JOURNAL
Unpublished
REFERENCE
3 (bases 1 to 593)
AUTHORS
Scherrret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE
Direct Submission
JOURNAL
Submitted (22-AUG-2000) Microbiology and Parasitology, University
of Queensland, St Lucia, QLD 4072, Australia
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and Hall,R.A.
Definitive studies of the relationships between West Nile and
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JOURNAL
REFERENCE 3 (bases 1 to 594)
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and Hall,R.A.
TITLE Direct Submission
JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University
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DEFINITION
ACCESSION AF297846
VERSION AF297846.1 GI:11991982
KEYWORDS Kunjin virus
ORGANISM Kunjin virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 600)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE The relationships between West Nile and Kunjin viruses
JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE 21469815
PUBMED 11585535
REFERENCE 2 (bases 1 to 600)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE Definitive studies of the relationships between West Nile and
Kunjin viruses
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 616)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE Direct Submission
JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University
of Queensland, St Lucia, QLD 4072, Australia
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DB 355 TCGCCACCGGAGTTGAGTAGACGGTGCTG 385

RESULT 14
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LOCUS Kunjin virus isolate CX255 nonstructural protein 5 gene, partial
DEFINITION
ACCESSION AF297845
VERSION AF297845.1 GI:11991980
KEYWORDS Kunjin virus
ORGANISM Kunjin virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 616)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE The relationships between West Nile and Kunjin viruses
JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE 21469816
PUBMED 11585535
REFERENCE 2 (bases 1 to 616)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE Definitive studies of the relationships between West Nile and
Kunjin viruses
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 616)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE Direct Submission
JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University
of Queensland, St Lucia, QLD 4072, Australia
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JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE 21469816
PUBMED 11585535
REFERENCE 2 (bases 1 to 657)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE Definitive studies of the relationships between West Nile and
Kunjin viruses
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 657)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE Direct Submission
JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University
of Queensland, St Lucia, QLD 4072, Australia
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Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 386 TCGCCACCGGAAGTTGAGTAGACGGTGTG 416

RESULT 17
AF196536
LOCUS West Nile virus isolate AraDj polyprotein gene, partial cds.
DEFINITION linear VRL 05-MAR-2002
ACCESSION AF196536
VERSION AF196536.1 GI:15865586
KEYWORDS
SOURCE West Nile virus
ORGANISM West Nile virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 659)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE The relationships between West Nile and Kunjin viruses
JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE 21469816
PUBMED 11585535
REFERENCE 2 (bases 1 to 659)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE Definitive studies of the relationships between West Nile and
Kunjin viruses
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 659)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE Direct Submission
JOURNAL Submitted (20-OCT-1999) Department of Microbiology and
Parasitology, University of Queensland, St. Lucia, Brisbane, QLD
4072, Australia
FEATURES
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Db 391 TCGCCACCGGAAGTTGAGTAGACGGTGCTG 421
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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
West Nile virus
Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
1 (bases 1 to 669)
Scherrer,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
The relationships between West Nile and Kunjin viruses
Emerging Infect. Dis. 7 (4), 697-705 (2001)
21459816
PUBMED
REFERENCE
2 (bases 1 to 669)
Scherrer,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
Definitive studies of the relationships between West Nile and
Kunjin viruses
Unpublished
JOURNAL
REFERENCE
3 (bases 1 to 669)
Scherrer,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
Direct Submission
Submitted (20-OCT-1999) Department of Microbiology and
Parasitology, University of Queensland, St. Lucia, Brisbane, QLD
4072, Australia
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.8e-07;
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Db 391 TCGCCACCGGAAGTTGAGTAGACGGTGCTG 421
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RESULT 19
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
West Nile virus
Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
1 (bases 1 to 670)
Scherrer,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
The relationships between West Nile and Kunjin viruses
Emerging Infect. Dis. 7 (4), 697-705 (2001)
21459816
PUBMED
REFERENCE
2 (bases 1 to 670)
Scherrer,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
Definitive studies of the relationships between West Nile and
Kunjin viruses
Unpublished
JOURNAL
REFERENCE
3 (bases 1 to 670)
Scherrer,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
Direct Submission
Submitted (20-OCT-1999) Department of Microbiology and
Parasitology, University of Queensland, St. Lucia, Brisbane, QLD
4072, Australia
Location/Qualifiers
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/mol_type="genomic RNA"
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Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 389 TCGCCACCGGAAGTTGAGTAGACGGTGCTG 419
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RESULT 20
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LOCUS
DEFINITION
ACCESSION

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Query Match          100.0%; Score 31; DB 14; Length 669;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
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Db 388 TCGCCACCGGAAGTTGAGTAGACGGTGCTG 418
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RESULT 19
AF196542
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
West Nile virus
Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
1 (bases 1 to 670)
Scherrer,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
The relationships between West Nile and Kunjin viruses
Emerging Infect. Dis. 7 (4), 697-705 (2001)
21459816
PUBMED
REFERENCE
2 (bases 1 to 670)
Scherrer,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
Definitive studies of the relationships between West Nile and
Kunjin viruses
Unpublished
JOURNAL
REFERENCE
3 (bases 1 to 670)
Scherrer,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
Direct Submission
Submitted (20-OCT-1999) Department of Microbiology and
Parasitology, University of Queensland, St. Lucia, Brisbane, QLD
4072, Australia
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Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 389 TCGCCACCGGAAGTTGAGTAGACGGTGCTG 419
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RESULT 20
AF017254
LOCUS
DEFINITION
ACCESSION

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VERSION	AF017254.2	GI:11497617	
KEYWORDS	West Nile virus		
SOURCE	West Nile virus		
ORGANISM	West Nile virus		
REFERENCE	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group.		
AUTHORS	1 (bases 1 to 1524)		
TITLE	Yamshchikov, V.F., Wengler, G., Brinton, M.A. and Compans, R.W.		
JOURNAL	A stable infectious clone of West Nile flavivirus		
REFERENCE	2 (bases 1 to 1524)		
AUTHORS	Yamshchikov, V.F. and Brinton, M.A.		
TITLE	Direct Submission		
JOURNAL	Submitted (04-AUG-1997) OVRP/DVP, FDA, 29 Lincoln Drive, Bethesda, MD 20892, USA		
REFERENCE	3 (bases 1 to 1524)		
AUTHORS	Yamshchikov, V.F. and Brinton, M.A.		
TITLE	Direct Submission		
JOURNAL	Submitted (01-DEC-2000) OVRP/DVP, FDA, 29 Lincoln Drive, Bethesda, MD 20892, USA		
REMARK	Sequence update by submitter		
COMMENT	On Dec 1, 2000 this sequence version replaced gi:2394279.		
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RESULT 21			
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LOCUS	AY278442	10842 bp	RNA linear VZL 03-MAY-2003
DEFINITION	West Nile virus isolate LEIV-Vlg00-27924, complete genome.		
ACCESSION	AY278442		
VERSION	AY278442.1	GI:30349731	
KEYWORDS	West Nile virus (WNV)		
SOURCE	West Nile virus		
ORGANISM	West Nile virus		
REFERENCE	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group.		
AUTHORS	1 (bases 1 to 10842)		
TITLE	Sadykova, G.K., Prilipov, A.G., Kinney, R.M., Samokhvalov, E.I., Savage, H.M., Alkhovsky, S.V., Tsychia, R., Gromashevsky, V.L., Usachev, E.V., Mokhonov, V.V., Voronina, A.G., Butenko, A.M., Lariichev, V.F., Gubler, D.J. and Lvov, D.K.		
JOURNAL	Analysis of a new variant of West Nile virus		
REFERENCE	2 (bases 1 to 10842)		

AUTHORS	Sadykova, G.K., Prilipov, A.G., Kinney, R.M., Samokhvalov, E.I., Savage, H.M., Alkhovsky, S.V., Tsychia, R., Gromashevsky, V.L., Usachev, E.V., Mokhonov, V.V., Voronina, A.G., Butenko, A.M., Lariichev, V.F., Gubler, D.J. and Lvov, D.K.
TITLE	Direct Submission
JOURNAL	Submitted (17-APR-2003) Molecular Genetic, Ivanovsky Virology Institute, Gamalei 16, Moscow 123098, Russia
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Db 10522 TCCGCCACCGAAGTTGAGTAGACGCTGCTG 10552

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DEFINITION

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VERSION

KEYWORDS

SOURCE

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JOURNAL

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AUTHORS

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JOURNAL

FEATURES

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ORIGIN

Query Match 100.0%; Score 31; DB 14; Length 10845;

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Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 23

AF317203

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

1 (bases 1 to 10972)

2 (bases 1 to 10972)

West Nile virus

West Nile virus

Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;

Flavivirus; Japanese encephalitis virus group.

1 (bases 1 to 10972)

Platonov, A.E., Karan, L., Yazishina, S., Obukhov, I.L., Shipulina, O.

and Shipulin, G.A.

Genetic similarity of West Nile viruses caused epidemics in

Volgograd 1999 and Romania 1996

Unpublished

2 (bases 1 to 10972)

AUTHORS

Karan,L., Yazishina,S., Obukhov,I.L., Shipulina,O., Shipulin,G.A.
and Platonov,A.E.
Direct Submission
Submitted (26-Oct-2000) Central Research Institute of Epidemiology,
Novogireevskaya Str. 3A, Moscow 111123, Russia
Location/Qualifiers

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Query Match 100.0%; Score 31; DB 14; Length 10972;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCGCCACCGGAAGTTGAGTAGACGGTGCTG 31
DB 10490 TCCGCCACCGGAAGTTGAGTAGACGGTGCTG 10520

RESULT 24

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DEFINITION West Nile virus isolate KN3829 polyprotein gene, complete cds.
ACCESSION AY262283
VERSION AY262283.1 GI:30230630
KEYWORDS
SOURCE West Nile virus (WNV)
ORGANISM West Nile virus

REFERENCE

1 (bases 1 to 10984)
AUTHORS Charrel,R.N., Braut,A.C., Gallian,P., Lemasson,J.-J., Murgue,B.,
Muri,S., Pastorino,B., Zeller,H., de Chesse,R., de Micco,P. and de
Lamballerie,X.

TITLE

Evolutionary relationship between Old World West Nile virus
strains. Evidence for viral gene flow between africa, the middle
east, and europe
Virology 315 (2), 381-388 (2003)
MEDLINE 14585341
PUBMED 14585341

REFERENCE

2 (bases 1 to 10984)
AUTHORS Braut,A.C. and de Lamballerie,X.
TITLE Direct Submission
JOURNAL Submitted (25-MAR-2003) Division of Vector-Borne Infectious
Diseases, Centers for Disease Control and Prevention, P.O. Box
2087, Fort Collins, CO 80522, USA

FEATURES

source

1. .10984
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/mol_type="genomic RNA"
/isolate="KN3829"
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ORIGIN

Query Match 100.0%; Score 31; DB 14; Length 10989;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DEFINITION

AF260968
AF260968.1 GI:9930135
West Nile virus
West Nile virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
1 (bases 1 to 11029)
Bowen, M., Meyer, R.F., McKinney, N., Morrill, W. and Lanciotti, R.
Complete genomic sequence of West Nile virus strain Eg101
Unpublished
2 (bases 1 to 11029)
Bowen, M., Meyer, R.F., McKinney, N., Morrill, W. and Lanciotti, R.
Direct Submission
Submitted (27-APR-2000) Arbovirus Diseases Branch, Centers for
Disease Control & Prevention, Rampart Road, Fort Collins, CO 80521,
USA
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7681. .10395
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Query Match 100.0%; Score 31; DB 14; Length 11029;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCGCCACCGGAAGTTGAGTAGACGCTGCTG 31
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Db 10522 TCGCCACCGGAAGTTGAGTAGACGCTGCTG 10552
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RESULT 27
AF260969 LOCUS 11029 bp RNA linear VRL 27-AUG-2000
West Nile virus strain R097-50, complete genome.
DEFINITION
ACCESSION AF260969
VERSION AF260969.1 GI:9930137
KEYWORDS
SOURCE
ORGANISM
West Nile virus
Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
1 (bases 1 to 11029)
Savage,H.M., Ceianu,C., Nicolescu,G., Karabatsos,N., Lanciotti,R.,
Vladimirescu,A., Laviu,L., Ungureanu,A., Romanca,C. and Teai,T.F.
Entomologic and avian investigations of an epidemic of West Nile
fever in Romania in 1996, with serologic and molecular
Characterization of a virus isolate from mosquitoes
Am. J. Trop. Med. Hyg. 61 (4), 600-611 (1999)
20014331
PUBMED 10548295
REFERENCE
2 (bases 1 to 11029)
Bowen,M., Meyer,R.F., McKinney,N., Morrill,W. and Lanciotti,R.
Direct Submission
Submitted (27-APR-2000) Arbovirus Diseases Branch, Centers for
Disease Control & Prevention, Rampart Road, Fort Collins, CO 80521,
QMWLLLYFHRRDLRLMANAICSAVPVNVPTGRTTWSIHAGGEMTTEDMLEVNRVY
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USA

FEATURES
Source

Location/Qualifiers

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1. 11029
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/country="Romania"
/note="1996"
97. 110398
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ISRLQRCGSGVFIHNDVEMWMDRYKYPETQGLAKIIOKAHKGSGVGLRSVLEH
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97. 465

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466. .741

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742. .966

/product="membrane protein M"

mat_peptide

957. 2469

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mat_peptide

2470. .3525

/product="non-structural protein 1 NS1"

mat_peptide

3526. .4218

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mat_peptide

4219. .4611

/product="non-structural protein 2B NS2B"

mat_peptide

4612. .6468

/product="non-structural protein 3 NS3"

mat_peptide

6469. .6915

/product="non-structural protein 4A NS4A"

mat_peptide

6916. .7680

/product="non-structural protein NS4B"

mat_peptide

7681. .10395

/product="non-structural protein NS5"

ORIGIN

Query Match 100.0%; Score 31; DB 14; Length 11029;

Best Local Similarity 100.0%; Pred. No. 2.1e-07;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCCACCGGAAGTTGAGTAGACGGTGCTG 31

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Db 10522 TCCGCCACCGGAAGTTGAGTAGACGGTGCTG 10552

RESULT 28

AF404757

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

10522

10522

10522

10522

10522

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10522

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VFVLLILPAVAYSFNCIGMGNRDFLEGVATWDLVLEGDSCVTIMSKQPTIDVK
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ORIGIN

Query Match 100.0%; Score 31; DB 14; Length 11029;

Best Local Similarity 100.0%; Pred. No. 2.1e-07;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCCACCGGAAGTTGAGTAGACGGTGCTG 31

|||||

Db 10522 TCCGCCACCGGAAGTTGAGTAGACGGTGCTG 10552


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3'UTR          175...->463
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 7e-07;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2  CCGCCACCGGAAGTTGAGTAGACGGTGCTG 31
          |||||
Db      299 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 328

RESULT 32
AF297854
LOCUS      Kunjin virus isolate WK436 nonstructural protein 5 gene, partial
cfs.
DEFINITION
ACCESSION  AF297854
VERSION    AF297854.1 GI:11991998
KEYWORDS
SOURCE     Kunjin virus
ORGANISM   Kunjin virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
REFERENCE  1 (bases 1 to 542)
AUTHORS   Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
          Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE     The relationships between West Nile and Kunjin viruses
JOURNAL   Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE   21469816
PUBMED
REFERENCE  2 (bases 1 to 542)
AUTHORS   Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
          and Hall,R.A.
TITLE     Definitive studies of the relationships between West Nile and
          Kunjin viruses
JOURNAL   Unpublished
REFERENCE  3 (bases 1 to 542)
AUTHORS   Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
          and Hall,R.A.
TITLE     Direct Submission
JOURNAL   Submitted (22-AUG-2000) Microbiology and Parasitology, University
          of Queensland, St Lucia, QLD 4072, Australia
FEATURES
source
Location/Qualifiers
1..542
/organism="Kunjin virus"
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/db_xref="GI:11991999"
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ORIGIN
Query Match          96.8%; Score 30; DB 14; Length 542;
Best Local Similarity 100.0%; Pred. No. 7e-07;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      363 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 392

RESULT 33
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LOCUS      Kunjin virus nonstructural protein (NS5) gene, 3' end of cds.
DEFINITION
ACCESSION  L48978

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ORIGIN
Query Match          96.8%; Score 30; DB 14; Length 587;
Best Local Similarity 100.0%; Pred. No. 7e-07;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGCCACCGGAAGTTGAGTAGACGGTGCTG 31
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Db 355 CGCCACCGGAAGTTGAGTAGACGGTGCTG 384

RESULT 35
AF297844
LOCUS
DEFINITION
Kunjin virus isolate CHI6549E nonstructural protein 5 gene, partial
cde.
ACCESSION
AF297844
VERSION
AF297844.1 GI:11991978
KEYWORDS
Kunjin virus
ORGANISM
Kunjin virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
1 (bases 1 to 601)
AUTHORS
Scherrret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE
The relationships between West Nile and Kunjin viruses
JOURNAL
Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE
21469816
PUBMED
11585535
REFERENCE
2 (bases 1 to 601)
AUTHORS
Scherrret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE
Definitive studies of the relationships between West Nile and
Kunjin viruses
JOURNAL
Unpublished
REFERENCE
3 (bases 1 to 607)
AUTHORS
Scherrret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE
Direct Submission
JOURNAL
Submitted (22-AUG-2000) Microbiology and Parasitology, University
of Queensland, St Lucia, QLD 4072, Australia
FEATURES
Location/Qualifiers
1..607
/organism="Kunjin virus"
/mol_type="genomic RNA"
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CDS
Query Match          96.8%; Score 30; DB 14; Length 601;
Best Local Similarity 100.0%; Pred. No. 7.1e-07;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGCCACCGGAAGTTGAGTAGACGGTGCTG 31
    |||||
Db 362 CGCCACCGGAAGTTGAGTAGACGGTGCTG 391

RESULT 36
AF297844
LOCUS
DEFINITION
Kunjin virus isolate CHI6465C nonstructural protein 5 gene, partial
cde.
ACCESSION
AF297844
VERSION
AF297844.1 GI:11991972
KEYWORDS
Kunjin virus
ORGANISM
Kunjin virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
1 (bases 1 to 607)
AUTHORS
Scherrret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE
The relationships between West Nile and Kunjin viruses
JOURNAL
Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE
21469816
PUBMED
11585535
REFERENCE
2 (bases 1 to 607)
AUTHORS
Scherrret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE
Definitive studies of the relationships between West Nile and
Kunjin viruses
JOURNAL
Unpublished
REFERENCE
3 (bases 1 to 607)
AUTHORS
Scherrret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.
and Hall,R.A.
TITLE
Direct Submission
JOURNAL
Submitted (22-AUG-2000) Microbiology and Parasitology, University
of Queensland, St Lucia, QLD 4072, Australia
FEATURES
Location/Qualifiers
1..607
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/db_xref="taxon:11077"
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 7.1e-07;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGCCACCGGAAGTTGAGTAGACGGTGCTG 31
    |||||
Db 375 CGCCACCGGAAGTTGAGTAGACGGTGCTG 404

RESULT 37
AF297856
LOCUS
DEFINITION
Kunjin virus isolate P1553 nonstructural protein 5 gene, partial
cde.
ACCESSION
AF297856
VERSION
AF297856.1 GI:11992002
KEYWORDS
Kunjin virus
ORGANISM
Kunjin virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
REFERENCE
1 (bases 1 to 609)
AUTHORS
Scherrret,J.H., Poldinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V.,
Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE
The relationships between West Nile and Kunjin viruses
JOURNAL
Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE
21469816
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11585535
REFERENCE 2 (bases 1 to 609)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.
TITLE Definitive studies of the relationships between West Nile and Kunjin viruses
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 609)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.
TITLE Direct Submission
JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University of Queensland, St Lucia, QLD 4072, Australia
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LOCUS Kunjin virus isolate MRM5373 RNA linear VRL 05-MAR-2002
DEFINITION Kunjin virus isolate MRM5373 nonstructural protein 5 gene, partial cds.
ACCESSION AF297859
VERSION AF297859.1 GI:11992008
KEYWORDS
SOURCE Kunjin virus
ORGANISM Kunjin virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 620)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V., Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE The relationships between West Nile and Kunjin viruses
JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE 21469816
PUBMED 11585535
REFERENCE 2 (bases 1 to 620)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.
TITLE Definitive studies of the relationships between West Nile and Kunjin viruses
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 620)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.
TITLE Definitive studies of the relationships between West Nile and Kunjin viruses
JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University of Queensland, St Lucia, QLD 4072, Australia
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Db 371 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 400
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DEFINITION Kunjin virus isolate CH16514C nonstructural protein 5 gene, partial cds.
ACCESSION AF297842
VERSION AF297842.1 GI:11991974
KEYWORDS
SOURCE Kunjin virus
ORGANISM Kunjin virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group.
REFERENCE 1 (bases 1 to 622)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V., Lipkin,W.I., Briese,T., Gould,E.A. and Hall,R.A.
TITLE The relationships between West Nile and Kunjin viruses
JOURNAL Emerging Infect. Dis. 7 (4), 697-705 (2001)
MEDLINE 21469816
PUBMED 11585535
REFERENCE 2 (bases 1 to 622)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.
TITLE Definitive studies of the relationships between West Nile and Kunjin viruses
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 622)
AUTHORS Scherret,J.H., Poidinger,M., Mackenzie,J.S., Broom,A.K., Deubel,V. and Hall,R.A.
TITLE Direct Submission
JOURNAL Submitted (22-AUG-2000) Microbiology and Parasitology, University of Queensland, St Lucia, QLD 4072, Australia
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DEFINITION	West Nile virus strain 645 bp RNA linear VRL 21-MAY-2003									
ACCESSION	AY187012									
VERSION	AY187012.1 GI:30983578									
KEYWORDS										
SOURCE	West Nile virus (WNV)									
ORGANISM	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Japanese encephalitis virus group.									
REFERENCE	1 (bases 1 to 645)									
AUTHORS	Beasley,D.W., Davis,C.T., Guzman,H., Vanlandingham,D.L., Travassos da Rosa,A.P., Parsons,R.E., Higgs,S., Tesh,R.B. and Barrett,A.D.									
TITLE	Limited evolution of West Nile virus has occurred during its southwesterly spread in the United States									
JOURNAL	Virology 309 (2), 190-195 (2003)									
MEDLINE	22644768									
PubMed	12758166									
REFERENCE	2 (bases 1 to 645)									
AUTHORS	Beasley,D.W.C., Davis,C.T., Guzman,H., Vanlandingham,D.L., Travassos da Rosa,A.P.A., Parsons,R.E., Higgs,S., Tesh,R.B. and Barrett,A.D.T.									
TITLE	Direct Submission									
JOURNAL	Submitted (26-NOV-2002) Pathology, University of Texas Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA									
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    Beasley,D.W., Davis,C.T., Guzman,H., Vanlandingham,D.L., Travassos
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    Limited evolution of West Nile virus has occurred during its
    southwesterly spread in the United States
    Virology 309 (2), 190-195 (2003)
  JOURNAL
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    Beasley,D.W.C., Davis,C.T., Guzman,H., Vanlandingham,D.L.,
    Travassos da Rosa,A.P.A., Parsons,R.E., Higgs,S., Tesh,R.B. and
    Barrett,A.D.T.
    Direct Submission
    Submitted (26-NOV-2002) Pathology, University of Texas Medical
    Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
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  VERSION
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  SOURCE
    West Nile virus
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    Flavivirus; Japanese encephalitis virus group.
  REFERENCE
    1 (bases 1 to 10945)
    Jia,X.Y., Briese,T., Jordan,I., Rambaut,A., Chi,H.C.,
```

Mackenzie, J.S., Hall, R.A., Scherret, J. and Lipkin, W.I.
Genetic analysis of West Nile New York 1999 encephalitis virus
Lancet 354 (9194), 1971-1972 (1999)
20086017
10622305
2 (bases 1 to 10945)
Jia, X.Y., Briese, T., Jordan, I. and Lipkin, W.I.
Direct Submission
Submitted (06-NOV-1999) Emerging Diseases Laboratory, Dept.
Microbiology & Molecular Genetics and Neurology, University of
California, Irvine, 3101 Gillespie Neuroscience Facility, Irvine,
CA 92697-4292, USA

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RESULT 49

AF206518 10975 bp DNA linear VRL 08-MAY-2000
LOCUS West Nile virus isolate 2741, complete genome.
DEFINITION Flavivirus; Japanese encephalitis virus group.
ACCESSION AF206518
VERSION AF206518.2 GI:7717200
KEYWORDS West Nile virus

SOURCE

ORGANISM West Nile virus
REFERENCE 1 (bases 1 to 10975)
AUTHORS Anderson, J.F., Andreadis, T.G., Vosebrinck, C.R., Tirrell, S.,
Wakem, B.M., French, R.A., Garmendia, A.E. and Van Kruiningen, H.J.

TITLE

Isolation of West Nile virus from mosquitoes, crows, and a Cooper's hawk in Connecticut

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LLMVGISLIREKRAAKKAGSLCLALAGTGLFNPMILAGLIAADPNRKRGP
TEWTAAGLMEALVGLAELDIDSMALPMTIAGLMEAFVISGKSTDMWERTADISW
ESDAETGSSERVDVRLDDGDFNOLMNDGAPWKIWMLEMACLAISAYTPWAILPSV
GFWTILQYTKRGVLDTPPKYKKGDTTGVYRIMTRGLLGSQAGAVNVEGVFH
TLWHTTGAALESGBRDLDPYWSKEDRLCYGPKWLOHKNWQDEQOMIVVEPGK
VKNQTKPFVFTPEGEIYAVTLPDFTGSGPIVDKNGDVLGYNGVIMENGSIYIS
AIVQGERMDEPIPAGEPEMLRKKOITVLDLHPGAGKTRILPOIKEAINRRLRTAV
LAPTVAAEMAEALRGLPIRYQTSVTEHNGNEIVDMVCHATLTHRLMSPHRVPY
NLPMDEAHTPASIAARGYISTKVELGEAAAIPMTATPPGTSDDPPSPESPISDLQ
TEIPDRAMNSGEMTEYIGKTVWFVFSVMGNEIALCLQRAKGVQLNRKKSIEY
PKCNDNDVITDISEMGANFKASRVDSRSVKPTIITEGEGRVILGEPSAVTAA
SAAQRRGRVNPQVDEYCYGHTNEDDSNFAHTEARIMLDNNMNGLIAOFYQ
PEREKVYTWGEYRLRGERKNFLELLRTADLPVWLKYVAAAGVSYHRRWCFCGPR
TNTILDNNEVEVITKGERKILRPRWIDARVYSDHQAOKAFKDFASGKRSGIOLIEV
LCKMPEHFGKTEALDNTYVATAEKGRHARMALELPDALQIALLIALLSVMTMG
VFLLMQKIGIKGLGGVAVGVATFFCWMAEVPGTKIAGMLLLSLLMLIILPIPEK
QRSQDNLQAVFLICVMTLVSAVANEMGLDKTSDISLFGRIEVENKFSMGFEFL
LDRPATASLVATVTLPLKHLITSDYINTSLTSINQVQASALFTIARGFPFVDV
GVSALLAAGCWQVTLVTVTAATLLFCHYAYMVPQWQAEAMRQAORTAAGIMKNA
VVDGIVATDVPELERTPIQKVKQIIMLILVSLAAVVPVSVKTVREAGILITAAAV
TLWENGASVWNAITAGLCHIMRGWLSCLITWTLIKWMEKPKLKGAGKRTLGE
VWKLRLQMTKEFTYRKALIEVDRSAAKHARKENGVTHGPHVSRGTAKURLVER
RFLPEVGVVIDLGGCGGYYMATQKRVQVGYTKGPGHEEPQLVQSYGWNIVTM
KSGVDVYFPRSECCDTLDCDIGESSAEVEEHTIRVLEWVEDWLRGPREFCVKVL
CYPMPKVIKEMELLQRRYGGGLVRNPLSRNSNTHMYVWSRAGSNVHSVNMSTQVLLG
RMEKRTWGPQVEDVNLGSGTRAVGKPLNLSDTSKIKNRIERLREYSSTWHDENH
PYRTWYHGSYDVKPTGSASLVANGVRLSKSPDITINVTWMTADTTPGQORVEK
EKVDYKAPPPGVKXVNLNETNWLWAFILAREKPRMCSREEFIRKVNNAALGAMFE
EQNQRSAEVEDPKFMDVDEEAREHLRGECCTCIYMMGKREKPKGFEKAGKSR
AIFWMLGARFLFEALGNLBNHWRKNSGGVEGLQKGLYILREVHTRPGGKI
YADTAGMDTRIITRADLENEAKVLELLDGEHRLARAIITLYTRHKVWVRPAADGR
TVMDVLSREDORSGQVTVYALNTFTNLAVQLVRMEGEVIGPDDVEKLTGKGPVKY
RTWLENGEERLSMAVSGDDCVKPLDDREATSLHFLNAMSVRKDIQEWKPSGTWY
DMQVQFPCSNHTELLMKDCRTLVPQCRQDELGRARISPGAGWNRVDRACLAASYA
QWMLLYFHRRDLRLMANAICSAVPVNVPTGRTTWSIHAGGEMWTTEDMLEVNRVW
IEENEMWEDKTVPSKRSYSGREDIWCGLSIGTTRATWAEINQVAINQVRAIIG
DEKYVDVMSLSKREDTTLIVEDTVL"

ORIGIN

Query Match 96.8%; Score 30; DB 14; Length 10989;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCGCCACCGGAAGTTCAGTAGCGGTGCTG 31
DB 10503 CCGCCACCGGAAGTTCAGTAGCGGTGCTG 10532

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 25, 2005, 00:26:37 ; Search time 157.747 Seconds
(without alignments)
1163.332 Million cell updates/sec

Title: US-10-688-489-59

Perfect score: 31

Sequence: 1 tcgcaccggaagttagtagacgtgctg 31

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : N_Geneseq_16Dec04.*

1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002as.*

7: Geneseqn2002bs.*

8: Geneseqn2003as.*

9: Geneseqn2003bs.*

10: Geneseqn2003cs.*

11: Geneseqn2003ds.*

12: Geneseqn2004as.*

13: Geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	31	ADN36737	Adn36737 West Nile
2	30	96.8	10945	ADN32078	Adn32078 Genomic D
3	30	96.8	10945	ADN36768	Adn36768 West Nile
4	30	96.8	10975	ADN98022	Adn98022 West Nile
5	30	96.8	11029	ABZ68481	Abz68481 Nucleotid
6	30	96.8	11029	ABV74821	Abv74821 West Nile
7	30	96.8	11029	ADN98023	Adn98023 West Nile
8	28	90.3	10962	ADK13681	Adk13681 West Nile
9	22	71.0	22	ADN36746	Adn36746 West Nile
10	21	67.7	21	ADN36741	Adn36741 West Nile
11	21	67.7	21	ADN36745	Adn36745 West Nile
12	21	67.7	21	ADN36748	Adn36748 West Nile
13	20	64.5	20	ADN36749	Adn36749 West Nile
14	20	64.5	20	ADN36740	Adn36740 West Nile
15	20	64.5	20	ADN36747	Adn36747 West Nile
16	19	61.3	19	ADN36744	Adn36744 West Nile
17	19	61.3	19	ADN36738	Adn36738 West Nile
18	18	58.1	18	ADN36742	Adn36742 West Nile
19	18	58.1	19	ADN36739	Adn36739 West Nile
20	18	58.1	26	ADN36825	Adn36825 West Nile

ACN01373	WNV Hamme	17	54.8	17	6	ACN01373
ACN04650	WNV Zinzy	17	54.8	17	6	ACN04650
ACN07292	WNV Amber	17	54.8	17	6	ACN07292
ACN09625	WNV minus	17	54.8	17	6	ACN09625
ACN07461	WNV minus	17	54.8	17	6	ACN07461
ACN09628	WNV minus	17	54.8	17	6	ACN09628
ACN01372	WNV Hamme	17	54.8	17	6	ACN01372
ACN13635	WNV minus	17	54.8	17	6	ACN13635
ACN07462	WNV minus	17	54.8	17	6	ACN07462
ACN09624	WNV minus	17	54.8	17	6	ACN09624
ACN05425	WNV DNazy	17	54.8	17	6	ACN05425
ACN04649	WNV Zinzy	17	54.8	17	6	ACN04649
ACN09626	WNV minus	17	54.8	17	6	ACN09626
ACN07290	WNV Amber	17	54.8	17	6	ACN07290
ACN07291	WNV Amber	17	54.8	17	6	ACN07291
ACN07463	WNV minus	17	54.8	17	6	ACN07463
ACN07465	WNV minus	17	54.8	17	6	ACN07465
ACN09627	WNV minus	17	54.8	17	6	ACN09627
ACN07293	WNV Amber	17	54.8	17	6	ACN07293
ACN07464	WNV minus	17	54.8	17	6	ACN07464
Adn36743	West Nile	18	54.8	18	12	Adn36743
Abi04952	Drosophila	17	54.8	17	6	Abi04952
ACN14228	WNV minus	17	51.6	17	6	ACN14228
ACN12344	WNV minus	17	51.6	17	6	ACN12344
ACN03350	WNV Inozy	17	51.6	17	6	ACN03350
Aaf08395	Fusarium	16	51.6	16	6	Aaf08395
Abz71129	Mycobacte	16	51.6	16	6	Abz71129
Aah51995	Mycobacte	16	51.6	16	6	Aah51995
Abi28588	Drosophila	16	51.6	16	6	Abi28588
Continuation (15 o		16	51.6	16	6	Continuation (15 o
Continuation (15 o		16	51.6	16	6	Continuation (15 o
ACN07294	WNV Amber	17	48.4	17	6	ACN07294
ACN12345	WNV minus	17	48.4	17	6	ACN12345
ACN09623	WNV minus	17	48.4	17	6	ACN09623
Adn36782	West Nile	21	48.4	21	12	Adn36782
Adn36863	West Nile	22	48.4	22	12	Adn36863
ACI27596	Human mic	25	48.4	25	9	ACI27596
Adn36864	West Nile	28	48.4	28	12	Adn36864
Adn36780	West Nile	69	48.4	69	12	Adn36780
Adn36779	West Nile	87	48.4	87	12	Adn36779
Abx83471	Corn ear-	214	48.4	214	10	Abx83471
ACH03748	Wheat ste	436	48.4	436	9	ACH03748
ACH03761	Wheat ste	551	48.4	551	10	ACH03761
ACH03758	Corn ster	600	48.4	600	9	ACH03758
ACH03757	Corn ster	616	48.4	616	9	ACH03757
Abq42685	Oligonuci	673	48.4	673	9	Abq42685
Abq42684	Oligonuci	1795	48.4	1795	6	Abq42684
Aah65402	C glutam	1795	48.4	1795	6	Aah65402
AdL65984	C. glutam	1863	48.4	1863	5	AdL65984
AdR85016	Aspergill	1969	48.4	1969	11	AdR85016
ACC57669	Mouse pro	2448	48.4	2448	13	ACC57669
Aat11083	Mouse JAK	3246	48.4	3246	8	Aat11083
AdR4429	Aspergill	4016	48.4	4016	2	AdR4429
Adq97983	Mouse can	8448	48.4	8448	13	Adq97983
Continuation (19 o		35998	48.4	35998	12	Continuation (19 o
Aah68525	C glutam	110000	48.4	110000	10	Aah68525
ACN04651	WNV Zinzy	349980	48.4	349980	5	ACN04651
ACN03349	WNV Inozy	45.2	48.4	45.2	17	ACN03349
Aaas3431	Human thi	17	45.2	17	6	Aaas3431
Aa123156	Human bre	103	45.2	103	3	Aa123156
Aa37214	Novel hum	127	45.2	127	4	Aa37214
Aa40667	Human sec	151	45.2	151	4	Aa40667
Aa114294	Human bre	220	45.2	220	2	Aa114294
Aa42671	Human 5'	231	45.2	231	4	Aa42671
Aa41295	Human sec	236	45.2	236	3	Aa41295
ABV08938	Human pro	370	45.2	370	5	ABV08938
Aa41295	Human sec	400	45.2	400	2	Aa41295
ADQ84440	Human tum	408	45.2	408	12	ADQ84440
ADQ85224	Human tum	408	45.2	408	12	ADQ85224
Adq83268	Human tum	408	45.2	408	13	Adq83268
Aav33191	Secrated	419	45.2	419	2	Aav33191
Aa40834	Secrated	419	45.2	419	2	Aa40834
Adm77856	Human CDN	419	45.2	419	11	Adm77856

C 94	14	45.2	419	12	ADP19132	Adp19132 Human sec
C 95	14	45.2	425	5	AAZ40815	Aaz40815 Secreted
C 96	14	45.2	425	5	AAS84649	Aas84649 DNA encod
C 97	14	45.2	425	11	ADM7792	Adm7792 Human cDN
C 98	14	45.2	425	12	ADP19113	Adp19113 Human sec
C 99	14	45.2	427	5	ABV38826	Abv38826 Human pro
100	14	45.2	456	9	ACH39996	Ach39996 Human foe
101	14	45.2	515	6	ABV97326	Abv97326 Human pan
102	14	45.2	516	6	ABV96872	Abv96872 Human pan
C 103	14	45.2	516	13	ACN46696	Acn46696 Cotton pr
C 104	14	45.2	542	12	ADJ10678	Adj10678 Recombina
C 105	14	45.2	564	3	AAC08029	Aac08029 Human sec
C 106	14	45.2	574	13	ADR65698	Adr65698 Cotton CD
C 107	14	45.2	576	6	ACN51680	Acn51680 Cotton an
C 108	14	45.2	654	4	ABA09109	Abao9109 Human HSP
C 109	14	45.2	659	13	ADR63650	Adr63650 Cotton CD
C 110	14	45.2	668	5	AAH64916	Aah64916 Human sec
C 111	14	45.2	941	12	ADO40822	Ado40822 DNA encod
C 112	14	45.2	1087	11	ACN84344	Acn84344 Breast ca
C 113	14	45.2	1100	2	AAV18890	Aav18890 Rat Hyper
C 114	14	45.2	1100	3	AAV75037	Aav75037 cDNA enco
C 115	14	45.2	1100	10	ADG32027	Adg32027 Rat hyper
C 116	14	45.2	1149	10	ACF68233	Acf68233 Photorhab
C 117	14	45.2	1455	3	AAF21889	Aaf21889 Human bre
C 118	14	45.2	1659	13	ADS48819	Ads48819 Bacterial
C 119	14	45.2	1738	9	ADA13428	Ada13428 Human rho
120	14	45.2	1738	9	ADA13428	Ada13428 Human rho
121	14	45.2	1738	10	ADG47133	Adg47133 Human rho
122	14	45.2	1738	10	ADG47133	Adg47133 Human rho
123	14	45.2	1738	12	ADQ86031	Adq86031 Human tum
C 124	14	45.2	1845	5	AAS89517	Aas89517 DNA encod
C 125	14	45.2	1854	11	ADM03408	Adm03408 Human cDN
C 126	14	45.2	1912	5	AAS84651	Aas84651 DNA encod
C 127	14	45.2	1955	4	AAO09956	Aao09956 Human dru
C 128	14	45.2	1959	3	AAAS59835	Aas59835 Human SEC
C 129	14	45.2	1959	3	AAAS53429	Aas53429 Human thi
C 130	14	45.2	2010	4	ABL22235	Abi22235 Drosophil
C 131	14	45.2	2114	13	ADQ85985	Adq85985 Human tum
C 132	14	45.2	2180	11	ADN95847	Adn95847 Human BEC
C 133	14	45.2	2180	13	ACN40882	Acn40882 Tumour-as
C 134	14	45.2	2187	3	AAI292220	Aai292220 Human thi
C 135	14	45.2	2187	6	AAI72961	Aai72961 Human thi
C 136	14	45.2	2310	11	ABD11602	Abd11602 Pseudomon
C 137	14	45.2	2655	5	AAS89516	Aas89516 DNA encod
C 138	14	45.2	2816	4	ABL13687	Abi13687 Drosophil
C 139	14	45.2	3085	4	ABL16797	Abi16797 Drosophil
140	14	45.2	3562	5	ABA16080	Abal6080 Human ner
141	14	45.2	3564	5	ABA16079	Abal6079 Human ner
142	14	45.2	3564	5	ABA16081	Abal6081 Human ner
C 143	14	45.2	3858	4	ABL13828	Abi13828 Drosophil
C 144	14	45.2	4488	4	ABL17095	Abi17095 Drosophil
145	14	45.2	4618	4	ABL22234	Abi22234 Drosophil
C 146	14	45.2	4851	8	ACN37619	Acn37619 Prokaryot
C 147	14	45.2	5186	4	ABL13686	Abi13686 Drosophil
C 148	14	45.2	6307	6	ABL33341	Abi33341 Human im
C 149	14	45.2	6898	6	ABN80223	Abn80223 Human che
C 150	14	45.2	6932	13	ADR84543	Adr84543 Aspergill
C 151	14	45.2	8046	4	ABL17094	Abi17094 Drosophil
C 152	14	45.2	10428	12	ADJ81646	Adj81646 Human tyr
C 153	14	45.2	18796	4	AAS59517	Aas59517 Propionib
C 154	14	45.2	18796	8	ACF64446	Acf64446 Propionib
C 155	14	45.2	20261	4	ABL16796	Abi16796 Drosophil
C 156	14	45.2	24593	1	AAAS0226	Aas0226 Sequence
C 157	14	45.2	24596	1	AAAS0182	Aas0182 Complete
C 158	14	45.2	34719	12	ADP90617	Adp90617 Micromono
C 159	14	45.2	43712	12	ADQ18757	Adq18757 Human sof
C 160	14	45.2	47318	11	ACN44730	Acn44730 Human gen
C 161	14	45.2	66566	3	AAAS3450	Aas3450 Human thi
C 162	14	45.2	110000	3	AAF22305	Continuation (4 of
C 163	14	45.2	110000	3	AAF22305	Continuation (10 of
C 164	14	45.2	110000	3	AAF22305	Continuation (4 of
C 165	14	45.2	185035	6	ABT10147	Abt10147 Human bre
C 166	14	45.2	185035	8	ACA64951	Aca64951 Human FEN
C 167	14	45.2	185035	12	ADQ20284	Adq20284 Human sof
C 168	13	41.9	13	5	ABH13266	Abh13266 Oligonucl
C 169	13	41.9	13	5	ABH13267	Abh13267 Oligonucl
C 170	13	41.9	17	6	ACN09622	Acn09622 WNV minus
C 171	13	41.9	17	6	ACN03348	Acn03348 WNV Inozy
C 172	13	41.9	17	6	ACN14229	Acn14229 WNV minus
C 173	13	41.9	18	2	AAV44610	Aav44610 Human unc
174	13	41.9	19	12	ADN36783	Adn36783 West Nile
175	13	41.9	40	3	AAZ96102	Aaz96102 Polyuucle
C 176	13	41.9	52	6	AAI72468	Aai72468 D. melano
C 177	13	41.9	52	8	ACA02212	ACA02212 D. melano
C 178	13	41.9	59	4	AAI14118	Aai14118 Antibody
C 179	13	41.9	87	2	AAV08087	Aav08087 Fragment
C 180	13	41.9	87	2	AAV08087	AAV08087 Synthetic
C 181	13	41.9	88	6	AAI72469	Aai72469 D. melano
C 182	13	41.9	88	8	ACA02213	ACA02213 D. melano
C 183	13	41.9	100	8	ACD69141	AcD69141 E. coli K
C 184	13	41.9	216	11	ABD15615	Abd15615 Pseudomon
C 185	13	41.9	300	6	ABL73959	Abi73959 Corn taes
C 186	13	41.9	302	4	AAAS59160	Aas59160 Human can
C 187	13	41.9	313	4	AAH71336	Aah71336 Human cer
C 188	13	41.9	334	3	AAA31143	Aaa31143 Plant mic
C 189	13	41.9	343	6	ABQ85935	Abq85935 Arabidops
C 190	13	41.9	358	6	ABQ85702	Abq85702 Arabidops
C 191	13	41.9	366	4	ABQ85441	Abq85441 DNA encod
C 192	13	41.9	368	9	ACH46578	Ach46578 Human inf
C 193	13	41.9	375	13	ACN50396	Acn50396 Cotton ma
C 194	13	41.9	390	2	AAV08037	Aav08037 Light cha
C 195	13	41.9	390	2	AAZ06301	Aaz06301 Human chi
C 196	13	41.9	413	8	ABX44157	Abx44157 Bovine ES
C 197	13	41.9	424	6	ABT06970	Abt06970 Human ova
C 198	13	41.9	424	6	ABT06970	Abt06970 Human ova
C 199	13	41.9	429	8	ABX72848	Abx72848 Human ova
C 200	13	41.9	445	11	ADM65226	Adm65226 Bovine ES
C 201	13	41.9	445	11	ADM65181	Adm65181 Human Y C
C 202	13	41.9	446	11	ADM65178	Adm65178 Human Y C
C 203	13	41.9	454	3	AAA31071	Aaa31071 Plant mic
C 204	13	41.9	458	6	ABL93710	Abi93710 Arabidops
C 205	13	41.9	462	5	ABV49656	Abv49656 Human pro
C 206	13	41.9	464	6	ABN25122	Abn25122 Human ORF
C 207	13	41.9	468	4	ABA26645	AbA26645 Probe #51
C 208	13	41.9	473	9	ACH35927	Ach35927 Human end
C 209	13	41.9	474	3	AAC42810	Aac42810 Arabidops
C 210	13	41.9	490	8	ABZ55607	Abz55607 Aspergill
C 211	13	41.9	498	10	ADE81712	Ade81712 Arabidops
C 212	13	41.9	499	2	AAQ40729	Aaq40729 Human eps
C 213	13	41.9	500	13	ACN45774	Acn45774 Cotton pr
C 214	13	41.9	501	6	ABQ42601	Abq42601 Oligonucl
C 215	13	41.9	501	6	ABQ42601	Abq42601 Oligonucl
C 216	13	41.9	507	6	ABN68232	Abn68232 Streptoco
C 217	13	41.9	511	6	ABQ21475	Abq21475 Oligonucl
C 218	13	41.9	511	6	ABQ21474	Abq21474 Oligonucl
C 219	13	41.9	519	13	ACN45487	Acn45487 Cotton pr
C 220	13	41.9	519	10	ADE59753	Ade59753 Rat gene
C 221	13	41.9	528	6	ABZ14654	Abz14654 Arabidops
C 222	13	41.9	528	13	ACN60951	Acn60951 Cotton, gy
C 223	13	41.9	529	5	AAH87936	Aah87936 Peppermin
C 224	13	41.9	546	4	ABL13169	Abi13169 Drosophil
C 225	13	41.9	546	9	ACH27564	Ach27564 Human adu
C 226	13	41.9	549	3	AAC94357	Aac94357 Cat flea
C 227	13	41.9	559	6	ABQ16264	Abq16264 Oligonucl
C 228	13	41.9	559	3	ABQ16265	Abq16265 Oligonucl
C 229	13	41.9	566	3	ABK40030	Abk40030 Arabidops
C 230	13	41.9	579	6	ABK76120	Abk76120 Bacillus
C 231	13	41.9	580	4	AAI93755	Aai93755 Human pol
C 232	13	41.9	583	6	ABQ60208	Abq60208 Human col
C 233	13	41.9	597	4	ABL22817	Abi22817 Drosophil
C 234	13	41.9	600	6	ABK48977	Abk48977 Physice-b
C 235	13	41.9	602	6	ABV96080	Abv96080 Human pan
C 236	13	41.9	603	10	ADF00887	Adf00887 Bacterial
C 237	13	41.9	612	13	ACN46486	Acn46486 Cotton pr
C 238	13	41.9	624	11	ABD03668	Abd03668 Pseudomon
C 239	13	41.9	628	4	AAK91018	Aak91018 Human dig

C 240	13	41.9	628	5	AA332053	Aas32053 Human liv	C 313	13	41.9	1320	10	ADC61134	Adc61134 Baeyer-Vi
C 241	13	41.9	628	6	ABN90408	Abn90408 Human liv	314	13	41.9	1324	3	AAC45583	Aac45583 Arabidops
C 242	13	41.9	628	11	ADJ15321	Adj15321 Human liv	315	13	41.9	1325	3	AAC33679	Aac33679 Arabidops
C 243	13	41.9	630	4	AA080468	Aa080468 Human sec	C 316	13	41.9	1326	5	AAH68314	Aah68314 C glutami
C 244	13	41.9	651	8	ACA30042	Aca30042 Prokaryot	C 317	13	41.9	1332	13	ADS61662	AdS61662 Bacterial
C 245	13	41.9	651	10	ADH85534	Adh85534 Enterococ	C 318	13	41.9	1338	4	ABL28569	AbL28569 Drosophil
C 246	13	41.9	651	11	ABD15572	Abd15572 Pseudomon	C 319	13	41.9	1342	9	ABK65332	Abk65332 Arabidops
C 247	13	41.9	654	10	ADC93120	Adc93120 E. faeciu	C 320	13	41.9	1342	6	ADAI5462	AdaI5462 DNA encod
C 248	13	41.9	657	10	ADP00507	Adp00507 Bacterial	C 321	13	41.9	1342	10	ADD30225	Add30225 Plant yie
C 249	13	41.9	660	4	AAK66329	Aak66329 Human imm	C 322	13	41.9	1342	12	ADI43616	Adi43616 Plant tra
C 250	13	41.9	666	6	ABQ22365	Abq22365 Oligonucl	C 323	13	41.9	1342	12	ADO02314	Ado02314 Thalecres
C 251	13	41.9	666	6	ABQ22364	Abq22364 Oligonucl	C 324	13	41.9	1342	12	ADO03426	Ado03426 Thalecres
C 252	13	41.9	667	4	AAF71326	Aaf71326 Corynebac	C 325	13	41.9	1342	12	ADQ16261	Adq16261 Thalecres
C 253	13	41.9	677	6	ABQ65789	Abq65789 Arabidops	C 326	13	41.9	1345	6	ABN60012	Abn60012 Novel hum
C 254	13	41.9	684	3	AAZ36248	Aaz36248 cDNA enco	C 327	13	41.9	1353	6	ABN101533	Abn101533 Murine ap
C 255	13	41.9	686	3	AAFI4763	Aafi4763 Aspergill	C 328	13	41.9	1359	11	ABD13452	Abd13452 Pseudomon
C 256	13	41.9	717	2	AAV44637	Aav44637 Human unc	C 329	13	41.9	1360	2	AAV21282	Aav21282 Mus muscu
C 257	13	41.9	732	12	ACH87446	Ach87446 Human gen	C 330	13	41.9	1376	12	ADL90359	Adl90359 Clostridi
C 258	13	41.9	743	5	AA591497	Aa591497 DNA encod	C 331	13	41.9	1376	12	ADL90357	Adl90357 Clostridi
C 259	13	41.9	751	4	AA523274	Aa523274 DNA encod	C 332	13	41.9	1376	12	ADL90353	Adl90353 Clostridi
C 260	13	41.9	752	4	AAH03559	Aah03559 Human cdn	C 333	13	41.9	1376	12	ADL90355	Adl90355 Clostridi
C 261	13	41.9	753	10	ADP81903	Adp81903 Leukaemia	C 334	13	41.9	1381	12	ADN60478	Adn60478 B. lichen
C 262	13	41.9	761	6	ABQ32387	Abq32387 Oligonucl	C 335	13	41.9	1385	12	ADL90351	Adl90351 Clostridi
C 263	13	41.9	761	6	ABQ32386	Abq32386 Oligonucl	C 336	13	41.9	1404	11	ABD05514	Abd05514 Pseudomon
C 264	13	41.9	780	11	ABD15488	Abd15488 Pseudomon	C 337	13	41.9	1405	12	ADN60474	Adn60474 B. lichen
C 265	13	41.9	795	8	ABZ51382	Abz51382 Aspergill	C 338	13	41.9	1411	3	AAC46753	Aac46753 Arabidops
C 266	13	41.9	800	12	ADL18184	Adl18184 P. aerugi	C 339	13	41.9	1431	3	AAC46348	Aac46348 Arabidops
C 267	13	41.9	803	2	AAZ24839	Aaz24839 Human sec	C 340	13	41.9	1433	3	ABL08297	AbL08297 Drosophil
C 268	13	41.9	803	8	ADA40091	Ada40091 Human sec	C 341	13	41.9	1435	3	ACL040039	Acl040039 Arabidops
C 269	13	41.9	803	10	ADC73665	Adc73665 Human sec	C 342	13	41.9	1447	5	AA565340	Aa565340 DNA encod
C 270	13	41.9	814	3	AAF08534	Aaf08534 Fusarium	C 343	13	41.9	1462	4	ABL09327	AbL09327 Drosophil
C 271	13	41.9	825	8	ACA51699	Aca51699 Prokaryot	C 344	13	41.9	1464	4	AA54301	Aa54301 Pseudomon
C 272	13	41.9	831	5	AA578026	Aa578026 DNA encod	C 345	13	41.9	1497	2	AAQ03572	Aaq03572 Sequence
C 273	13	41.9	833	11	ADP65985	Adp65985 Mouse EST	C 346	13	41.9	1497	2	AAQ03571	Aaq03571 Sequence
C 274	13	41.9	849	11	ABD13423	Abd13423 Pseudomon	C 347	13	41.9	1497	2	AAQ03367	Aaq03367 Phenol ox
C 275	13	41.9	852	12	ACH87068	Ach87068 Human gen	C 348	13	41.9	1525	3	AAQ03358	Aaq03358 Arabidops
C 276	13	41.9	862	8	ACA48745	Aca48745 Prokaryot	C 349	13	41.9	1530	2	AAV21283	Aav21283 Mus muscu
C 277	13	41.9	879	12	ADN72326	Adn72326 Thale cre	C 350	13	41.9	1548	13	ADR85685	Adr85685 Aspergill
C 278	13	41.9	909	13	ADA58012	Ada58012 Bacterial	C 351	13	41.9	1548	13	ADR84911	Adr84911 Aspergill
C 279	13	41.9	936	10	ADC23800	Adc23800 DNA sequ	C 352	13	41.9	1548	13	ADR85498	Adr85498 Aspergill
C 280	13	41.9	936	12	ADH35901	Adh35901 Chemical	C 353	13	41.9	1548	13	ADR85098	Adr85098 Aspergill
C 281	13	41.9	936	12	ADG93602	Adg93602 Nitrilase	C 354	13	41.9	1558	8	ABZ34834	Abz34834 Coding se
C 282	13	41.9	936	12	ADI62199	Adi62199 DNA encod	C 355	13	41.9	1563	11	ABD03962	Abd03962 Pseudomon
C 283	13	41.9	936	12	ADI64320	Adi64320 DNA encod	C 356	13	41.9	1596	3	ADC61124	Adc61124 Baeyer-Vi
C 284	13	41.9	945	11	ABD15527	Abd15527 Pseudomon	C 357	13	41.9	1605	3	AAC42127	Aac42127 Arabidops
C 285	13	41.9	947	6	ABL89703	AbL89703 Human pol	C 358	13	41.9	1671	4	AA567852	Aaf567852 Corynebac
C 286	13	41.9	982	13	AD561352	Ad561352 Bacterial	C 359	13	41.9	1671	11	ABD03748	Abd03748 Pseudomon
C 287	13	41.9	990	3	AA333134	Aac333134 Arabidops	C 360	13	41.9	1680	11	ABD05483	Abd05483 Pseudomon
C 288	13	41.9	1002	8	ACF39335	Acf39335 Mycobacte	C 361	13	41.9	1685	3	AAC39029	Aac39029 Arabidops
C 289	13	41.9	1008	12	ADO07694	Ado07694 Mouse pol	C 362	13	41.9	1685	3	AAC39029	Aac39029 Arabidops
C 290	13	41.9	1030	3	AA45904	Aac45904 Arabidops	C 363	13	41.9	1695	12	ADJ35101	Adj35101 DNA encod
C 291	13	41.9	1035	3	AA47938	Aac47938 Arabidops	C 364	13	41.9	1730	5	AA588807	Aas88807 DNA encod
C 292	13	41.9	1045	6	ABK35230	Abk35230 Human cdn	C 365	13	41.9	1753	10	ADG32542	Adg32542 DNA encod
C 293	13	41.9	1049	3	AAK359933	Aac359933 Arabidops	C 366	13	41.9	1754	12	AAQ90837	Aax90837 Maize his
C 294	13	41.9	1058	3	AACT7714	Aac77714 Human can	C 367	13	41.9	1826	2	AAQ03578	Aaq03578 Synthetic
C 295	13	41.9	1065	13	ADR47154	Adr47154 Nocardiop	C 368	13	41.9	1833	2	AAQ03578	Aaq03578 Synthetic
C 296	13	41.9	1085	4	ABA09563	Aba09563 Human bk2	C 369	13	41.9	1833	2	AAT05738	Aat05738 B. thurin
C 297	13	41.9	1085	4	AAK52774	Aak52774 Human pol	C 370	13	41.9	1833	2	AAT40340	Aat40340 Synthetic
C 298	13	41.9	1089	2	AAV21284	Aav21284 Mus muscu	C 371	13	41.9	1833	2	ADG25143	Adg25143 Codon opt
C 299	13	41.9	1097	3	AA42285	Aac42285 Arabidops	C 372	13	41.9	1833	3	AAZ59994	Aaz59994 Synthetic
C 300	13	41.9	1098	6	AB564870	Ab564870 DNA encod	C 373	13	41.9	1833	11	ACH95250	Ach95250 Klebsell
C 301	13	41.9	1104	11	ABD05533	Abd05533 Pseudomon	C 374	13	41.9	1834	13	AD561396	Ad561396 Bacterial
C 302	13	41.9	1116	6	ABK75724	Abk75724 Bacillus	C 375	13	41.9	1860	8	ACA30477	Aca30477 Prokaryot
C 303	13	41.9	1146	10	AD50518	Aad50518 Mycobacte	C 376	13	41.9	1995	11	ABD07179	Abd07179 Pseudomon
C 304	13	41.9	1212	6	ABZ13761	Abz13761 Arabidops	C 377	13	41.9	2000	10	ACC60755	Acc60755 Gene sequ
C 305	13	41.9	1250	5	AA578025	Aa578025 DNA encod	C 378	13	41.9	2000	10	ADK61933	Adk61933 Disease c
C 306	13	41.9	1257	11	ABD02288	Abd02288 Pseudomon	C 379	13	41.9	2009	1	AAAC91211	Aac36211 Arabidops
C 307	13	41.9	1266	10	ACF58067	Acf58067 D. melano	C 380	13	41.9	2017	3	AAN91804	Aan91804 Human pap
C 308	13	41.9	1268	3	AA363637	Aac363637 Arabidops	C 381	13	41.9	2024	12	ADG98281	Adg98281 Mouse ClG
C 309	13	41.9	1278	11	ABD03879	Abd03879 Pseudomon	C 382	13	41.9	2037	5	AH567460	Aah567460 C glutami
C 310	13	41.9	1287	6	ABZ14624	Abz14624 Arabidops	C 383	13	41.9	2043	6	ABZ13532	Abz13532 Arabidops
C 311	13	41.9	1288	6	ABQ14513	Abq14513 Oligonucl	C 384	13	41.9	2043	2	ABZ23149	Abz23149 Environme
C 312	13	41.9	1288	6	ABQ14512	Abq14512 Oligonucl	C 385	13	41.9	2049	2	AAQ03573	Aaq03573 Phenol ox

C 386	13	41.9	2049	2	AAQ03366	Raq03366 Phenol ox	C 459	13	41.9	3011	6	ABS73264	Abs73264 DNA encod
C 387	13	41.9	2052	8	ACA01241	ACA01241 C. glutam	C 460	13	41.9	3121	10	ADF77733	Adf77733 Cortisol
C 388	13	41.9	2061	13	ADS47086	Ads47086 Bacterial	461	13	41.9	3173	12	ADP74349	Adp74349 Laminaria
C 389	13	41.9	2073	13	AD567086	Ad567086 Bacterial	462	13	41.9	3189	5	AAS88658	Aas88658 DNA encod
C 390	13	41.9	2115	9	ADB09684	Adb09684 Allostococ	463	13	41.9	3315	12	ADJ40049	Adj40049 Plant cDN
C 391	13	41.9	2116	12	ADN43137	Adn43137 Brassica	464	13	41.9	3322	4	ABL17363	Ab17363 Drosophil
C 392	13	41.9	2116	12	ADN43139	Adn43139 Brassica	465	13	41.9	3382	12	ADL90335	Adl90335 Clostridi
C 393	13	41.9	2127	13	ADS96513	Ads96513 Drosophil	466	13	41.9	3382	12	ADL90339	Adl90339 Clostridi
C 394	13	41.9	2160	12	ADO06867	Ado06867 Brassica	467	13	41.9	3382	12	ADL90331	Adl90331 Clostridi
C 395	13	41.9	2161	10	ADA47066	Ada47066 Rat gene	468	13	41.9	3382	12	ADL90321	Adl90321 Clostridi
C 396	13	41.9	2201	13	ADR60687	Adr60687 Cotton cD	469	13	41.9	3388	12	ADL90323	Adl90323 Clostridi
C 397	13	41.9	2203	5	AAS98810	Aas98810 DNA encod	470	13	41.9	3388	12	ADL90337	Adl90337 Clostridi
C 398	13	41.9	2209	4	AAS59649	Aas59649 Propionib	471	13	41.9	3388	12	ADL90333	Adl90333 Clostridi
C 399	13	41.9	2209	8	ACF4578	Acf4578 Propionib	472	13	41.9	3388	12	ADL90329	Adl90329 Clostridi
C 400	13	41.9	2231	4	ABL21017	Ab121017 Drosophil	473	13	41.9	3391	12	ADL90325	Adl90325 Clostridi
C 401	13	41.9	2242	13	ADR08381	Adr08381 Full leng	474	13	41.9	3397	12	ADL90327	Adl90327 Clostridi
C 402	13	41.9	2286	5	AAS88808	Aas88808 DNA encod	475	13	41.9	3433	4	ABL08296	Ab108296 Drosophil
C 403	13	41.9	2289	12	ADO63761	Ado63761 Novel hum	476	13	41.9	3483	12	ADQ21230	Adq21230 Human sof
C 404	13	41.9	2297	12	ADO23480	Ado23480 Human sof	477	13	41.9	3484	12	ADQ86815	Adq86815 Human tum
C 405	13	41.9	2359	12	ADO06881	Ado06881 Brassica	478	13	41.9	3487	9	ACD19151	Ac19151 E. coli 0
C 406	13	41.9	2361	6	AAQ40743	Aaq40743 Human kin	479	13	41.9	3514	4	ABL29371	Ab129371 Drosophil
C 407	13	41.9	2367	4	AAK94257	Aak94257 Human ful	480	13	41.9	3517	12	ADH42438	Adh42438 Novel hum
C 408	13	41.9	2367	12	ADL30839	Adl30839 Full leng	481	13	41.9	3517	12	ADH42436	Adh42436 Novel hum
C 409	13	41.9	2367	13	ADO68011	Ado68011 Recombina	482	13	41.9	3517	12	ADH42432	Adh42432 Novel hum
C 410	13	41.9	2385	10	ADD30303	Add30303 Plant yie	483	13	41.9	3569	4	AAF32715	Aaf32715 Human sec
C 411	13	41.9	2385	11	ABD13394	Abd13394 Pseudomon	484	13	41.9	3593	10	ADJ92148	Adj92148 Human hai
C 412	13	41.9	2385	12	ADJ44208	Adj44208 Plant tra	485	13	41.9	3594	10	ADC01465	Adc01465 Enterohae
C 413	13	41.9	2442	4	AAK94333	Aak94333 Human ful	486	13	41.9	3612	13	ADI79957	Adi79957 DNA of hu
C 414	13	41.9	2442	12	ADN30990	Adn30990 Full leng	487	13	41.9	3614	4	ABL24163	Ab124163 Drosophil
C 415	13	41.9	2477	11	ADN02480	Adn02480 Thiamine	488	13	41.9	3737	6	ABQ69219	Abq69219 Listeria
C 416	13	41.9	2538	4	AAH15911	Aah15911 Drosophil	489	13	41.9	3741	11	ADO77948	Ado77948 Brassica
C 417	13	41.9	2540	4	AAH33292	Aah33292 Human col	490	13	41.9	3747	3	AAC42770	Aac42770 Arabidops
C 418	13	41.9	2590	12	ADM98992	Adm98992 Diterpene	491	13	41.9	3770	11	ADL33403	Adl33403 Human tra
C 419	13	41.9	2600	12	ADL90317	Adl90317 Clostridi	492	13	41.9	3815	4	ABL15910	Ab115910 Drosophil
C 420	13	41.9	2600	12	ADL90319	Adl90319 Clostridi	493	13	41.9	3824	11	ADL33402	Adl33402 Human tra
C 421	13	41.9	2600	12	ADL90315	Adl90315 Clostridi	494	13	41.9	3832	7	ADJ73121	Adj73121 Human kid
C 422	13	41.9	2609	12	ADL90313	Adl90313 Clostridi	495	13	41.9	3832	8	ABV76014	Abv76014 Human EGF
C 423	13	41.9	2619	12	ADL90434	Adl90434 Clostridi	496	13	41.9	3832	10	ADG42127	Adg42127 Human bra
C 424	13	41.9	2623	4	ABL13168	Ab113168 Drosophil	497	13	41.9	3832	10	ADK61114	Adk61114 Ovarian c
C 425	13	41.9	2625	12	ADL90448	Adl90448 Clostridi	498	13	41.9	3832	11	ADN95678	Adn95678 Human BEC
C 426	13	41.9	2625	12	ADL90432	Adl90432 Clostridi	499	13	41.9	3838	10	ADA53335	Ada53335 Human cod
C 427	13	41.9	2625	12	ADL90450	Adl90450 Clostridi	500	13	41.9	3863	4	ABL06097	Ab106097 Drosophil
C 428	13	41.9	2625	12	ADL90446	Adl90446 Clostridi							
C 429	13	41.9	2637	12	ADL90438	Adl90438 Clostridi							
C 430	13	41.9	2640	12	ADL90311	Adl90311 Clostridi							
C 431	13	41.9	2642	10	ADL90343	Adl90343 Human cod							
C 432	13	41.9	2643	12	ADL90343	Adl90343 Clostridi							
C 433	13	41.9	2643	12	ADL90440	Adl90440 Clostridi							
C 434	13	41.9	2667	12	ADL90442	Adl90442 Clostridi							
C 435	13	41.9	2673	3	AACT6488	Aac76488 Human ORF							
C 436	13	41.9	2691	4	ABL17111	Ab117111 Drosophil							
C 437	13	41.9	2733	4	ABL08396	Ab108396 Drosophil							
C 438	13	41.9	2733	12	ADG98280	Adg98280 Rat Clg g							
C 439	13	41.9	2778	4	ABU22816	Abu22816 Drosophil							
C 440	13	41.9	2817	4	AAS52282	Aas52282 E. coli D							
C 441	13	41.9	2817	8	ACA19189	Aca19189 Prokaryot							
C 442	13	41.9	2820	2	AAQ87969	Aaq87969 E.coli is							
C 443	13	41.9	2820	2	AAQ79721	Aaq79721 Isoleucyl							
C 444	13	41.9	2837	2	AAV09621	Aav09621 Human SSR							
C 445	13	41.9	2837	10	ADA18592	Ada18592 Human DNA							
C 446	13	41.9	2839	2	AAQ46540	Aaq46540 Human SSR							
C 447	13	41.9	2839	3	AAZ92742	Aaz92742 cDNA enco							
C 448	13	41.9	2839	13	ADR25016	Adr25016 Breast ca							
C 449	13	41.9	2839	13	ACN39211	Acn39211 Tumour-as							
C 450	13	41.9	2858	10	ADB63809	Adb63809 Human cDN							
C 451	13	41.9	2859	11	ADB02340	Adb02340 Pseudomon							
C 452	13	41.9	2878	12	ADO39648	Ado39648 Yeast Bdf							
C 453	13	41.9	2888	10	ADA52697	Ada52697 Human cod							
C 454	13	41.9	2889	4	ABL20819	Ab120819 Drosophil							
C 455	13	41.9	2901	4	ABL09328	Ab109328 Drosophil							
C 456	13	41.9	2974	4	ABL26427	Ab126427 Drosophil							
C 457	13	41.9	2978	12	ADQ96147	Adq96147 T cell ac							
C 458	13	41.9	3011	6	ABS73262	Abs73262 DNA encod							

ALIGNMENTS

RESULT 1
ADN36737
ID ADN36737 standard; DNA; 31 BP.
XX
AC ADN36737;
XX
DT 15-JUL-2004 (first entry)
DE West Nile virus detection-related oligonucleotide probe SeqID59.
XX
KW hybridisation assay probe; nucleic acid detection;
KW target-complementary sequence; flavivirus; West Nile virus; WNV;
KW RNA virus; infection; meningitis; encephalitis;
XX high throughput screening; probe; ss.
OS West Nile virus.
XX
PN WO2004036190-A2.
XX
PD 29-APR-2004.
XX
PF 10-OCT-2003; 2003WO-US033639.
XX
PR 16-OCT-2002; 2002US-0418891P.
PR 25-NOV-2002; 2002US-0429006P.
PR 24-FEB-2003; 2003US-0449810P.

XX (GENP-) GEN-PROBE INC.
 XX Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
 XX WPI; 2004-389590/36.
 XX
 XX New hybridization assay probe comprising target-complementary sequence of
 XX bases, useful in detecting flavivirus, e.g. West Nile virus.
 XX
 XX Claim 18; SEQ ID NO 59; 135pp; English.
 XX
 XX This invention relates to a novel hybridisation assay probe, for
 XX detecting a nucleic acid, which is a probe sequence that comprises a
 XX target-complementary sequence of bases, and optionally one or more base
 XX sequences that are not complementary to the nucleic acid that is to be
 XX detected. The hybridisation assay probes and the kits are useful in
 XX detecting and amplifying a target nucleic acid sequence, for example
 XX flavivirus like West Nile virus, that may be present in a biological
 XX sample. West Nile virus (WNV) is an RNA virus that primarily infects
 XX birds and culex mosquitoes, with humans and horses serving as incidental
 XX hosts. Infection of humans can lead to meningitis or encephalitis. The
 XX invention may allow for accurate and efficient high throughput screening.
 XX The present sequence is that of an oligonucleotide probe which is related
 XX to the invention.
 XX
 XX Sequence 31 BP; 6 A; 8 C; 11 G; 6 T; 0 U; 0 Other;
 XX
 XX
 XX Query Match 100.0%; Score 31; DB 12; Length 31;
 XX Best Local Similarity 100.0%; Pred. No. 3.3e-08;
 XX Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 TCGCCACCGGAAGTTGAGTAGACGCTGCTG 31
 XX |||||
 XX Db 1 TCGCCACCGGAAGTTGAGTAGACGCTGCTG 31
 XX
 XX
 XX RESULT 2
 XX ADR32078
 XX ID ADR32078 standard; DNA; 10945 BP.
 XX AC ADR32078;
 XX
 XX 18-NOV-2004 (first entry)
 XX
 XX Genomic DNA of a West Nile virus.
 XX
 XX analysis; target; real time PCR; ds; genomic.
 XX
 XX West Nile virus.
 XX
 XX WO2004072230-A2.
 XX
 XX 26-AUG-2004.
 XX
 XX 10-FEB-2004; 2004WO-US0002012.
 XX
 XX 10-FEB-2003; 2003US-00361004.
 XX
 XX (CLEA-) CLEARANT INC.
 XX
 XX Mckenney K, Gillmeister L, Marlowe K, Armistead D;
 XX WPI; 2004-625843/60.
 XX
 XX Analyzing a target nucleic acid sequence in a biological material by real
 XX time PCR using nucleic acid primers that are separated by at least 750
 XX nucleic acid residues in the target sequence.
 XX
 XX Disclosure; SEQ ID NO 5; 96pp; English.
 XX
 XX The invention relates to a novel method for analysing a target nucleic
 XX acid sequence in a biological material. The method comprises adding at

CC least two nucleic acid primers that hybridise under stringent conditions
 CC to predetermined nucleic acid sequences of the target nucleic acid
 CC sequence that are separated by at least 750 nucleic acid residues,
 CC amplifying the target nucleic acid sequence by PCR, and detecting and
 CC quantifying the target nucleic acid sequence. The methods and
 CC compositions of the present invention are useful for analysing a target
 CC nucleic acid sequence in a biological material by real time PCR using
 CC nucleic acid primers that are separated by at least 750 nucleic acid
 CC residues in the target sequence. This polynucleotide sequence represents
 CC the genomic DNA of a West Nile virus used in the target analysis method
 CC of the invention.
 XX
 XX Sequence 10945 BP; 2999 A; 2457 C; 3143 G; 2346 T; 0 U; 0 Other;
 XX
 XX Query Match 96.8%; Score 30; DB 13; Length 10945;
 XX Best Local Similarity 100.0%; Pred. No. 1.1e-07;
 XX Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 2 CCGCCACCGGAAGTTGAGTAGACGCTGCTG 31
 XX |||||
 XX Db 10481 CCGCCACCGGAAGTTGAGTAGACGCTGCTG 10510
 XX
 XX
 XX RESULT 3
 XX ADR67768
 XX ID ADR67768 standard; DNA; 10945 BP.
 XX AC ADR67768;
 XX
 XX 18-NOV-2004 (first entry)
 XX
 XX West Nile virus DNA detected by novel detection method.
 XX
 XX ds; detection; pathogen.
 XX
 XX West Nile virus.
 XX
 XX WO2004072231-A2.
 XX
 XX 26-AUG-2004.
 XX
 XX 10-FEB-2004; 2004WO-US0002013.
 XX
 XX 10-FEB-2003; 2003US-00361002.
 XX
 XX (CLEA-) CLEARANT INC.
 XX
 XX Mckenney K, Gillmeister L, Marlowe K, Armistead D;
 XX WPI; 2004-625844/60.
 XX
 XX Determining level of potentially active biological pathogens in
 XX biological material, by adding nucleic acid primer pairs to biological
 XX material, amplifying target nucleic acid by PCR, detecting and
 XX quantifying target nucleic acid.
 XX
 XX Disclosure; SEQ ID NO 5; 111pp; English.
 XX
 XX The invention relates to a method of determining (M1) level of
 XX potentially active biological pathogens in biological material, involves
 XX adding at least two nucleic acid primer pairs to biological material,
 XX amplifying target nucleic acid sequences by PCR, and detecting and
 XX quantifying target nucleic acid sequences, where quantity of the nucleic
 XX acid sequences is proportional to number of biological pathogens in
 XX biological material. (M1) is useful for determining level of potentially
 XX active biological pathogens in a biological material such as cells,
 XX tissues, blood or blood components, proteins, bone, teeth, skin grafts,
 XX botanicals, food, ligaments, tendons, nerves, bone, teeth, skin grafts,
 XX bone marrow, heart valves, cartilage, cornea, arteries, veins, organs,
 XX lipids, carbohydrates, collagen, chitin and its derivatives, forensic
 XX samples, mummified material, human or animal remains, stem cells, islet
 XX of Langerhans cells, cells for transplantation, red blood cells, white
 XX blood cells or platelets. The biological pathogen is chosen from

CC bacteria, viruses, fungi and single cell parasites. The biological
 CC pathogen is chosen from Aspergillus, Candida, Histoplasma
 CC Saccharomyces, Coccidioides, Cryptococcus, Escherichia, Bacillus,
 CC Campylobacter, Helicobacter, Listeria, Clostridium, Streptococcus,
 CC Enterococcus, Staphylococcus, Brucella, Haemophilus, Salmonella,
 CC Yersinia, Pseudomonas, Serratia, Enterobacter, Klebsiella, Proteus,
 CC Citrobacter, Corynebacterium, Propionibacterium and Coccidia. The
 CC biological pathogen is chosen from Adeno-associated virus (AAV),
 CC California encephalitis virus, Coronavirus, Coxsackievirus-A,
 CC Coxsackievirus-B, Eastern equine encephalitis virus (EDEV), Echovirus,
 CC Hantavirus, Hepatitis A virus (HAV), Hepatitis C virus (HCV), Hepatitis
 CC delta virus (HDV), Hepatitis E virus (HEV), Hepatitis G virus (HGV), HIV,
 CC Human T-lymphotrophic virus (HTLV), Influenza virus (Flu virus), Measles
 CC virus (Rubella), Mumps virus, Norwalk virus, Parainfluenza virus, Polio
 CC virus, Rabies virus, Respiratory syncytial virus, Rhinovirus, Rubella
 CC virus, Saint Louis encephalitis virus, Western equine encephalitis virus
 CC (WEEV), Yellow fever virus, Adenovirus, Cytomegalovirus (CMV), Epstein-
 CC Barr virus (EBV), Hepatitis B virus (HBV), Herpes simplex virus 1, Herpes
 CC simplex virus 2, Molluscum contagiosum, Papilloma virus (HPV), Smallpox
 CC virus (Variola), Vaccinia virus, Venezuelan equine encephalitis virus
 CC (VEEV), Ebola virus, West Nile virus, Human Parvovirus B19 and Rotavirus.
 CC (M1) is useful for determining the effectiveness of a sterilization
 CC process applied to a biological material. (M1) is useful in determining
 CC whether the biological pathogen is inactive or active. (M1) enables
 CC a biological material as shown by amplification of first target sequence
 CC and whether the biological pathogen is inactive or active. (M1) enables
 CC evaluation of the effectiveness of sterilization processes, and
 CC determination of both the original level and the residual level of
 CC potentially active biological pathogens. This sequence corresponds to a
 CC West Nile virus DNA detected by the method of the invention.

SQ Sequence 10945 BP; 2999 A; 2457 C; 3143 G; 2346 T; 0 U; 0 Other;

Query Match 96.8%; Score 30; DB 13; Length 10945;
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGGCCACCGGAAGTTGAGTAGACGGTGCTG 31
 DB 10481 CGGCCACCGGAAGTTGAGTAGACGGTGCTG 10510

RESULT 4
 ADN98022
 ID ADN98022 standard; DNA; 10975 BP.

AC ADN98022;

DT 29-JUL-2004 (first entry)

DE West Nile Virus isolate 2741 complete genome sequence.

KW ds; West Nile Virus; envelope protein; glycoprotein E; flavivirus;
 KW Japanese encephalitis virus; Dengue virus; St Louis encephalitis virus.

OS West Nile virus.

PN WO2004040263-A2.

PD 13-MAY-2004.

PF 31-OCT-2003; 2003WO-US034823.

XX 31-OCT-2002; 2002US-0422755P.

PR 06-JUN-2003; 2003US-0476513P.

XX (HEAL-) HEALTH RES INC.

PI Wong SJ, Pei-Yong S;

XX WPI; 2004-400223/37.

DR GENBANK; AF206518.

XX New diagnostic kit comprising West Nile Virus (WNV) envelope protein
 PT reactive with antibody against WNV and cross-reactive with antibody
 PT against a flavivirus, useful in diagnosing flavivirus infection caused by
 PT DENV, WNV, JEV or SLEV.

PS Disclosure; Fig 37; 212pp; English.

XX The invention relates to a diagnostic kit comprising at least one
 CC isolated and purified polypeptide comprising a West Nile Virus (WNV)
 CC envelope (E) protein or its immunogenic fragment having a native
 CC conformation or non-denatured structure and that is reactive with
 CC antibodies against WNV and cross-reactive with antibodies against a
 CC flavivirus. The diagnostic kit is useful in diagnosing flavivirus
 CC infection caused by DENV, WNV, JEV or SLEV. This sequence corresponds to
 CC the complete nucleotide sequence of the WNV isolate 2741.

XX SQ Sequence 10975 BP; 3007 A; 2460 C; 3149 G; 2359 T; 0 U; 0 Other;

Query Match 96.8%; Score 30; DB 12; Length 10975;
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGGCCACCGGAAGTTGAGTAGACGGTGCTG 31
 DB 10505 CGGCCACCGGAAGTTGAGTAGACGGTGCTG 10534

RESULT 5
 ABZ68481
 ID ABZ68481 standard; DNA; 11029 BP.

XX AC ABZ68481;

XX DT 22-APR-2003 (first entry)

XX DE Nucleotide sequence of the genome of West Nile virus IS-98-ST1.

XX KW WNV; IS-98-ST1; Flavivirus; infection; encephalitis; gene; ss.

XX OS West Nile virus.

PH Key Location/Qualifiers
 FT CDS 97..10397
 FT /*tag= a
 FT /product= "polyprotein"

XX WO200281511-A1.

XX 17-OCT-2002.

XX 04-APR-2002; 2002WO-FR001168.

XX 04-APR-2001; 2001FR-00004599.

XX 06-SEP-2001; 2001FR-00011525.

XX (INSP) INST PASTEUR.

XX (KIMR-) KIMRON VETERINARY INST.

XX Despres P, Deubel V, Guenet J, Drouet M, Malkinson M, Banet C;
 PI Frenkiel M, Courageot M, Coulbaly F, Catteau A, Flamand M, Weber P;
 PI Ceccaldi P;

XX WPI; 2003-058498/05.

XX P-PSDB; ABP70647.

XX New neurovirulent strain of West Nile virus, useful in diagnosis and
 PT screening for antiviral agents, also related nucleic acids, proteins and
 PT antibodies.

XX Claim 1; Page 34-49; 68pp; French.

XX The present sequence represents the genome of a strain of West Nile virus

CC (WNV), designated IS-98-ST1. This strain is a neuroinvasive and
 CC neurovirulent strain of WNV. Polynucleotides and polypeptides derived
 CC from the IS-98-ST1 genome are useful for diagnosis and prognosis of
 CC Flavivirus infection, specifically WNV-mediated encephalitis. They are
 CC also useful to raise specific antibodies, for recombinant expression of
 CC WNV proteins or peptides (for diagnosis, production of antibodies and
 CC identification of specific binding partners in cells), for identifying
 CC cellular genes implicated in resistance to viral infection, and for
 CC screening for anti-Flavivirus agents
 XX
 SQ Sequence 11029 BP; 3019 A; 2471 C; 3167 G; 2372 T; 0 U; 0 Other;
 Query Match 96.8%; Score 30; DB 8; Length 11029;
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 31
 Db 10523 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 10552
 RESULT 6
 ABV74821
 ID ABV74821 standard; DNA; 11029 BP.
 XX
 AC ABV74821;
 XX
 DT 28-MAR-2003 (first entry)
 XX
 DE West Nile virus strain NY99-flamingo 382-99 complete genome.
 XX
 KW Virucide; hepatotropic; antiinflammatory; antiviral; OAS;
 KW 2'-5'-oligoadenylate synthase; Flavivirus infection; gene; ss.
 XX
 OS West Nile Virus.
 XX
 FH Key Location/Qualifiers
 FT CDS 97..10398
 FT /*tag= a
 FT /product= "West Nile Virus protein"
 XX
 PN WO200281741-A2.
 XX
 PD 17-OCT-2002.
 XX
 PF 04-APR-2002; 2002WO-FR001169.
 XX
 PR 04-APR-2001; 2001FR-00004598.
 XX
 PA (INSP) INST PASTEUR.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 XX
 XX Guenet J, Mashimo T, Simon-Chazottes D, Montagutelli X;
 PI Frenkiel M, Despres P, Deubel V, Bonhomme F, Lucas M;
 XX
 DR WPI; 2003-058566/05.
 DR P-PSDB; ABB98821.
 XX
 PT Identifying stimulators of oligoadenylate synthase family genes, useful
 PT as antiviral agents against Flavivirus, also mutated genes responsible
 PT for sensitivity to virus.
 XX
 PS Example 1; Page 52-67; 93pp; French.
 XX
 CC The present invention relates to a method for identifying compounds (I)
 CC that can stimulate a gene of the OAS (2'-5'-oligoadenylate synthase)
 CC family. The method comprises: (a) inducing expression of the OAS gene in
 CC a culture of cells from a non-human mammal (Flvr/Flvr or Flvr/Flvs;
 CC indicating resistance or sensitivity to Flavivirus infection); (b)
 CC treating cells with test compound; and (c) measuring activity of OAS gene
 CC relative to a control. (I) are potentially useful as antiviral agents for
 CC treating infections by Flaviviruses (e.g. hepatitis C; dengue; yellow
 CC fever and various forms of encephalitis). Genomic OAS DNA and derived

CC cDNA, also the encoded proteins, are useful: (a) for treating Flavivirus
 CC infection; (b) in screening for anti-flavivirus agents, and (c) for
 CC evaluating sensitivity of subjects to Flavivirus infection and their
 CC likely response to interferon treatment, e.g. to identify patients at
 CC risk of developing severe forms of such infections. The present sequence
 CC is West Nile Virus strain NY99-flamingo 382-99 (IS-98-ST1) complete
 CC genome, which was used in an example from the invention. West Nile Virus
 CC is one such Flavivirus
 XX
 SQ Sequence 11029 BP; 3019 A; 2471 C; 3167 G; 2372 T; 0 U; 0 Other;
 Query Match 96.8%; Score 30; DB 10; Length 11029;
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 31
 Db 10523 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 10552
 RESULT 7
 ADN98023
 ID ADN98023 standard; DNA; 11029 BP.
 XX
 AC ADN98023;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE West Nile Virus isolate 3356 complete genome sequence.
 XX
 KW ds; West Nile Virus; envelope protein; glycoprotein E; flavivirus;
 KW Japanese encephalitis virus; Dengue virus; St Louis encephalitis virus.
 XX
 OS West Nile virus.
 XX
 PN WO2004040263-A2.
 XX
 PD 13-MAY-2004.
 XX
 PF 31-OCT-2003; 2003WO-US034823.
 XX
 PR 31-OCT-2002; 2002US-0422755P.
 PR 06-JUN-2003; 2003US-0476513P.
 XX
 PA (HEAL-) HEALTH RES INC.
 XX
 PI Wong SJ, Pei-Yong S;
 XX
 DR WPI; 2004-400223/37.
 DR GENBANK; AF404756.
 XX
 PT New diagnostic kit comprising West Nile Virus (WNV) envelope protein
 PT reactive with antibody against WNV and cross-reactive with antibody
 PT against a flavivirus, useful in diagnosing flavivirus infection caused by
 PT DENV, WNV, JEV or SLEV.
 XX
 PS Disclosure; Fig 38; 212pp; English.
 XX
 CC The invention relates to a diagnostic kit comprising at least one
 CC isolated and purified polypeptide comprising a West Nile Virus (WNV)
 CC envelope (E) protein or its immunogenic fragment having a native
 CC conformation or non-denatured structure and that is reactive with
 CC antibodies against WNV and cross-reactive with antibodies against a
 CC flavivirus. The diagnostic kit is useful in diagnosing flavivirus
 CC infection caused by DENV, WNV, JEV or SLEV. This sequence corresponds to
 CC the complete nucleotide sequence of the WNV isolate 3356.
 XX
 SQ Sequence 11029 BP; 3017 A; 2466 C; 3172 G; 2374 T; 0 U; 0 Other;
 Query Match 96.8%; Score 30; DB 12; Length 11029;
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 2 CGCCACCGGAAGTTGAGTAGACGGTGCTG 31
Db 10523 CGCCACCGGAAGTTGAGTAGACGGTGCTG 10552

RESULT 8
ADK13681
ID ADK13681 standard; DNA; 10962 BP.
XX
AC ADK13681;
XX
DT 20-MAY-2004 (first entry)
XX
DE West Nile Virus DNA sequence, SEQ ID 1.
XX
KW Virucide; Immunostimulant; flavivirus;
XX envelope protein domain III polypeptide; envelope protein; gene; ss.
OS West Nile virus.
XX
FH Key Location/Qualifiers
FT CDS 97..10389
FT /*tag= a
FT /product= "West Nile Virus protein"
XX
PN WO2004016586-A2.
XX
PD 26-FEB-2004.
XX
PF 18-AUG-2003; 2003WO-US025681.
XX
PR 16-AUG-2002; 2002US-0403893P.
XX 06-FEB-2003; 2003US-0445581P.
XX (TEXA ) UNIV TEXAS SYSTM.
XX
PI Barrett A, Beasley D, Holbrook M;
XX
DR WPI; 2004-203756/19.
DR P-PSDB; ADK13682.
XX
PT Diagnosing flavivirus infection by contacting a sample from a human or
PT animal with a flavivirus envelope protein domain III polypeptide, and
PT detecting formation of a immunocomplex between the envelope protein and
PT antibodies in the sample.
XX
PS Disclosure; SEQ ID NO 1; 110pp; English.
XX
CC The present invention relates to a method for screening for a flavivirus
CC in a subject or animal host. The method comprises: contacting a sample
CC from the subject with a composition comprising a flavivirus envelope
CC protein domain III polypeptide (ADK13683-ADK13701) under conditions that
CC permit formation of specific immunocomplex between an antibody in the
CC sample and the envelope protein domain III polypeptide; and detecting
CC whether a specific immunocomplex is formed. The present sequence is the
CC coding sequence for West Nile Virus protein, from which E protein
CC envelope protein domain III polypeptide (ADK13683) is derived.
XX
SQ Sequence 10962 BP; 2997 A; 2497 C; 3100 G; 2368 T; 0 U; 0 Other;

Query Match 90.3%; Score 28; DB 12; Length 10962;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GCCACCGGAAGTTGAGTAGACGGTGCTG 31
Db 10460 GCCACCGGAAGTTGAGTAGACGGTGCTG 10487

RESULT 9
ADN36746
ID ADN36746 standard; DNA; 22 BP.
XX
Qy 2 CGCCACCGGAAGTTGAGTAGACGGTGCTG 31
Db 10523 CGCCACCGGAAGTTGAGTAGACGGTGCTG 10552

ADN36746;
15-JUL-2004 (first entry)
West Nile virus detection-related PCR primer SeqID68.
hybridisation assay probe; nucleic acid detection;
target-complementary sequence; flavivirus; West Nile virus; WNV;
RNA virus; infection; meningitis; encephalitis;
high throughput screening; PCR; primer; ss.
West Nile virus.
WO2004036190-A2.
29-APR-2004.
10-OCT-2003; 2003WO-US033639.
16-OCT-2002; 2002US-0418891P.
25-NOV-2002; 2002US-0429006P.
24-FEB-2003; 2003US-0449810P.
(GENP-) GEN-PROBE INC.
Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
WPI; 2004-389590/36.
New hybridization assay probe comprising target-complementary sequence of
bases, useful in detecting flavivirus, e.g. West Nile virus.
Claim 26; SEQ ID NO 68; 135pp; English.
This invention relates to a novel hybridisation assay probe, for
detecting a nucleic acid, which is a probe sequence that comprises a
target-complementary sequence of bases, and optionally one or more base
sequences that are not complementary to the nucleic acid that is to be
detected. The hybridisation assay probes and the kits are useful in
detecting and amplifying a target nucleic acid sequence, for example
flavivirus like West Nile virus, that may be present in a biological
sample. West Nile virus (WNV) is an RNA virus that primarily infects
birds and culex mosquitoes, with humans and horses serving as incidental
hosts. Infection of humans can lead to meningitis or encephalitis. The
invention may allow for accurate and efficient high throughput screening.
The present sequence is that of a PCR primer which is related to the
invention.
Sequence 22 BP; 5 A; 2 C; 10 G; 5 T; 0 U; 0 Other;

Query Match 71.0%; Score 22; DB 12; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.0056;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GGAAGTTGAGTAGACGGTGCTG 31
Db 1 GGAAGTTGAGTAGACGGTGCTG 22

RESULT 10
ADN36741
ID ADN36741 standard; DNA; 21 BP.
XX
AC ADN36741;
XX
DT 15-JUL-2004 (first entry)
XX
DE West Nile virus detection-related oligonucleotide probe SeqID63.
XX
KW hybridisation assay probe; nucleic acid detection;
KW target-complementary sequence; flavivirus; West Nile virus; WNV;
KW RNA virus; infection; meningitis; encephalitis;
KW high throughput screening; probe; ss.

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XX OS West Nile virus.
XX PN WO2004036190-A2.
XX PD 29-APR-2004.
XX PF 10-OCT-2003; 2003WO-US033639.
XX PR 16-OCT-2002; 2002US-0418891P.
XX PR 25-NOV-2002; 2002US-0429006P.
XX PR 24-FEB-2003; 2003US-0449810P.
XX PA (GENP-) GEN-PROBE INC.
XX PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX DR WPI; 2004-389590/36.
XX PT New hybridization assay probe comprising target-complementary sequence of
XX PT bases, useful in detecting flavivirus, e.g. West Nile virus.
XX PS Claim 26; SEQ ID NO 63; 135pp; English.
XX CC This invention relates to a novel hybridisation assay probe, for
XX CC detecting a nucleic acid, which is a probe sequence that comprises a
XX CC target-complementary sequence of bases, and optionally one or more base
XX CC sequences that are not complementary to the nucleic acid that is to be
XX CC detected. The hybridisation assay probes and the kits are useful in
XX CC detecting and amplifying a target nucleic acid sequence, for example
XX CC flavivirus like West Nile virus, that may be present in a biological
XX CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
XX CC birds and culex mosquitoes, with humans and horses serving as incidental
XX CC hosts. Infection of humans can lead to meningitis or encephalitis. The
XX CC invention may allow for accurate and efficient high throughput screening.
XX CC The present sequence is that of an oligonucleotide probe which is related
XX CC to the invention.
XX SQ Sequence 21 BP; 5 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 67.7%; Score 21; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TCCGCCACCGGAAGTTGAGTA 21
Db 1 TCCGCCACCGGAAGTTGAGTA 21

RESULT 11
ADN36745
ID ADN36745 standard; DNA; 21 BP.
XX AC ADN36745;
XX DT 15-JUL-2004 (first entry)
XX DE West Nile virus detection-related PCR primer SeqID67.
XX KW hybridisation assay probe; nucleic acid detection;
XX KW target-complementary sequence; flavivirus; West Nile virus; WNV;
XX KW RNA virus; infection; meningitis; encephalitis;
XX KW high throughput screening; PCR; primer; ss.
XX OS West Nile virus.
XX PN WO2004036190-A2.
XX PD 29-APR-2004.
XX PF 10-OCT-2003; 2003WO-US033639.
XX PR 16-OCT-2002; 2002US-0418891P.
XX PR 25-NOV-2002; 2002US-0429006P.
XX PR 24-FEB-2003; 2003US-0449810P.
XX PA (GENP-) GEN-PROBE INC.
XX PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX DR WPI; 2004-389590/36.
XX PT New hybridization assay probe comprising target-complementary sequence of
XX PT bases, useful in detecting flavivirus, e.g. West Nile virus.
XX PS Claim 26; SEQ ID NO 63; 135pp; English.
XX CC This invention relates to a novel hybridisation assay probe, for
XX CC detecting a nucleic acid, which is a probe sequence that comprises a
XX CC target-complementary sequence of bases, and optionally one or more base
XX CC sequences that are not complementary to the nucleic acid that is to be
XX CC detected. The hybridisation assay probes and the kits are useful in
XX CC detecting and amplifying a target nucleic acid sequence, for example
XX CC flavivirus like West Nile virus, that may be present in a biological
XX CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
XX CC birds and culex mosquitoes, with humans and horses serving as incidental
XX CC hosts. Infection of humans can lead to meningitis or encephalitis. The
XX CC invention may allow for accurate and efficient high throughput screening.
XX CC The present sequence is that of an oligonucleotide probe which is related
XX CC to the invention.
XX SQ Sequence 21 BP; 5 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 67.7%; Score 21; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TCCGCCACCGGAAGTTGAGTA 21
Db 1 TCCGCCACCGGAAGTTGAGTA 21

RESULT 12
ADN36748
ID ADN36748 standard; DNA; 21 BP.
XX AC ADN36748;
XX DT 15-JUL-2004 (first entry)
XX DE West Nile virus detection-related PCR primer SeqID70.
XX KW hybridisation assay probe; nucleic acid detection;
XX KW target-complementary sequence; flavivirus; West Nile virus; WNV;
XX KW RNA virus; infection; meningitis; encephalitis;
XX KW high throughput screening; PCR; primer; ss.
XX OS West Nile virus.
XX PN WO2004036190-A2.
XX PD 29-APR-2004.
XX PF 10-OCT-2003; 2003WO-US033639.
XX PR 16-OCT-2002; 2002US-0418891P.
XX PR 25-NOV-2002; 2002US-0429006P.
XX PR 24-FEB-2003; 2003US-0449810P.
XX PA (GENP-) GEN-PROBE INC.
XX PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX DR WPI; 2004-389590/36.
XX PT New hybridization assay probe comprising target-complementary sequence of

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PT bases, useful in detecting flavivirus, e.g. West Nile virus.
 XX Claim 26; SEQ ID NO 70; 135pp; English.
 XX This invention relates to a novel hybridisation assay probe, for
 CC detecting a nucleic acid, which is a probe sequence that comprises a
 CC target-complementary sequence of bases, and optionally one or more base
 CC sequences that are not complementary to the nucleic acid that is to be
 CC detected. The hybridisation assay probes and the kits are useful in
 CC detecting and amplifying a target nucleic acid sequence, for example
 CC flavivirus like West Nile virus, that may be present in a biological
 CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
 CC birds and culex mosquitoes, with humans and horses serving as incidental
 CC hosts. Infection of humans can lead to meningitis or encephalitis. The
 CC invention may allow for accurate and efficient high throughput screening.
 CC The present sequence is that of a PCR primer which is related to the
 CC invention.
 XX SQ Sequence 21 BP; 5 A; 2 C; 9 G; 5 T; 0 U; 0 Other;
 Query Match 67.7%; Score 21; DB 12; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.021;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 GAAGTTGAGTAGACGGTGCTG 31
 |||||
 Db 1 GAAGTTGAGTAGACGGTGCTG 21
 |||||
 RESULT 13
 ADN36749
 ID ADN36749 standard; DNA; 20 BP.
 XX AC ADN36749;
 XX DT 15-JUL-2004 (first entry)
 XX DE West Nile virus detection-related PCR primer SeqID71.
 XX KW hybridisation assay probe; nucleic acid detection;
 KW target-complementary sequence; flavivirus; West Nile virus; WNV;
 KW RNA virus; infection; meningitis; encephalitis;
 KW high throughput screening; PCR; primer; ss.
 XX OS West Nile virus.
 XX OS WO2004036190-A2.
 XX PD 29-APR-2004.
 XX PF 10-OCT-2003; 2003WO-US033639.
 XX PR 16-OCT-2002; 2002US-0418891P.
 XX PR 25-NOV-2002; 2002US-0429006P.
 XX PR 24-FEB-2003; 2003US-0449810P.
 XX PA (GENP-) GEN-PROBE INC.
 XX PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
 XX WPI; 2004-389590/36.
 XX New hybridization assay probe comprising target-complementary sequence of
 PT bases, useful in detecting flavivirus, e.g. West Nile virus.
 XX Claim 26; SEQ ID NO 71; 135pp; English.
 XX This invention relates to a novel hybridisation assay probe, for
 CC detecting a nucleic acid, which is a probe sequence that comprises a
 CC target-complementary sequence of bases, and optionally one or more base
 CC sequences that are not complementary to the nucleic acid that is to be
 CC detected. The hybridisation assay probes and the kits are useful in
 CC detecting and amplifying a target nucleic acid sequence, for example
 CC flavivirus like West Nile virus, that may be present in a biological
 CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
 CC birds and culex mosquitoes, with humans and horses serving as incidental
 CC hosts. Infection of humans can lead to meningitis or encephalitis. The
 CC invention may allow for accurate and efficient high throughput screening.
 CC The present sequence is that of a PCR primer which is related to the
 CC invention.
 XX SQ Sequence 21 BP; 5 A; 2 C; 9 G; 5 T; 0 U; 0 Other;
 Query Match 67.7%; Score 21; DB 12; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.021;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 GAAGTTGAGTAGACGGTGCTG 31
 |||||
 Db 1 GAAGTTGAGTAGACGGTGCTG 21
 |||||
 RESULT 14
 ADN36740
 ID ADN36740 standard; DNA; 20 BP.
 XX AC ADN36740;
 XX DT 15-JUL-2004 (first entry)
 XX DE West Nile virus detection-related oligonucleotide probe SeqID62.
 XX KW hybridisation assay probe; nucleic acid detection;
 KW target-complementary sequence; flavivirus; West Nile virus; WNV;
 KW RNA virus; infection; meningitis; encephalitis;
 KW high throughput screening; probe; ss.
 XX OS West Nile virus.
 XX OS WO2004036190-A2.
 XX PD 29-APR-2004.
 XX PF 10-OCT-2003; 2003WO-US033639.
 XX PR 16-OCT-2002; 2002US-0418891P.
 XX PR 25-NOV-2002; 2002US-0429006P.
 XX PR 24-FEB-2003; 2003US-0449810P.
 XX PA (GENP-) GEN-PROBE INC.
 XX PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
 XX WPI; 2004-389590/36.
 XX New hybridization assay probe comprising target-complementary sequence of
 PT bases, useful in detecting flavivirus, e.g. West Nile virus.
 XX Claim 26; SEQ ID NO 62; 135pp; English.
 XX This invention relates to a novel hybridisation assay probe, for
 CC detecting a nucleic acid, which is a probe sequence that comprises a
 CC target-complementary sequence of bases, and optionally one or more base
 CC sequences that are not complementary to the nucleic acid that is to be
 CC detected. The hybridisation assay probes and the kits are useful in
 CC detecting and amplifying a target nucleic acid sequence, for example
 CC flavivirus like West Nile virus, that may be present in a biological
 CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
 CC birds and culex mosquitoes, with humans and horses serving as incidental
 CC hosts. Infection of humans can lead to meningitis or encephalitis. The
 CC invention may allow for accurate and efficient high throughput screening.
 CC The present sequence is that of an oligonucleotide probe which is related
 CC to the invention.
 XX SQ Sequence 20 BP; 4 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

CC flavivirus like West Nile virus, that may be present in a biological
 CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
 CC birds and culex mosquitoes, with humans and horses serving as incidental
 CC hosts. Infection of humans can lead to meningitis or encephalitis. The
 CC invention may allow for accurate and efficient high throughput screening.
 CC The present sequence is that of a PCR primer which is related to the
 CC invention.
 XX SQ Sequence 20 BP; 5 A; 2 C; 8 G; 5 T; 0 U; 0 Other;
 Query Match 64.5%; Score 20; DB 12; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.081;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 AAGTTGAGTAGACGGTGCTG 31
 |||||
 Db 1 AAGTTGAGTAGACGGTGCTG 20
 |||||
 RESULT 14
 ADN36740
 ID ADN36740 standard; DNA; 20 BP.
 XX AC ADN36740;
 XX DT 15-JUL-2004 (first entry)
 XX DE West Nile virus detection-related oligonucleotide probe SeqID62.
 XX KW hybridisation assay probe; nucleic acid detection;
 KW target-complementary sequence; flavivirus; West Nile virus; WNV;
 KW RNA virus; infection; meningitis; encephalitis;
 KW high throughput screening; probe; ss.
 XX OS West Nile virus.
 XX OS WO2004036190-A2.
 XX PD 29-APR-2004.
 XX PF 10-OCT-2003; 2003WO-US033639.
 XX PR 16-OCT-2002; 2002US-0418891P.
 XX PR 25-NOV-2002; 2002US-0429006P.
 XX PR 24-FEB-2003; 2003US-0449810P.
 XX PA (GENP-) GEN-PROBE INC.
 XX PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
 XX WPI; 2004-389590/36.
 XX New hybridization assay probe comprising target-complementary sequence of
 PT bases, useful in detecting flavivirus, e.g. West Nile virus.
 XX Claim 26; SEQ ID NO 62; 135pp; English.
 XX This invention relates to a novel hybridisation assay probe, for
 CC detecting a nucleic acid, which is a probe sequence that comprises a
 CC target-complementary sequence of bases, and optionally one or more base
 CC sequences that are not complementary to the nucleic acid that is to be
 CC detected. The hybridisation assay probes and the kits are useful in
 CC detecting and amplifying a target nucleic acid sequence, for example
 CC flavivirus like West Nile virus, that may be present in a biological
 CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
 CC birds and culex mosquitoes, with humans and horses serving as incidental
 CC hosts. Infection of humans can lead to meningitis or encephalitis. The
 CC invention may allow for accurate and efficient high throughput screening.
 CC The present sequence is that of an oligonucleotide probe which is related
 CC to the invention.
 XX SQ Sequence 20 BP; 4 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 64.5%; Score 20; DB 12; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.081;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGCCACCGAAGTTGAGT 20
 DB 1 TCGCCACCGAAGTTGAGT 20

RESULT 15
 ADN36747
 ID ADN36747 standard; DNA; 20 BP.
 XX AC ADN36747;
 XX DT 15-JUL-2004 (first entry)
 XX DE West Nile virus detection-related PCR primer SeqID69.
 XX KW hybridisation assay probe; nucleic acid detection;
 KW target-complementary sequence; flavivirus; West Nile virus; WNV;
 KW RNA virus; infection; meningitis; encephalitis;
 KW high throughput screening; PCR; primer; ss.
 XX OS West Nile virus.
 XX PN WO2004036190-A2.
 XX PD 29-APR-2004.
 XX PF 10-OCT-2003; 2003WO-US033639.
 XX PR 16-OCT-2002; 2002US-0418891P.
 XX PR 25-NOV-2002; 2002US-0429006P.
 XX PR 24-FEB-2003; 2003US-0449810P.
 XX PA (GENP-) GEN-PROBE INC.
 XX PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
 XX WPI; 2004-389590/36.
 XX PF New hybridization assay probe comprising target-complementary sequence of
 PT bases, useful in detecting flavivirus, e.g. West Nile virus.
 XX PS Claim 26; SEQ ID NO 69; 135pp; English.
 XX CC This invention relates to a novel hybridisation assay probe, for
 CC detecting a nucleic acid, which is a probe sequence that comprises a
 CC target-complementary sequence of bases, and optionally one or more base
 CC sequences that are not complementary to the nucleic acid that is to be
 CC detected. The hybridisation assay probes and the kits are useful in
 CC detecting and amplifying a target nucleic acid sequence, for example
 CC flavivirus like West Nile virus, that may be present in a biological
 CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
 CC birds and culex mosquitoes, with humans and horses serving as incidental
 CC hosts. Infection of humans can lead to meningitis or encephalitis. The
 CC invention may allow for accurate and efficient high throughput screening.
 CC The present sequence is that of a PCR primer which is related to the
 CC invention.
 XX SQ Sequence 20 BP; 5 A; 2 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 64.5%; Score 20; DB 12; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.081;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GAAGTTGAGTAGACGGTGCT 30
 DB 1 GAAGTTGAGTAGACGGTGCT 20

RESULT 16
 ADN36748
 ID ADN36748 standard; DNA; 19 BP.
 XX AC ADN36748;
 XX DT 15-JUL-2004 (first entry)
 XX DE West Nile virus detection-related oligonucleotide probe SeqID60.
 XX KW hybridisation assay probe; nucleic acid detection;

ADN36744
 ID ADN36744 standard; DNA; 19 BP.
 XX AC ADN36744;
 XX DT 15-JUL-2004 (first entry)
 XX DE West Nile virus detection-related oligonucleotide probe SeqID66.
 XX KW hybridisation assay probe; nucleic acid detection;
 KW target-complementary sequence; flavivirus; West Nile virus; WNV;
 KW RNA virus; infection; meningitis; encephalitis;
 KW high throughput screening; probe; ss.
 XX OS West Nile virus.
 XX PN WO2004036190-A2.
 XX PD 29-APR-2004.
 XX PF 10-OCT-2003; 2003WO-US033639.
 XX PR 16-OCT-2002; 2002US-0418891P.
 XX PR 25-NOV-2002; 2002US-0429006P.
 XX PR 24-FEB-2003; 2003US-0449810P.
 XX PA (GENP-) GEN-PROBE INC.
 XX PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
 XX WPI; 2004-389590/36.
 XX PF New hybridization assay probe comprising target-complementary sequence of
 PT bases, useful in detecting flavivirus, e.g. West Nile virus.
 XX PS Claim 26; SEQ ID NO 66; 135pp; English.
 XX CC This invention relates to a novel hybridisation assay probe, for
 CC detecting a nucleic acid, which is a probe sequence that comprises a
 CC target-complementary sequence of bases, and optionally one or more base
 CC sequences that are not complementary to the nucleic acid that is to be
 CC detected. The hybridisation assay probes and the kits are useful in
 CC detecting and amplifying a target nucleic acid sequence, for example
 CC flavivirus like West Nile virus, that may be present in a biological
 CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
 CC birds and culex mosquitoes, with humans and horses serving as incidental
 CC hosts. Infection of humans can lead to meningitis or encephalitis. The
 CC invention may allow for accurate and efficient high throughput screening.
 CC The present sequence is that of an oligonucleotide probe which is related
 CC to the invention.
 XX SQ Sequence 19 BP; 5 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 61.3%; Score 19; DB 12; Length 19;
 Best Local Similarity 100.0%; Pred. No. 0.31;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CGCCACCGAAGTTGAGTA 21
 DB 1 CGCCACCGAAGTTGAGTA 19

RESULT 17
 ADN36738
 ID ADN36738 standard; DNA; 19 BP.
 XX AC ADN36738;
 XX DT 15-JUL-2004 (first entry)
 XX DE West Nile virus detection-related oligonucleotide probe SeqID60.
 XX KW hybridisation assay probe; nucleic acid detection;

```
KW target-complementary sequence; flavivirus; West Nile virus; WNV;
KW RNA virus; infection; meningitis; encephalitis;
KW high throughput screening; probe; ss.
XX
OS West Nile virus.
XX
PN WO2004036190-A2.
XX
PD 29-APR-2004.
XX
XX
XX 10-OCT-2003; 2003WO-US033639.
XX
XX 16-OCT-2002; 2002US-0418891P.
PR
PR 25-NOV-2002; 2002US-0429006P.
PR
PR 24-FEB-2003; 2003US-0449810P.
XX
XX (GENP-) GEN-PROBE INC.
XX
XX Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
PI
XX WPI; 2004-389590/36.
XX
XX New hybridization assay probe comprising target-complementary sequence of
PT bases, useful in detecting flavivirus, e.g. West Nile virus.
PT
XX Claim 26; SEQ ID NO 60; 135pp; English.
XX
XX This invention relates to a novel hybridisation assay probe, for
CC detecting a nucleic acid, which is a probe sequence that comprises a
CC target-complementary sequence of bases, and optionally one or more base
CC sequences that are not complementary to the nucleic acid that is to be
CC detected. The hybridisation assay probes and the kits are useful in
CC detecting and amplifying a target nucleic acid sequence, for example
CC flavivirus like West Nile virus, that may be present in a biological
CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC birds and culex mosquitoes, with humans and horses serving as incidental
CC hosts. Infection of humans can lead to meningitis or encephalitis. The
CC invention may allow for accurate and efficient high throughput screening.
CC The present sequence is that of an oligonucleotide probe which is related
CC to the invention.
XX
XX Sequence 19 BP; 4 A; 6 C; 6 G; 3 T; 0 U; 0 Other;
SQ
Query Match 61.3%; Score 19; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.31; 0; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0;
QY 1 TCCGCCACCGGAAGTTGAG 19
DB 1 TCCGCCACCGGAAGTTGAG 19
XX
RESULT 18
ADN36742
ID ADN36742 standard; DNA; 18 BP.
XX
XX ADN36742;
AC
XX
XX 15-JUL-2004 (first entry)
DT
XX
XX West Nile virus detection-related PCR primer SeqID64.
DE
XX
XX hybridisation assay probe; nucleic acid detection;
KW target-complementary sequence; flavivirus; West Nile virus; WNV;
KW RNA virus; infection; meningitis; encephalitis;
KW high throughput screening; PCR; primer; ss.
XX
XX West Nile virus.
OS
XX
XX WO2004036190-A2.
PN
XX 29-APR-2004.
PR
PR
XX
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PF 10-OCT-2003; 2003WO-US033639.
XX
XX 16-OCT-2002; 2002US-0418891P.
PR
PR 25-NOV-2002; 2002US-0429006P.
PR
PR 24-FEB-2003; 2003US-0449810P.
XX
XX (GENP-) GEN-PROBE INC.
XX
XX Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
PI
XX WPI; 2004-389590/36.
XX
XX New hybridization assay probe comprising target-complementary sequence of
PT bases, useful in detecting flavivirus, e.g. West Nile virus.
PT
XX Claim 26; SEQ ID NO 64; 135pp; English.
XX
XX This invention relates to a novel hybridisation assay probe, for
CC detecting a nucleic acid, which is a probe sequence that comprises a
CC target-complementary sequence of bases, and optionally one or more base
CC sequences that are not complementary to the nucleic acid that is to be
CC detected. The hybridisation assay probes and the kits are useful in
CC detecting and amplifying a target nucleic acid sequence, for example
CC flavivirus like West Nile virus, that may be present in a biological
CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC birds and culex mosquitoes, with humans and horses serving as incidental
CC hosts. Infection of humans can lead to meningitis or encephalitis. The
CC invention may allow for accurate and efficient high throughput screening.
CC The present sequence is that of a PCR primer which is related to the
CC invention.
XX
XX Sequence 18 BP; 4 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
SQ
Query Match 58.1%; Score 18; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2; 0; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0;
QY 3 CGCCACCGGAAGTTGAGT 20
DB 1 CGCCACCGGAAGTTGAGT 18
XX
RESULT 19
ADN36739
ID ADN36739 standard; DNA; 19 BP.
XX
XX ADN36739;
AC
XX
XX 15-JUL-2004 (first entry)
DT
XX
XX West Nile virus detection-related oligonucleotide probe SeqID61.
DE
XX
XX hybridisation assay probe; nucleic acid detection;
KW target-complementary sequence; flavivirus; West Nile virus; WNV;
KW RNA virus; infection; meningitis; encephalitis;
KW high throughput screening; probe; ss.
XX
XX West Nile virus.
OS
XX
XX Key Location/Qualifiers
FH modified_base 1 /*tag= a
FT /mod_base= i
FT
XX
XX WO2004036190-A2.
PN
XX 29-APR-2004.
PR
PR
XX 10-OCT-2003; 2003WO-US033639.
PF
XX
XX 16-OCT-2002; 2002US-0418891P.
PR
PR 25-NOV-2002; 2002US-0429006P.
PR
PR 24-FEB-2003; 2003US-0449810P.
XX
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XX (GENP-) GEN-PROBE INC.
XX
XX Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX
XX WPI; 2004-389590/36.
XX
XX New hybridization assay probe comprising target-complementary sequence of
XX bases, useful in detecting flavivirus, e.g. West Nile virus.
XX
XX Disclosure; SEQ ID NO 61; 135pp; English.
XX
XX This invention relates to a novel hybridisation assay probe, for
XX detecting a nucleic acid, which is a probe sequence that comprises a
XX target-complementary sequence of bases, and optionally one or more base
XX sequences that are not complementary to the nucleic acid that is to be
XX detected. The hybridisation assay probes and the kits are useful in
XX detecting and amplifying a target nucleic acid sequence, for example
XX flavivirus like West Nile virus, that may be present in a biological
XX sample. West Nile virus (WNV) is an RNA virus that primarily infects
XX birds and culex mosquitoes, with humans and horses serving as incidental
XX hosts. Infection of humans can lead to meningitis or encephalitis. The
XX invention may allow for accurate and efficient high throughput screening.
XX The present sequence is that of an oligonucleotide probe which is related
XX to the invention.
XX
XX Sequence 19 BP; 4 A; 6 C; 6 G; 2 T; 0 U; 1 Other;
XX
XX Query Match 58.1%; Score 18; DB 12; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 1.2;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 CCGCCACCGAGTTGAG 19
XX
XX Db 2 CCGCCACCGAGTTGAG 19
XX
XX RESULT 20
XX ADN36825/C
XX ID ADN36825 standard; RNA; 26 BP.
XX
XX AC ADN36825;
XX
XX 15-JUL-2004 (first entry)
XX
XX DE West Nile virus detection-related oligonucleotide probe SeqID147.
XX
XX KW hybridisation assay probe; nucleic acid detection;
XX target-complementary sequence; flavivirus; West Nile virus; WNV;
XX RNA virus; infection; meningitis; encephalitis;
XX KW high throughput screening; probe; ss.
XX
XX OS West Nile virus.
XX
XX Key Location/Qualifiers
XX modified_base 1..26
XX /*tag= a
XX /mod_base= OTHER
XX FT FT
XX FT /note= "OTHER= 2'-methoxyethoxy (2'-MOE) nucleotides"
XX
XX PN WO2004036190-A2.
XX
XX 29-APR-2004.
XX
XX 10-OCT-2003; 2003WO-US033639.
XX
XX 16-OCT-2002; 2002US-0418991P.
XX PR 25-NOV-2002; 2002US-0429006P.
XX PR 24-FEB-2003; 2003US-0449810P.
XX
XX (GENP-) GEN-PROBE INC.
XX
XX Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX
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XX WPI; 2004-389590/36.
XX
XX New hybridization assay probe comprising target-complementary sequence of
XX bases, useful in detecting flavivirus, e.g. West Nile virus.
XX
XX Example 1; SEQ ID NO 147; 135pp; English.
XX
XX This invention relates to a novel hybridisation assay probe, for
XX detecting a nucleic acid, which is a probe sequence that comprises a
XX target-complementary sequence of bases, and optionally one or more base
XX sequences that are not complementary to the nucleic acid that is to be
XX detected. The hybridisation assay probes and the kits are useful in
XX detecting and amplifying a target nucleic acid sequence, for example
XX flavivirus like West Nile virus, that may be present in a biological
XX sample. West Nile virus (WNV) is an RNA virus that primarily infects
XX birds and culex mosquitoes, with humans and horses serving as incidental
XX hosts. Infection of humans can lead to meningitis or encephalitis. The
XX invention may allow for accurate and efficient high throughput screening.
XX The present sequence is that of an oligonucleotide probe which is related
XX to the invention.
XX
XX Sequence 26 BP; 6 A; 10 C; 6 G; 0 T; 4 U; 0 Other;
XX
XX Query Match 58.1%; Score 18; DB 12; Length 26;
XX Best Local Similarity 100.0%; Pred. No. 1.2;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 14 GTTGAGTAGACGGTCTG 31
XX
XX Db 26 GTTGAGTAGACGGTCTG 9
XX
XX RESULT 21
XX ACN01373
XX ID ACN01373 standard; RNA; 17 BP.
XX
XX AC ACN01373;
XX
XX 22-APR-2004 (first entry)
XX
XX DE WNV Hammerhead Ribozyme substrate SEQ ID NO 1363.
XX
XX KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
XX virucide; neuroprotective; antibacterial; replication; pancreatitis;
XX KW encephalitis; myocarditis; meningitis; infection; hepatitis;
XX KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
XX KW Amberzyme; Zinzyme; ss.
XX
XX OS West Nile Virus.
XX
XX PN WO200268637-A2.
XX
XX 06-SEP-2002.
XX
XX 19-OCT-2001; 2001WO-US048350.
XX
XX 20-OCT-2000; 2000US-0242411P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX PA (BLAT/) BLATT L.
XX PA (MCSW/) MCSWIGGEN J A.
XX
XX Blatt L, Mcswiggen JA;
XX
XX WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
XX (WNV), useful for treating a condition related to WNV infection e.g.
XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
XX Claim 23; SEQ ID NO 1363; 495pp; English.
XX
```

CC The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention

XX
SQ Sequence 17 BP; 4 A; 2 C; 7 G; 0 T; 4 U; 0 Other;

Query Match 54.8%; Score 17; DB 6; Length 17;
Best Local Similarity 76.5%; Pred. No. 4.5;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 13 AGTTGAGTAGACGGTGC 29
||:||||:||||:|
Db 1 AGUGAGUAGACGGGUC 17

RESULT 22
ACN04650
ID ACN04650 standard; RNA; 17 BP.
XX
AC ACN04650;
XX
DT 22-APR-2004 (first entry)
XX
DE WNV Zinzyme substrate SEQ ID NO 4653.
XX
KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
KW Amberzyme; Zinzyme; ss.

XX West Nile Virus.
XX WO200268637-A2.
XX 06-SEP-2002.
XX 19-OCT-2001; 2001WO-US048350.
XX 20-OCT-2000; 2000US-0242411P.
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGGEN J A.
XX Blatt L, Mcswiggen JA;
XX WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
XX (WNV), useful for treating a condition related to WNV infection e.g.
XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
XX Claim 23; SEQ ID NO 4653; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication
XX of the West Nile Virus (WNV). The nucleic acid molecules are useful for
XX treating a condition related to WNV infection e.g. pancreatitis,
XX encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
XX molecule is selected from the group of ribozymes consisting of
XX Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The

CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention

XX
SQ Sequence 17 BP; 5 A; 1 C; 7 G; 0 T; 4 U; 0 Other;

Query Match 54.8%; Score 17; DB 6; Length 17;
Best Local Similarity 76.5%; Pred. No. 4.5;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 11 GAAGTTGAGTAGACGGT 27
||||:||||:|
Db 1 GAAGUGAGUAGACGGU 17

RESULT 23
ACN07292
ID ACN07292 standard; RNA; 17 BP.
XX
AC ACN07292;
XX
DT 22-APR-2004 (first entry)
XX
DE WNV Amberzyme substrate SEQ ID NO 7295.
XX
KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
KW Amberzyme; Zinzyme; ss.

XX West Nile Virus.
XX WO200268637-A2.
XX 06-SEP-2002.
XX 19-OCT-2001; 2001WO-US048350.
XX 20-OCT-2000; 2000US-0242411P.
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGGEN J A.
XX Blatt L, Mcswiggen JA;
XX WPI; 2002-706994/76.

XX The invention relates to nucleic acid molecules that modulate replication
XX of the West Nile Virus (WNV). The nucleic acid molecules are useful for
XX treating a condition related to WNV infection e.g. pancreatitis,
XX encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
XX molecule is selected from the group of ribozymes consisting of
XX Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
XX nucleic acid molecules further comprise at least five ribose residues, at
XX least ten 2'-O-methyl modifications, phosphorothioate linkages on at
XX least three of the 5' terminal nucleotides and a 3' end modification of a
XX 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
XX are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
XX in the specification. The present sequence is that of a nucleic acid
XX molecule of the invention

```
XX SQ Sequence 17 BP; 5 A; 2 C; 7 G; 0 T; 3 U; 0 Other;
Query Match 54.8%; Score 17; DB 6; Length 17;
Best Local Similarity 82.4%; Pred. No. 4.5;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 9 CGGAAGTTGAGTAGACG 25
DB 1 CGGAAGUUGAGUAGCG 17

RESULT 24
ACN09625/c
ID ACN09625 standard; RNA; 17 BP.
XX AC ACN09625;
XX KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
XX KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
XX KW encephalitis; myocarditis; meningitis; infection; hepatitis;
XX KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
XX KW Amberzyme; Zinzyme; ss.
XX OS West Nile Virus.
XX XX WO200268637-A2.
XX PN 06-SEP-2002.
XX PD 19-OCT-2001; 2001WO-US048350.
XX PF 20-OCT-2000; 2000US-024241P.
XX PR (RIBO-) RIBOZYME PHARM INC.
XX PA (BLAT/) BLATT L.
XX PA (MCSW/) MCSWIGGEN J A.
XX XX Blatt L, Mcswiggen JA;
XX PI WPI; 2002-706994/76.
XX DR New nucleic acid molecule that modulates replication of West Nile Virus
XX PT (WNV), useful for treating a condition related to WNV infection e.g.
XX PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX PS Claim 23; SEQ ID NO 9628; 495pp; English.
XX CC The invention relates to nucleic acid molecules that modulate replication
XX CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
XX CC treating a condition related to WNV infection e.g. pancreatitis,
XX CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
XX CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
XX CC molecule is selected from the group of ribozymes consisting of
XX CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
XX CC nucleic acid molecules further comprise at least five ribose residues, at
XX CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
XX CC least three of the 5' terminal nucleotides and a 3' end modification of a
XX CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
XX CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
XX CC in the specification. The present sequence is that of a nucleic acid
XX CC molecule of the invention
XX SQ Sequence 17 BP; 3 A; 8 C; 1 G; 0 T; 5 U; 0 Other;
Query Match 54.8%; Score 17; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 10 GGAAGTTGAGTAGACG 26
DB 17 GGAAGTTGAGTAGACG 1

RESULT 25
ACN07461/c
ID ACN07461 standard; RNA; 17 BP.
XX AC ACN07461;
XX XX 22-APR-2004 (first entry)
XX DE WNV minus strand Hammerhead Ribozyme substrate SEQ ID NO 7464.
XX XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
XX KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
XX KW encephalitis; myocarditis; meningitis; infection; hepatitis;
XX KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
XX KW Amberzyme; Zinzyme; ss.
XX OS West Nile Virus.
XX XX WO200268637-A2.
XX PN 06-SEP-2002.
XX PD 19-OCT-2001; 2001WO-US048350.
XX PF 20-OCT-2000; 2000US-024241P.
XX PR (RIBO-) RIBOZYME PHARM INC.
XX PA (BLAT/) BLATT L.
XX PA (MCSW/) MCSWIGGEN J A.
XX XX Blatt L, Mcswiggen JA;
XX PI WPI; 2002-706994/76.
XX DR New nucleic acid molecule that modulates replication of West Nile Virus
XX PT (WNV), useful for treating a condition related to WNV infection e.g.
XX PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX PS Claim 23; SEQ ID NO 7464; 495pp; English.
XX CC The invention relates to nucleic acid molecules that modulate replication
XX CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
XX CC treating a condition related to WNV infection e.g. pancreatitis,
XX CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
XX CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
XX CC molecule is selected from the group of ribozymes consisting of
XX CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
XX CC nucleic acid molecules further comprise at least five ribose residues, at
XX CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
XX CC least three of the 5' terminal nucleotides and a 3' end modification of a
XX CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
XX CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
XX CC in the specification. The present sequence is that of a nucleic acid
XX CC molecule of the invention
XX SQ Sequence 17 BP; 5 A; 7 C; 2 G; 0 T; 3 U; 0 Other;
Query Match 54.8%; Score 17; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GTTGAGTAGACGGTGCT 30
DB 17 GTTGAGTAGACGGTGCT 1

RESULT 26
ACN09628/c
```

ID ACN09628 standard; RNA; 17 BP.
 XX ACN09628;
 XX DT 22-APR-2004 (first entry)
 XX WNV minus strand Inozyme substrate SEQ ID NO 9631.
 XX
 XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
 KW Amberzyme; Zinzyne; ss.
 XX
 XX West Nile Virus.
 XX WO200268637-A2.
 XX PD 06-SEP-2002.
 XX PF 19-OCT-2001; 2001WO-US048350.
 XX PR 20-OCT-2000; 2000US-0242411P.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 XX PI Blatt L, Mcswiggen JA;
 XX WPI; 2002-706994/76.
 XX
 XX New nucleic acid molecule that modulates replication of West Nile Virus
 PT (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 XX
 XX Claim 23; SEQ ID NO 9631; 495pp; English.
 XX
 XX The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyne. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention
 XX
 XX Sequence 17 BP; 2 A; 5 C; 6 G; 0 T; 4 U; 0 Other;
 SQ
 Query Match 54.8%; Score 17; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4.5;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CCGCCACCGGAAGTTGA 18
 Db 17 CCGCCACCGGAAGTTGA 1
 RESULT 27
 ACN01372
 ID ACN01372 standard; RNA; 17 BP.
 XX ACN01372;
 XX DT 22-APR-2004 (first entry)
 XX WNV Hammerhead Ribozyme substrate SEQ ID NO 1362.
 DE

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
 KW Amberzyme; Zinzyne; ss.
 XX
 XX West Nile Virus.
 XX WO200268637-A2.
 XX PD 06-SEP-2002.
 XX PF 19-OCT-2001; 2001WO-US048350.
 XX PR 20-OCT-2000; 2000US-0242411P.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 XX PI Blatt L, Mcswiggen JA;
 XX WPI; 2002-706994/76.
 XX
 XX New nucleic acid molecule that modulates replication of West Nile Virus
 PT (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 XX
 XX Claim 23; SEQ ID NO 1362; 495pp; English.
 XX
 XX The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyne. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention
 XX
 XX Sequence 17 BP; 5 A; 3 C; 6 G; 0 T; 3 U; 0 Other;
 SQ
 Query Match 54.8%; Score 17; DB 6; Length 17;
 Best Local Similarity 82.4%; Pred. No. 4.5;
 Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 8 CCGGAAGTTGAGTAGAC 24
 Db 1 CCGGAAGTTGAGTAGAC 17
 RESULT 28
 ACN13635/c
 ID ACN13635 standard; RNA; 17 BP.
 XX ACN13635;
 XX DT 22-APR-2004 (first entry)
 XX WNV minus strand DNazyme substrate SEQ ID NO 13638.
 DE
 XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
 KW Amberzyme; Zinzyne; ss.
 XX

OS West Nile Virus.
 XX WO200268637-A2.
 XX
 XX PD 06-SEP-2002.
 XX
 XX PF 19-OCT-2001; 2001WO-US048350.
 XX
 XX PR 20-OCT-2000; 2000US-0242411P.
 XX
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX (BLAT/) BLATT L.
 XX (MCSW/) MCSWIGGEN J A.
 XX
 XX PI Blatt L, Mcswiggen JA;
 XX WPI; 2002-706994/76.
 XX
 XX New nucleic acid molecule that modulates replication of West Nile Virus (WNV), useful for treating a condition related to WNV infection e.g. pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 XX
 XX PS Claim 23; SEQ ID NO 13638; 495pp; English.
 XX
 XX The invention relates to nucleic acid molecules that modulate replication of the West Nile Virus (WNV). The nucleic acid molecules are useful for treating a condition related to WNV infection e.g. pancreatitis, encephalitis, myocarditis, meningitis, neurologic infection, hepatitis, liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid molecule is selected from the group of ribozymes consisting of Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The nucleic acid molecules further comprise at least five ribose residues, at least ten 2'-O-methyl modifications, phosphorothioate linkages on at least three of the 5' terminal nucleotides and a 3' end modification of a 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080 are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given in the specification. The present sequence is that of a nucleic acid molecule of the invention
 XX
 XX SQ Sequence 17 BP; 3 A; 6 C; 2 G; 0 T; 6 U; 0 Other;
 Query Match 54.8%; Score 17; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4.5;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 ACCGGAAGTTGAGTAGA 23
 Db 17 ACCGGAAGTTGAGTAGA 1
 RESULT 29
 ACN07462/c
 ID ACN07462 standard; RNA; 17 BP.
 XX
 XX ACN07462;
 AC
 DT 22-APR-2004 (first entry)
 XX
 DE WNV minus strand Hammerhead Ribozyme substrate SEQ ID NO 7465.
 XX
 XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic; virucide; neuroprotective; antibacterial; replication; pancreatitis; encephalitis; myocarditis; meningitis; infection; hepatitis; liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme; Amberzyme; Zinzyme; ss.
 OS
 XX West Nile Virus.
 OS
 XX WO200268637-A2.
 XX
 XX PD 06-SEP-2002.
 XX
 XX PF 19-OCT-2001; 2001WO-US048350.

XX
 PR 20-OCT-2000; 2000US-0242411P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 XX (BLAT/) BLATT L.
 XX (MCSW/) MCSWIGGEN J A.
 XX
 XX PI Blatt L, Mcswiggen JA;
 XX WPI; 2002-706994/76.
 XX
 XX New nucleic acid molecule that modulates replication of West Nile Virus (WNV), useful for treating a condition related to WNV infection e.g. pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 XX
 XX PS Claim 23; SEQ ID NO 7465; 495pp; English.
 XX
 XX The invention relates to nucleic acid molecules that modulate replication of the West Nile Virus (WNV). The nucleic acid molecules are useful for treating a condition related to WNV infection e.g. pancreatitis, encephalitis, myocarditis, meningitis, neurologic infection, hepatitis, liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid molecule is selected from the group of ribozymes consisting of Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The nucleic acid molecules further comprise at least five ribose residues, at least ten 2'-O-methyl modifications, phosphorothioate linkages on at least three of the 5' terminal nucleotides and a 3' end modification of a 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080 are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given in the specification. The present sequence is that of a nucleic acid molecule of the invention
 XX
 XX SQ Sequence 17 BP; 4 A; 7 C; 1 G; 0 T; 5 U; 0 Other;
 Query Match 54.8%; Score 17; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4.5;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 AAGTTGAGTAGACGGTG 28
 Db 17 AAGTTGAGTAGACGGTG 1
 RESULT 30
 ACN09624/c
 ID ACN09624 standard; RNA; 17 BP.
 XX
 XX ACN09624;
 AC
 DT 22-APR-2004 (first entry)
 XX
 DE WNV minus strand Inozyme substrate SEQ ID NO 9627.
 XX
 XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic; virucide; neuroprotective; antibacterial; replication; pancreatitis; encephalitis; myocarditis; meningitis; infection; hepatitis; liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme; Amberzyme; Zinzyme; ss.
 OS
 XX West Nile Virus.
 OS
 XX WO200268637-A2.
 XX
 XX PD 06-SEP-2002.
 XX
 XX PF 19-OCT-2001; 2001WO-US048350.
 XX
 XX PR 20-OCT-2000; 2000US-0242411P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 XX (BLAT/) BLATT L.
 XX (MCSW/) MCSWIGGEN J A.

PI Blatt L, Mcswiggen JA;
 XX WPI; 2002-706994/76.
 XX New nucleic acid molecule that modulates replication of West Nile Virus
 PT (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 XX Claim 23; SEQ ID NO 9627; 495pp; English.
 XX The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention
 XX SQ Sequence 17 BP; 4 A; 7 C; 2 G; 0 T; 4 U; 0 Other;
 Query Match 54.8%; Score 17; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4.5;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 AGTGTAGTAGCGGTGC 29
 DB 17 AGTGTAGTAGCGGTGC 1
 RESULT 31
 ACN05425
 ID ACN05425 standard; RNA; 17 BP.
 AC ACN05425;
 XX 22-APR-2004 (first entry)
 XX WNV DNAzyme substrate SEQ ID NO 5428.
 XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
 KW Amberzyme; Zinzyme; ss.
 XX West Nile Virus.
 OS WO200268637-A2.
 XX 06-SEP-2002.
 XX 19-OCT-2001; 2001WO-US048350.
 XX 20-OCT-2000; 2000US-0242411P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 XX Blatt L, Mcswiggen JA;
 XX WPI; 2002-706994/76.
 XX New nucleic acid molecule that modulates replication of West Nile Virus
 PT (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 PT

XX Claim 23; SEQ ID NO 5428; 495pp; English.
 XX The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention
 XX SQ Sequence 17 BP; 3 A; 2 C; 7 G; 0 T; 5 U; 0 Other;
 Query Match 54.8%; Score 17; DB 6; Length 17;
 Best Local Similarity 70.6%; Pred. No. 4.5;
 Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 QY 15 TTGAGTAGACGGTGCTG 31
 DB 1 UUGAGUAGACGGUGCUG 17
 RESULT 32
 ACN04649
 ID ACN04649 standard; RNA; 17 BP.
 AC ACN04649;
 XX 22-APR-2004 (first entry)
 XX WNV Zinzyme substrate SEQ ID NO 4652.
 XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
 KW Amberzyme; Zinzyme; ss.
 XX West Nile Virus.
 OS WO200268637-A2.
 XX 06-SEP-2002.
 XX 19-OCT-2001; 2001WO-US048350.
 XX 20-OCT-2000; 2000US-0242411P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 XX Blatt L, Mcswiggen JA;
 XX WPI; 2002-706994/76.
 XX New nucleic acid molecule that modulates replication of West Nile Virus
 PT (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 XX Claim 23; SEQ ID NO 4652; 495pp; English.
 XX The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis.
 CC

CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid molecule is selected from the group of ribozymes consisting of Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The nucleic acid molecules further comprise at least five ribose residues, at least ten 2'-O-methyl modifications, phosphorothioate linkages on at least three of the 5' terminal nucleotides and a 3' end modification of a 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080 are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given in the specification. The present sequence is that of a nucleic acid molecule of the invention

XX Sequence 17 BP; 5 A; 3 C; 6 G; 0 T; 3 U; 0 Other;
SQ Query Match 54.8%; Score 17; DB 6; Length 17;
Best Local Similarity 82.4%; Pred. No. 4.5;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 6 CACCGGAAGTTGAGTAG 22
Db 1 CACCGGAAGUUGAGUAG 17

RESULT 33
ACN09626/C
ID ACN09626 standard; RNA; 17 BP.

XX ACN09626;

XX 22-APR-2004 (first entry)

DE WNV minus strand Inozyme substrate SEQ ID NO 9629.

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW viricide; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
KW Amberzyme; Zinzyme; ss.

XX West Nile Virus.

XX WO200268637-A2.

XX 06-SEP-2002.

XX 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.

XX (BLAT/) BLATT L.

XX (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus (WNV), useful for treating a condition related to WNV infection e.g. pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

PS Claim 23; SEQ ID NO 9629; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication of the West Nile Virus (WNV). The nucleic acid molecules are useful for treating a condition related to WNV infection e.g. pancreatitis, encephalitis, myocarditis, meningitis, neurologic infection, hepatitis, liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid molecule is selected from the group of ribozymes consisting of Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The nucleic acid molecules further comprise at least five ribose residues, at least ten 2'-O-methyl modifications, phosphorothioate linkages on at least three of the 5' terminal nucleotides and a 3' end modification of a 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080

CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given in the specification. The present sequence is that of a nucleic acid molecule of the invention

XX Sequence 17 BP; 3 A; 6 C; 3 G; 0 T; 5 U; 0 Other;

QY Query Match 54.8%; Score 17; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCGGAAGTTGAGTAGAC 24
Db 17 CCGGAAGTTGAGTAGAC 1

RESULT 34
ACN07290
ID ACN07290 standard; RNA; 17 BP.

XX ACN07290;

XX 22-APR-2004 (first entry)

DE WNV Amberzyme substrate SEQ ID NO 7293.

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW viricide; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
KW Amberzyme; Zinzyme; ss.

XX West Nile Virus.

XX WO200268637-A2.

XX 06-SEP-2002.

XX 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.

XX (BLAT/) BLATT L.

XX (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus (WNV), useful for treating a condition related to WNV infection e.g. pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

PS Claim 23; SEQ ID NO 7293; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication of the West Nile Virus (WNV). The nucleic acid molecules are useful for treating a condition related to WNV infection e.g. pancreatitis, encephalitis, myocarditis, meningitis, neurologic infection, hepatitis, liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid molecule is selected from the group of ribozymes consisting of Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The nucleic acid molecules further comprise at least five ribose residues, at least ten 2'-O-methyl modifications, phosphorothioate linkages on at least three of the 5' terminal nucleotides and a 3' end modification of a 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080 are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given in the specification. The present sequence is that of a nucleic acid molecule of the invention

XX Sequence 17 BP; 4 A; 6 C; 5 G; 0 T; 2 U; 0 Other;

QY Query Match 54.8%; Score 17; DB 6; Length 17;

Best Local Similarity 88.2%; Pred. No. 4.5;		Pred. No. 4.5;		Pred. No. 4.5;	
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;		Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;		Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	
QY	2	CGCCACCGGAAGTTGA 18			
DB	1	CGCCACCGGAAGUUGA 17			
RESULT 35					
ID	ACN07291	ACN07291 standard; RNA; 17 BP.			
XX	AC	ACN07291;			
XX	DT	22-APR-2004 (first entry)			
XX	DE	WNV Amberzyme substrate SEQ ID NO 7294.			
XX	KW	WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;			
XX	KW	virucide; neuroprotective; antibacterial; replication; pancreatitis;			
XX	KW	encephalitis; myocarditis; meningitis; infection; hepatitis;			
XX	KW	liver failure; cancer; cirrhosis; Hammerhead; inozyme; DNAzyme;			
XX	KW	Amberzyme; Zinzyne; ss.			
XX	OS	West Nile Virus.			
XX	PN	WO200268637-A2.			
XX	PD	06-SEP-2002.			
XX	PF	19-OCT-2001; 2001WO-US048350.			
XX	PR	20-OCT-2000; 2000US-0242411P.			
XX	PA	(RIBO-) RIBOZYME PHARM INC.			
XX	PA	(BLAT/) BLATT L.			
XX	PA	(MCSW/) MCSWIGGEN J A.			
XX	PI	Blatt L, Mcswiggen JA;			
XX	WPI	2002-706994/76.			
XX	PT	New nucleic acid molecule that modulates replication of West Nile Virus			
XX	PT	(WNV), useful for treating a condition related to WNV infection e.g.			
XX	PT	pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.			
XX	PS	Claim 23; SEQ ID NO 7294; 495pp; English.			
XX	CC	The invention relates to nucleic acid molecules that modulate replication			
XX	CC	of the West Nile Virus (WNV). The nucleic acid molecules are useful for			
XX	CC	treating a condition related to WNV infection e.g. pancreatitis,			
XX	CC	encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,			
XX	CC	liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid			
XX	CC	molecule is selected from the group of ribozymes consisting of			
XX	CC	Hammerhead, inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyne. The			
XX	CC	nucleic acid molecules further comprise at least five ribose residues, at			
XX	CC	least ten 2'-O-methyl modifications, phosphorothioate linkages on at			
XX	CC	least three of the 5' terminal nucleotides and a 3' end modification of a			
XX	CC	3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080			
XX	CC	are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given			
XX	CC	in the specification. The present sequence is that of a nucleic acid			
XX	CC	molecule of the invention			
XX	Sequence	17 BP; 4 A; 5 C; 6 G; 0 T; 2 U; 0 Other;			
Query Match 54.8%; Score 17; DB 6; Length 17;					
Best Local Similarity 88.2%; Pred. No. 4.5;					
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;					
QY	3	CGCCACCGGAAGTTGAG 19			
DB	1	CGCCACCGGAAGUUGAG 17			

Best Local Similarity 88.2%; Pred. No. 4.5;		Pred. No. 4.5;		Pred. No. 4.5;	
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;		Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;		Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	
QY	2	CGCCACCGGAAGTTGA 18			
DB	1	CGCCACCGGAAGUUGA 17			
RESULT 36					
ID	ACN07463/c	ACN07463 standard; RNA; 17 BP.			
XX	AC	ACN07463;			
XX	DT	22-APR-2004 (first entry)			
XX	DE	WNV minus strand Hammerhead Ribozyme substrate SEQ ID NO 7466.			
XX	KW	WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;			
XX	KW	virucide; neuroprotective; antibacterial; replication; pancreatitis;			
XX	KW	encephalitis; myocarditis; meningitis; infection; hepatitis;			
XX	KW	liver failure; cancer; cirrhosis; Hammerhead; inozyme; DNAzyme;			
XX	KW	Amberzyme; Zinzyne; ss.			
XX	OS	West Nile Virus.			
XX	PN	WO200268637-A2.			
XX	PD	06-SEP-2002.			
XX	PF	19-OCT-2001; 2001WO-US048350.			
XX	PR	20-OCT-2000; 2000US-0242411P.			
XX	PA	(RIBO-) RIBOZYME PHARM INC.			
XX	PA	(BLAT/) BLATT L.			
XX	PA	(MCSW/) MCSWIGGEN J A.			
XX	PI	Blatt L, Mcswiggen JA;			
XX	WPI	2002-706994/76.			
XX	PT	New nucleic acid molecule that modulates replication of West Nile Virus			
XX	PT	(WNV), useful for treating a condition related to WNV infection e.g.			
XX	PT	pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.			
XX	PS	Claim 23; SEQ ID NO 7466; 495pp; English.			
XX	CC	The invention relates to nucleic acid molecules that modulate replication			
XX	CC	of the West Nile Virus (WNV). The nucleic acid molecules are useful for			
XX	CC	treating a condition related to WNV infection e.g. pancreatitis,			
XX	CC	encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,			
XX	CC	liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid			
XX	CC	molecule is selected from the group of ribozymes consisting of			
XX	CC	Hammerhead, inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyne. The			
XX	CC	nucleic acid molecules further comprise at least five ribose residues, at			
XX	CC	least ten 2'-O-methyl modifications, phosphorothioate linkages on at			
XX	CC	least three of the 5' terminal nucleotides and a 3' end modification of a			
XX	CC	3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080			
XX	CC	are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given			
XX	CC	in the specification. The present sequence is that of a nucleic acid			
XX	CC	molecule of the invention			
XX	Sequence	17 BP; 3 A; 7 C; 2 G; 0 T; 5 U; 0 Other;			
Query Match 54.8%; Score 17; DB 6; Length 17;					
Best Local Similarity 100.0%; Pred. No. 4.5;					
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	9	CGGAAGTTGAGTAGACG 25			
DB	17	CGGAAGTTGAGTAGACG 1			

Best Local Similarity 88.2%; Pred. No. 4.5;		Pred. No. 4.5;		Pred. No. 4.5;	
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;		Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;		Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	
QY	3	CGCCACCGGAAGTTGAG 19			
DB	1	CGCCACCGGAAGUUGAG 17			
RESULT 37					
ID	ACN07465/c	ACN07465 standard; RNA; 17 BP.			
XX	ID	ACN07465 standard; RNA; 17 BP.			
XX	AC	ACN07465;			
XX	DT	22-APR-2004 (first entry)			
XX	DE	WNV minus strand Hammerhead Ribozyme substrate SEQ ID NO 7466.			
XX	KW	WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;			
XX	KW	virucide; neuroprotective; antibacterial; replication; pancreatitis;			
XX	KW	encephalitis; myocarditis; meningitis; infection; hepatitis;			
XX	KW	liver failure; cancer; cirrhosis; Hammerhead; inozyme; DNAzyme;			
XX	KW	Amberzyme; Zinzyne; ss.			
XX	OS	West Nile Virus.			
XX	PN	WO200268637-A2.			
XX	PD	06-SEP-2002.			
XX	PF	19-OCT-2001; 2001WO-US048350.			
XX	PR	20-OCT-2000; 2000US-0242411P.			
XX	PA	(RIBO-) RIBOZYME PHARM INC.			
XX	PA	(BLAT/) BLATT L.			
XX	PA	(MCSW/) MCSWIGGEN J A.			
XX	PI	Blatt L, Mcswiggen JA;			
XX	WPI	2002-706994/76.			
XX	PT	New nucleic acid molecule that modulates replication of West Nile Virus			
XX	PT	(WNV), useful for treating a condition related to WNV infection e.g.			
XX	PT	pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.			
XX	PS	Claim 23; SEQ ID NO 7294; 495pp; English.			
XX	CC	The invention relates to nucleic acid molecules that modulate replication			
XX	CC	of the West Nile Virus (WNV). The nucleic acid molecules are useful for			
XX	CC	treating a condition related to WNV infection e.g. pancreatitis,			
XX	CC	encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,			
XX	CC	liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid			
XX	CC	molecule is selected from the group of ribozymes consisting of			
XX	CC	Hammerhead, inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyne. The			
XX	CC	nucleic acid molecules further comprise at least five ribose residues, at			
XX	CC	least ten 2'-O-methyl modifications, phosphorothioate linkages on at			
XX	CC	least three of the 5' terminal nucleotides and a 3' end modification of a			
XX	CC	3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080			
XX	CC	are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given			
XX	CC	in the specification. The present sequence is that of a nucleic acid			
XX	CC	molecule of the invention			
XX	Sequence	17 BP; 4 A; 5 C; 6 G; 0 T; 2 U; 0 Other;			
Query Match 54.8%; Score 17; DB 6; Length 17;					
Best Local Similarity 88.2%; Pred. No. 4.5;					
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;					
QY	3	CGCCACCGGAAGTTGAG 19			
DB	1	CGCCACCGGAAGUUGAG 17			

DT 22-APR-2004 (first entry)
 XX WNV minus strand Hammerhead Ribozyme substrate SEQ ID NO 7468.
 DE
 XX
 XX WNV; West Nile Virus; antiinflammatory; cytotostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
 KW Amberzyme; Zinzyme; ss.
 XX
 XX West Nile Virus.
 OS
 XX
 XX WO200268637-A2.
 PN
 XX
 XX 06-SEP-2002.
 PD
 XX
 XX 19-OCT-2001; 2001WO-US048350.
 PP
 XX
 XX 20-OCT-2000; 2000US-0242411P.
 PR
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 PA
 XX
 PI Blatt L, Mcswiggen JA;
 PI
 XX
 XX WPI; 2002-706994/76.
 DR
 XX
 XX New nucleic acid molecule that modulates replication of West Nile Virus
 XX (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 PT
 XX
 XX Claim 23; SEQ ID NO 7468; 495pp; English.
 PS
 XX
 XX The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention
 XX
 XX Sequence 17 BP; 2 A; 6 C; 5 G; 0 T; 4 U; 0 Other;
 SQ
 Query Match 54.8%; Score 17; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4.5;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 CGCCACCGGAAGTTGAG 19
 DB 17 CGCCACCGGAAGTTGAG 1
 RESULT 38
 ACN09627/C
 ID ACN09627 standard; RNA; 17 BP.
 AC ACN09627;
 AC
 XX
 XX 22-APR-2004 (first entry)
 DT
 XX WNV minus strand Inozyme substrate SEQ ID NO 9630.
 DE
 XX
 XX WNV; West Nile Virus; antiinflammatory; cytotostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;

KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
 KW Amberzyme; Zinzyme; ss.
 XX
 XX West Nile Virus.
 OS
 XX
 XX WO200268637-A2.
 PN
 XX
 XX 06-SEP-2002.
 PD
 XX
 XX 19-OCT-2001; 2001WO-US048350.
 PP
 XX
 XX 20-OCT-2000; 2000US-0242411P.
 PR
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 PA
 XX
 PI Blatt L, Mcswiggen JA;
 PI
 XX
 XX WPI; 2002-706994/76.
 DR
 XX
 XX New nucleic acid molecule that modulates replication of West Nile Virus
 XX (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 PT
 XX
 XX Claim 23; SEQ ID NO 9630; 495pp; English.
 PS
 XX
 XX The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention
 XX
 XX Sequence 17 BP; 3 A; 5 C; 4 G; 0 T; 5 U; 0 Other;
 SQ
 Query Match 54.8%; Score 17; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4.5;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 CCACCGGAAGTTGAGTA 21
 DB 17 CCACCGGAAGTTGAGTA 1
 RESULT 39
 ACN07293
 ID ACN07293 standard; RNA; 17 BP.
 AC ACN07293;
 AC
 XX
 XX 22-APR-2004 (first entry)
 DT
 XX WNV Amberzyme substrate SEQ ID NO 7296.
 DE
 XX
 XX WNV; West Nile Virus; antiinflammatory; cytotostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
 KW Amberzyme; Zinzyme; ss.
 XX
 XX West Nile Virus.
 OS
 XX
 XX WO200268637-A2.
 PN

```

PD 06-SEP-2002.
XX
PF 19-OCT-2001; 2001WO-US048350.
XX
PR 20-OCT-2000; 2000US-0242411P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
XX
PI Blatt L, Mcswiggen JA;
XX
PS Claim 23; SEQ ID NO 7296; 495pp; English.
XX
CC The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
SQ Sequence 17 BP; 3 A; 2 C; 7 G; 0 T; 5 U; 0 Other;
Query Match 54.8%; Score 17; DB 6; Length 17;
Best Local Similarity 70.6%; Pred. No. 4.5;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 14 GTTGAGTAGACGGTGCT 30
Db 1 GUUGAGUAGACGGUGCU 17

RESULT 40
ACN07464/C
ID ACN07464 standard; RNA; 17 BP.
XX
AC ACN07464;
XX
DT 22-APR-2004 (first entry)
XX
DE WNV minus strand Hammerhead Ribozyme substrate SEQ ID NO 7467.
XX
KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
KW Amberzyme; Zinzyme; ss.
XX
OS West Nile Virus.
XX
PN WO200268637-A2.
XX
PD 06-SEP-2002.
XX
PF 19-OCT-2001; 2001WO-US048350.
XX
PR 20-OCT-2000; 2000US-0242411P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Mcswiggen JA;
XX
PS Claim 23; SEQ ID NO 7296; 495pp; English.
XX
CC The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
SQ Sequence 17 BP; 3 A; 2 C; 7 G; 0 T; 5 U; 0 Other;
Query Match 54.8%; Score 17; DB 6; Length 17;
Best Local Similarity 70.6%; Pred. No. 4.5;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 14 GTTGAGTAGACGGTGCT 30
Db 1 GUUGAGUAGACGGUGCU 17

RESULT 40
ACN07464/C
ID ACN07464 standard; RNA; 17 BP.
XX
AC ACN07464;
XX
DT 22-APR-2004 (first entry)
XX
DE WNV minus strand Hammerhead Ribozyme substrate SEQ ID NO 7467.
XX
KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
KW Amberzyme; Zinzyme; ss.
XX
OS West Nile Virus.
XX
PN WO200268637-A2.
XX
PD 06-SEP-2002.
XX
PF 19-OCT-2001; 2001WO-US048350.
XX
PR 20-OCT-2000; 2000US-0242411P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Mcswiggen JA;
XX
PS Claim 23; SEQ ID NO 7467; 495pp; English.
XX
CC The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
SQ Sequence 17 BP; 3 A; 2 C; 7 G; 0 T; 5 U; 0 Other;
Query Match 54.8%; Score 17; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCCACCGGAGCTTGAGT 20
Db 17 GCCACCGGAGCTTGAGT 1

RESULT 41
ADN36743
ID ADN36743 standard; DNA; 18 BP.
XX
AC ADN36743;
XX
DT 15-JUL-2004 (first entry)
XX
DE West Nile virus detection-related oligonucleotide probe SeqID65.
XX
KW hybridisation assay probe; nucleic acid detection;
KW target-complementary sequence; flavivirus; West Nile virus; WNV;
KW RNA virus; infection; meningitis; encephalitis;
KW high throughput screening; probe; ss.
XX
OS West Nile virus.
XX
FH Key Location/Qualifiers
FT modified_base 1 /tag= a
FT /mod_base= i
XX
PN WO2004036190-A2.
XX
PD 29-APR-2004.
XX
PF 10-OCT-2003; 2003WO-US033639.
XX
PR 16-OCT-2002; 2002US-0418891P.
XX
PR 25-NOV-2002; 2002US-0429006P.
XX
PR 24-FEB-2003; 2003US-0449810P.
XX
PA (GENP-) GEN-PROBE INC.
XX

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PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX WPI; 2004-389590/36.
XX New hybridization assay probe comprising target-complementary sequence of
PT bases, useful in detecting flavivirus, e.g. West Nile virus.
PT
XX Claim 26; SEQ ID NO 65; 135pp; English.
XX
CC This invention relates to a novel hybridisation assay probe, for
CC detecting a nucleic acid, which is a probe sequence that comprises a
CC target-complementary sequence of bases, and optionally one or more base
CC sequences that are not complementary to the nucleic acid that is to be
CC detected. The hybridisation assay probes and the kits are useful in
CC detecting and amplifying a target nucleic acid sequence, for example
CC flavivirus like West Nile virus, that may be present in a biological
CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC birds and culex mosquitoes, with humans and horses serving as incidental
CC hosts. Infection of humans can lead to meningitis or encephalitis. The
CC invention may allow for accurate and efficient high throughput screening.
CC The present sequence is that of an oligonucleotide probe which is related
CC to the invention.
XX
SQ Sequence 18 BP; 4 A; 4 C; 6 G; 3 T; 0 U; 1 Other;

Query Match 54.8%; Score 17; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCCACCGGAAGTTGAGT 20
DB 2 GCCACCGGAAGTTGAGT 18
|||||
RESULT 42
ABL04952/C
ID ABL04952 standard; cDNA; 52872 BP.
AC
XX ABL04952;
XX
XX 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 9338.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.
XX
XX WO200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US09231.
XX
XX 23-MAR-2000; 2000US-0191637P.
XX
XX 11-JUL-2000; 2000US-00614150.
XX
XX (PEKE) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
PI
XX WPI; 2001-656860/75.
XX
XX P-PSDB; ABB60849.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions.
PT
XX
XX Claim 1; SEQ ID NO 9338; 21pp + Sequence Listing; English.
PS
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is

CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 52872 BP; 15532 A; 11487 C; 10803 G; 15050 T; 0 U; 0 Other;

Query Match 54.8%; Score 17; DB 4; Length 52872;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CACCGGAAGTTGAGTAG 22
DB 19409 CACCGGAAGTTGAGTAG 19393
|||||
RESULT 43
ACN14228/C
ID ACN14228 standard; RNA; 17 BP.
AC
XX ACN14228;
XX
XX 22-APR-2004 (first entry)
XX
XX WNV minus strand Amberzyme substrate SEQ ID NO 14231.
XX
XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
KW Amberzyme; Zinzyme; ss.
XX
XX West Nile Virus.
XX
XX WO200268637-A2.
XX
XX 06-SEP-2002.
XX
XX 19-OCT-2001; 2001WO-US048350.
XX
XX 20-OCT-2000; 2000US-0242411P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGGEN J A.
XX
XX Blatt L, Mcswiggen JA;
XX
XX WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
PT (WNV), useful for treating a condition related to WNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
XX Claim 23; SEQ ID NO 14231; 495pp; English.
XX
XX The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid

CC molecule of the invention
 XX Sequence 17 BP; 2 A; 5 C; 7 G; 0 T; 3 U; 0 Other;
 SQ Query Match 51.6%; Score 16; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCGCCACCGGAAGTTG 17
 Db 16 CCGCCACCGGAAGTTG 1
 |||||

RESULT 44
 ACN12344/c
 ID ACN12344 standard; RNA; 17 BP.
 AC ACN12344;
 XX 22-APR-2004 (first entry)
 DT
 XX WNV minus strand Zinzyne substrate SEQ ID NO 12347.
 DE
 XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; inozyme; DNAzyme;
 KW Amberzyme; Zinzyne; ss.
 XX
 OS West Nile Virus.
 XX
 PN WO200268637-A2.
 XX
 PD 06-SEP-2002.
 XX
 PF 19-OCT-2001; 2001WO-US048350.
 XX
 PR 20-OCT-2000; 2000US-0242411P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGEN J A.
 XX
 PI Blatt L, Mcswiggen JA;
 XX
 XX WPI; 2002-706994/76.
 DR
 XX New nucleic acid molecule that modulates replication of West Nile Virus
 PT (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 XX
 PS Claim 23; SEQ ID NO 12347; 495pp; English.
 XX
 CC The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyne. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention
 XX
 SQ Sequence 17 BP; 4 A; 7 C; 3 G; 0 T; 3 U; 0 Other;
 Query Match 51.6%; Score 16; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCGCCACCGGAAGTTG 17
 Db 16 CCGCCACCGGAAGTTG 1
 |||||

RESULT 45
 ACN03350
 ID ACN03350 standard; RNA; 17 BP.
 AC ACN03350;
 XX 22-APR-2004 (first entry)
 DT
 XX WNV Inozyme substrate SEQ ID NO 3353.
 DE
 XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; inozyme; DNAzyme;
 KW Amberzyme; Zinzyne; ss.
 XX
 OS West Nile Virus.
 XX
 PN WO200268637-A2.
 XX
 PD 06-SEP-2002.
 XX
 PF 19-OCT-2001; 2001WO-US048350.
 XX
 PR 20-OCT-2000; 2000US-0242411P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGEN J A.
 XX
 PI Blatt L, Mcswiggen JA;
 XX
 XX WPI; 2002-706994/76.
 DR
 XX New nucleic acid molecule that modulates replication of West Nile Virus
 PT (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 XX
 PS Claim 23; SEQ ID NO 3353; 495pp; English.
 XX
 CC The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyne. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention
 XX
 SQ Sequence 17 BP; 3 A; 7 C; 5 G; 0 T; 2 U; 0 Other;
 Query Match 51.6%; Score 16; DB 6; Length 17;
 Best Local Similarity 87.5%; Pred. No. 17;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCGCCACCGGAAGTTG 17
 Db 2 CCGCCACCGGAAGTTG 17
 |||||

RESULT 46

AAAF08395/c
 ID AAFA08395 standard; cDNA; 628 BP.
 AC AAFA08395;
 XX
 DT 13-MAR-2001 (first entry)
 XX
 DE Fusarium venenatum EST SEQ ID NO:918.
 XX
 KW Multiple gene expression; filamentous fungal cell; EST;
 KW expressed sequence tag; Fusarium venenatum; Aspergillus niger;
 KW Aspergillus oryzae; Trichoderma reesei; identification; recombination;
 KW culture condition; environmental stress; spore morphogenesis;
 KW metabolic pathway engineering; catabolic pathway engineering; ss.
 XX
 OS Fusarium venenatum.
 XX
 PN WO200056762-A2.
 XX
 PD 28-SEP-2000.
 XX
 PF 22-MAR-2000; 2000WO-US007781.
 XX
 PR 22-MAR-1999; 99US-00273623.
 XX
 PA (NOVO) NOVO NORDISK BIOTECH INC.
 PA (NOVO) NOVO NORDISK AS.
 XX
 PI Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;
 XX
 DR WPI; 2000-594572/56.
 XX
 PT Monitoring differential expression of genes in filamentous fungal cells
 PT uses fluorescence-labeled nucleic acids isolated from the cells and a
 PT substrate of expressed sequence tags.
 XX
 PS Claim 86; Page 734; 3161pp; English.
 XX
 CC The present invention describes a method for monitoring differential
 CC expression of genes in a first filamentous fungal (FF) cell relative to
 CC expression of the same genes in one or more second filamentous fungal
 CC cells. The method uses fluorescence-labeled nucleic acids isolated from
 CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs
 CC are used in the methods for monitoring differential expression of genes
 CC in a first filamentous fungal (FF) cell relative to expression of the
 CC same genes in one or more second filamentous fungal cells. Monitoring the
 CC global expression of genes from FF cells allows the production potential
 CC of the microorganisms to be improved. New genes may be discovered,
 CC possible functions of unknown open reading frames can be identified and
 CC gene copy number variation and stability can be monitored. The expression
 CC of genes can be used to study how FF cells adapt to changes in culture
 CC conditions, environmental stress, spore morphogenesis, recombination,
 CC metabolic or catabolic pathway engineering. Using ESTs provides several
 CC advantages over genomic or random cDNA clones including elimination of
 CC redundancy as one spot on an array equals one gene or open reading frame,
 CC and organization of the microarrays based on function of the gene
 CC products to facilitate analysis of the results. AAFA07478 to AAFA11247
 CC represents ESTs from Fusarium venenatum; AAFA11248 to AAFA11853 represents
 CC ESTs from Aspergillus niger; AAFA11854 to AAFA14878 represents ESTs from
 CC Aspergillus oryzae; and AAFA14879 to AAFA15337 represents ESTs from
 CC Trichoderma reesei, which are all specifically claimed in the present
 CC invention
 XX
 SQ Sequence 628 BP; 128 A; 175 C; 144 G; 176 T; 0 U; 5 Other;
 Query Match 51.6%; Score 16; DB 3; Length 628;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 14 GTTGAGTAGACGGTGC 29
 DB 205 GTTGAGTAGACGGTGC 190

RESULT 47
 ABZ71129/c
 ID ABZ71129 standard; DNA; 1323 BP.
 XX
 AC ABZ71129;
 XX
 DT 28-APR-2003 (first entry)
 XX
 DE Mycobacterium tuberculosis protein encoding DNA SEQ ID NO:136.
 XX
 KW Mycobacterium tuberculosis; infection; antibacterial; tuberculostatic;
 KW immunostimulant; vaccine; gene therapy; mycobacterial infection; gene;
 KW da.
 XX
 OS Mycobacterium tuberculosis.
 XX
 PN WO2003000721-A2.
 XX
 PD 03-JAN-2003.
 XX
 PF 21-JUN-2002; 2002WO-GB002845.
 XX
 PR 22-JUN-2001; 2001GB-00015365.
 PR 07-SEP-2001; 2001GB-00021780.
 XX
 PA (MICR-) MICROBIOLOGICAL RES AUTHORITY.
 XX
 PI James BW, Bacon J, Marsh P;
 XX
 DR WPI; 2003-201403/19.
 DR P-PSDB; ABP57503.
 XX
 PT New mycobacterial peptide, its fragment, variant or derivative, useful as
 PT vaccine for treating or preventing mycobacterial infections, and as
 PT diagnostic reagents for identifying such infections.
 XX
 PS Claim 15; Page 243-244; 246pp; English.
 XX
 CC ABP57436 to ABP57504 represent mycobacterial amino acid sequences (I)
 CC encoded by ABZ71062 to ABZ71130 (II), which are isolated from
 CC Mycobacterium tuberculosis. (I) are encoded by genes (II) whose
 CC expression is induced or up-regulated during culture of a mycobacterium
 CC under conditions defined by a dissolved oxygen tension of at least 10%
 CC air saturation measured at 37 plus degrees Celsius when compared with a
 CC dissolved oxygen tension of at least 40% air saturation measured at 37
 CC plus degrees Celsius. (I) and (II) have antibacterial, tuberculostatic
 CC and immunostimulant activities, and can be used in vaccines and gene
 CC therapy. (I) and (II) can be used for the manufacture of a medicament for
 CC treating or preventing a mycobacterial infection. They can also be used
 CC for the manufacture of a diagnostic reagent for identifying a
 CC mycobacterial infection
 XX
 SQ Sequence 1323 BP; 228 A; 416 C; 450 G; 229 T; 0 U; 0 Other;
 Query Match 51.6%; Score 16; DB 10; Length 1323;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 GCCACCGGAAGTTGAG 19
 DB 1037 GCCACCGGAAGTTGAG 1022

RESULT 48
 AAH51995/c
 ID AAH51995 standard; DNA; 1326 BP.
 XX
 AC AAH51995;
 XX
 DT 04-SEP-2001 (first entry)
 XX
 DE Mycobacterium tuberculosis potential drug target gene SEQ ID 49.

```
XX Drug target; growth; organism viability; characterisation; ds.
KW Mycobacterium tuberculosis.
XX WO200135317-A1.
XX 17-MAY-2001.
XX 13-NOV-2000; 2000WO-US0311152.
XX 12-NOV-1999; 99US-0165086P.
XX 12-NOV-1999; 99US-0165124P.
XX 01-FEB-2000; 2000US-0179531P.
XX (REGC ) UNIV CALIFORNIA.
XX Eisenberg D, Rotstein SH, Marcotte EM;
XX WPI: 2001-329193/34.
XX P-PSDB; AAG81144.
XX Identifying nucleotide or polypeptide sequence for use as drug target,
PT involves providing algorithm that analyzes a functional relationship
PT between nucleotide or polypeptide sequences, and comparing the sequences.
XX Disclosure; Page 82; 207pp; English.
XX This invention relates to a method for identifying a nucleotide or
CC polypeptide sequence that may be a drug target, or essential for growth
CC or viability of an organism. Polynucleotide sequences AAH51947 - AAH52092
CC represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium
CC tuberculosis proteins which are potential drug targets. The DNA and
CC protein sequences are used to illustrate the method of the invention. The
CC method involves providing an unknown nucleotide or polypeptide sequences,
CC and comparing it to a number of sequences along with at least one
CC algorithm capable of analysing a functional relationship between
CC nucleotide and polypeptide sequences. The method is useful for
CC characterizing the function of nucleic acids and polypeptides that may be
CC useful as a target for a drug or essential for the growth or viability of
CC an organism
XX Sequence 1326 BP; 229 A; 416 C; 451 G; 230 T; 0 U; 0 Other;
SQ Query Match 51.6%; Score 16; DB 4; Length 1326;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GCCACCGGAAGTTGAG 19
| | | | | | | | | |
DB 1037 GCCACCGGAAGTTGAG 1022
RESULT 49
ABL28588/c
ID ABL28588 standard; DNA; 31068 BP.
XX ABL28588;
XX 26-MAR-2002 (first entry)
XX Drosophila melanogaster genomic polynucleotide SEQ ID NO 37237.
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ds.
XX Drosophila melanogaster.
OS WO200171042-A2.
XX 27-SEP-2001.
XX 23-MAR-2001; 2001WO-US009231.
```

```
XX 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX (PEKE ) PE CORP NY.
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI: 2001-656860/75.
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX Claim 1; SEQ ID NO 37237; 21pp + Sequence Listing; English.
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-
CC AB872072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX Sequence 31068 BP; 8424 A; 6977 C; 7023 G; 8644 T; 0 U; 0 Other;
SQ Query Match 51.6%; Score 16; DB 4; Length 31068;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 CGCCACCGGAAGTTGA 18
| | | | | | | | | |
DB 2641 CGCCACCGGAAGTTGA 2626
RESULT 50
AAI99682_14/c
Continuation (15 of 45) of AAI99682 from base 1400001 (Mycobacterium tuberculosis strain
WP Sequence split into 45 fragments LOCUS AAI99682 Accession AAI99682
WP Fragment Name Begin End
WP AAI99682_00 1 110000
WP AAI99682_01 100001 210000
WP AAI99682_02 200001 310000
WP AAI99682_03 300001 410000
WP AAI99682_04 400001 510000
WP AAI99682_05 500001 600001
WP AAI99682_06 600001 710000
WP AAI99682_07 700001 810000
WP AAI99682_08 800001 910000
WP AAI99682_09 900001 1010000
WP AAI99682_10 1000001 1110000
WP AAI99682_11 1100001 1210000
WP AAI99682_12 1200001 1310000
WP AAI99682_13 1300001 1410000
WP AAI99682_14 1400001 1510000
WP AAI99682_15 1500001 1610000
WP AAI99682_16 1600001 1710000
WP AAI99682_17 1700001 1810000
WP AAI99682_18 1800001 1910000
WP AAI99682_19 1900001 2010000
WP AAI99682_20 2000001 2110000
WP AAI99682_21 2100001 2210000
WP AAI99682_22 2200001 2310000
WP AAI99682_23 2300001 2410000
WP AAI99682_24 2400001 2510000
WP AAI99682_25 2500001 2610000
WP AAI99682_26 2600001 2710000
WP AAI99682_27 2700001 2810000
WP AAI99682_28 2800001 2910000
WP AAI99682_29 2900001 3010000
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WP	AAI9682_30	3000001	3110000
WP	AAI9682_31	3100001	3210000
WP	AAI9682_32	3200001	3310000
WP	AAI9682_33	3300001	3410000
WP	AAI9682_34	3400001	3510000
WP	AAI9682_35	3500001	3610000
WP	AAI9682_36	3600001	3710000
WP	AAI9682_37	3700001	3810000
WP	AAI9682_38	3800001	3910000
WP	AAI9682_39	3900001	4010000
WP	AAI9682_40	4000001	4110000
WP	AAI9682_41	4100001	4210000
WP	AAI9682_42	4200001	4310000
WP	AAI9682_43	4300001	4410000
WP	AAI9682_44	4400001	4411529

Query Match 51.6%; Score 16; DB 4; Length 110000;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCCACCGGAAGTTGAG 19
 |||||
 Db 50409 GCCACCGGAAGTTGAG 50394

Search completed: March 25, 2005, 08:12:57
 Job time : 210.747 secs

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OM nucleic - nucleic search, using sw model

Run on: March 25, 2005, 04:27:15 ; Search time 1236.08 Seconds
(without alignments)
954.628 Million cell updates/sec

Title: US-10-688-489-59
Perfect score: 31
Sequence: 1 tcgcaccggaagttagtagacggtgctg 31

Scoring table: OLIGO_NUC
Gapop_60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0
Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : EST:*

1:	gb_est1:*
2:	gb_est2:*
3:	gb_hic:*
4:	gb_est3:*
5:	gb_est4:*
6:	gb_est5:*
7:	gb_est6:*
8:	gb_gss1:*
9:	gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	58.1	731	8	BZ992042
2	17	54.8	545	6	CD309228
3	17	54.8	737	8	BH794414
4	17	54.8	895	7	CF824029
5	17	54.8	3008	3	AK029674
6	16	51.6	334	2	BF545230
7	16	51.6	410	1	AI029009
8	16	51.6	434	6	CD174634
9	16	51.6	438	6	CD177046
10	16	51.6	470	8	AQ951732
11	16	51.6	480	5	BQ559427
12	16	51.6	520	8	AZ952856
13	16	51.6	539	6	CA542435
14	16	51.6	587	7	CF895091
15	16	51.6	590	8	BZ179360
16	16	51.6	602	2	AW338466
17	16	51.6	604	8	AQ447015
18	16	51.6	607	7	CO430950
19	16	51.6	612	2	AW173515
20	16	51.6	614	2	AW173560
21	16	51.6	626	2	AW168911
22	16	51.6	627	2	AW172834
23	16	51.6	671	9	CE654959
24	16	51.6	691	8	BZ281548

C 98	15	48.4	598	1	AJ635684	AJ635684	AJ635684	C 171	14	45.2	174	2	BB568308	BB568308
C 99	15	48.4	599	7	CN993548	CN993548	Mdfw2048a	C 172	14	45.2	174	9	AG230344	AG230344
C 100	15	48.4	607	1	AJ565585	AJ565585	AJ565585	C 173	14	45.2	198	9	AL949703	AL949703
C 101	15	48.4	607	2	BF494611	BF494611	AT03307.5	C 174	14	45.2	215	1	AA344058	AA344058
C 102	15	48.4	609	1	AU168218	AU168218	AU168218	C 175	14	45.2	215	1	CO518355	CO518355
C 103	15	48.4	609	8	BH829233	BH829233	BACPP28-L	C 176	14	45.2	215	8	AZ817330	AZ817330
C 104	15	48.4	625	5	BQ619714	BQ619714	TaLr1172C	C 177	14	45.2	218	8	CO566654	CO566654
C 105	15	48.4	625	7	CF574030	CF574030	MCSA079B1	C 178	14	45.2	219	7	CO518085	CO518085
C 106	15	48.4	629	9	CC941817	CC941817	BOIDH63TR	C 179	14	45.2	229	7	D46547	D46547
C 107	15	48.4	632	1	AJ635681	AJ635681	AJ635681	C 180	14	45.2	229	9	CL166072	CL166072
C 108	15	48.4	632	8	BH427770	BH427770	BOGGO1TF	C 181	14	45.2	233	9	CL166072	CL166072
C 109	15	48.4	633	1	AV722172	AV722172	AV722172	C 182	14	45.2	234	1	AJ539592	AJ539592
C 110	15	48.4	634	5	BQ869429	BQ869429	QGD6C08.Y	C 183	14	45.2	242	2	BF552390	BF552390
C 111	15	48.4	634	7	CF474818	CF474818	RTW2.8.G	C 184	14	45.2	244	2	BE085873	BE085873
C 112	15	48.4	643	8	AZ509564	AZ509564	LM0352M04	C 185	14	45.2	248	8	AW436988	AW436988
C 113	15	48.4	648	6	CD767004	CD767004	AGENCOURT	C 186	14	45.2	248	8	CC364104	CC364104
C 114	15	48.4	650	2	BF503168	BF503168	AT19082.5	C 187	14	45.2	252	1	AJ548307	AJ548307
C 115	15	48.4	651	1	AV836130	AV836130	AV836130	C 188	14	45.2	267	7	D48060	D48060
C 116	15	48.4	656	2	BB212101	BB212101	BB212101	C 189	14	45.2	276	8	BH535546	BH535546
C 117	15	48.4	663	7	CV086807	CV086807	CS_gil_44	C 190	14	45.2	279	7	CF092422	CF092422
C 118	15	48.4	671	8	CC138192	CC138192	NDL_69O15	C 191	14	45.2	280	5	BY130019	BY130019
C 119	15	48.4	674	9	AG048990	AG048990	Pan trogl	C 192	14	45.2	287	9	CG861284	CG861284
C 120	15	48.4	675	9	CL159759	CL159759	104_349.1	C 193	14	45.2	287	9	CG861284	CG861284
C 121	15	48.4	676	2	BE759306	BE759306	an_3659.A	C 194	14	45.2	292	7	CO518322	CO518322
C 122	15	48.4	678	9	AG186550	AG186550	Pan trogl	C 195	14	45.2	298	2	BE019183	BE019183
C 123	15	48.4	685	6	CD211397	CD211397	HS1_60.E0	C 196	14	45.2	299	8	AQ084977	AQ084977
C 124	15	48.4	687	7	CV006256	CV006256	CS_gil_13	C 197	14	45.2	300	7	CN869974	CN869974
C 125	15	48.4	694	8	AZ274865	AZ274865	RPCI-23.1	C 198	14	45.2	302	1	AL839186	AL839186
C 126	15	48.4	694	8	BH390738	BH390738	AG-ND-175	C 199	14	45.2	303	2	BE942397	BE942397
C 127	15	48.4	697	7	CV006634	CV006634	CS_gil_14	C 200	14	45.2	303	5	BU025081	BU025081
C 128	15	48.4	703	7	CO902852	CO902852	Mdfct3059	C 201	14	45.2	304	7	CF096537	CF096537
C 129	15	48.4	707	9	AG338106	AG338106	Mus muscu	C 202	14	45.2	304	7	BY308785	BY308785
C 130	15	48.4	713	7	CF479516	CF479516	RTW3.22	C 203	14	45.2	307	5	CF094188	CF094188
C 131	15	48.4	725	2	BF501815	BF501815	AT17375.5	C 204	14	45.2	308	7	CF095319	CF095319
C 132	15	48.4	727	9	CNS0107H	AL146886	Anopheles	C 205	14	45.2	308	7	CF095319	CF095319
C 133	15	48.4	737	7	CF530757	CF530757	UI-N-FY0-	C 206	14	45.2	312	2	BF014710	BF014710
C 134	15	48.4	757	8	CC320942	CC320942	TAM32-24K	C 207	14	45.2	318	5	BY353388	BY353388
C 135	15	48.4	763	7	CO367755	CO367755	RTK1_36.H	C 208	14	45.2	319	1	AI425872	AI425872
C 136	15	48.4	765	6	CA275632	CA275632	SCBPSD103	C 209	14	45.2	320	2	BE520314	BE520314
C 137	15	48.4	780	9	CL537062	CL537062	OB_Ba004	C 210	14	45.2	320	2	BE920391	BE920391
C 138	15	48.4	786	5	BU224609	BU224609	603798022	C 211	14	45.2	320	7	F30607	F30607
C 139	15	48.4	790	9	CL672584	CL672584	PRO107b.B	C 212	14	45.2	321	2	BE272257	BE272257
C 140	15	48.4	803	9	CG095738	CG095738	FUIHD45TD	C 213	14	45.2	321	2	BF013532	BF013532
C 141	15	48.4	820	8	BH402915	BH402915	AG-ND-136	C 214	14	45.2	323	4	BG983137	BG983137
C 142	15	48.4	823	8	BZ803950	BZ803950	PUFFC34TB	C 215	14	45.2	324	7	CF096784	CF096784
C 143	15	48.4	825	8	BZ803957	BZ803957	PUFFC34TD	C 216	14	45.2	326	7	CO518236	CO518236
C 144	15	48.4	829	7	CV198371	CV198371	CGF100397	C 217	14	45.2	327	5	BY346062	BY346062
C 145	15	48.4	855	9	AG368695	AG368695	Mus muscu	C 218	14	45.2	327	7	CF096615	CF096615
C 146	15	48.4	856	9	AG418407	AG418407	Mus muscu	C 219	14	45.2	330	9	CC888047	CC888047
C 147	15	48.4	860	8	CC434233	CC434233	PUEFK37TD	C 220	14	45.2	331	7	CF096374	CF096374
C 148	15	48.4	868	4	BG249837	BG249837	602319317	C 221	14	45.2	331	1	AI416623	AI416623
C 149	15	48.4	881	6	CA479263	CA479263	AGENCOURT	C 222	14	45.2	333	5	BY103521	BY103521
C 150	15	48.4	895	4	BI199621	BI199621	602761295	C 223	14	45.2	333	5	BY103521	BY103521
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C 152	15	48.4	924	6	CB575660	CB575660	AGENCOURT	C 225	14	45.2	335	1	AA290815	AA290815
C 153	15	48.4	929	9	CG235378	CG235378	QGS3AW30TH	C 226	14	45.2	335	5	BQ912253	BQ912253
C 154	15	48.4	989	4	BI824531	BI824531	6030315124	C 227	14	45.2	339	7	CN308892	CN308892
C 155	15	48.4	1001	9	CNS0743W	AL436098	T7_end of	C 228	14	45.2	341	4	BG000840	BG000840
C 156	15	48.4	1028	8	CC219896	CC219896	CH261-99H	C 229	14	45.2	345	6	C74573	C74573
C 157	15	48.4	1064	7	CF879024	CF879024	tr1c019xd	C 230	14	45.2	347	7	W82480	W82480
C 158	15	48.4	1074	8	CC212262	CC212262	CH261-950	C 231	14	45.2	350	5	BY351083	BY351083
C 159	15	48.4	1101	9	CNS009NH	AL070811	Drosophil	C 232	14	45.2	350	7	CK092234	CK092234
C 160	15	48.4	1145	9	AG279110	AG279110	Mus muscu	C 233	14	45.2	352	5	BY143042	BY143042
C 161	15	48.4	1148	3	CNS0A41M	BX927347	Arabidops	C 234	14	45.2	352	7	CO288896	CO288896
C 162	15	48.4	1257	7	CK402323	CK402923	AUF_Ifinc	C 235	14	45.2	357	6	BY776654	BY776654
C 163	15	48.4	1309	3	AK040601	AK040601	Mus muscu	C 236	14	45.2	358	7	CF098729	CF098729
C 164	15	48.4	1372	3	AK038268	AK038268	Mus muscu	C 237	14	45.2	359	1	AA419008	AA419008
C 165	15	48.4	1381	3	AK088365	AK088365	Mus muscu	C 238	14	45.2	359	2	BF187402	BF187402
C 166	15	48.4	145.2	83	9	AGS0709H	AGS0709H	C 239	14	45.2	360	6	CS1251	CS1251
C 167	15	48.4	145.2	124	2	BE163607	QV3-HT046	C 240	14	45.2	360	6	C74308	C74308
C 168	15	48.4	145.2	125	5	BY281236	BY281236	C 241	14	45.2	360	7	CN640823	CN640823
C 169	15	48.4	145.2	154	5	BY003844	BY003844	C 242	14	45.2	362	6	CD748468	CD748468
C 170	15	48.4	145.2	164	8	AZ489976	1M0322P15	C 243	14	45.2	364	5	BY310897	BY310897

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C 247	14	45.2	370	5	BY106946	BY106946	BO106946	C 320	14	45.2	436	5	BU566410	BU566410	AGENCOURT
C 248	14	45.2	372	9	CC361903	CC361903	BO18K64TF	C 321	14	45.2	436	5	CD175246	CD175246	AGENCOURT
C 249	14	45.2	373	7	H23229	H23229	ym52907.si	C 322	14	45.2	438	6	CD176606	CD176606	AGENCOURT
C 250	14	45.2	374	9	BX652187	BX652187	Arabidops	C 323	14	45.2	438	6	CD386216	CD386216	AGENCOURT
C 251	14	45.2	374	5	BY028350	BY028350	Arabidops	C 324	14	45.2	438	8	AQ076186	AQ076186	CIT-HSP-2
C 252	14	45.2	379	4	BF992409	BF992409	IL0-GN021	C 325	14	45.2	438	8	AQ076186	AQ076186	CIT-HSP-2
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C 255	14	45.2	385	1	AJ551561	AJ551561	z810f11.8	C 328	14	45.2	439	6	CD388905	CD388905	AGENCOURT
C 256	14	45.2	387	1	AJ548167	AJ548167	AJ548167	C 329	14	45.2	440	2	BB864870	BB864870	BB864870
C 257	14	45.2	387	5	BY093031	BY093031	BY093031	C 330	14	45.2	441	1	AV743817	AV743817	AV743817
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C 261	14	45.2	392	5	BY311810	BY311810	BY311810	C 334	14	45.2	442	7	CN960300	CN960300	7800_1001
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C 263	14	45.2	394	6	BY707461	BY707461	CL324425	C 336	14	45.2	444	5	BX453099	BX453099	BX453099
C 264	14	45.2	394	9	CL324425	CL324425	RPC144_47	C 337	14	45.2	447	5	BQ914502	BQ914502	QHB10M11.
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C 266	14	45.2	397	5	BY228605	BY228605	BY228605	C 339	14	45.2	448	5	BY272775	BY272775	BY272775
C 267	14	45.2	398	7	CN235129	CN235129	WLB080F02	C 340	14	45.2	448	5	BY393523	BY393523	BY393523
C 268	14	45.2	399	4	BM686994	BM686994	UI-B-CQ1-	C 341	14	45.2	448	6	CB571826	CB571826	AGENCOURT
C 269	14	45.2	400	6	CD298434	CD298434	AGENCOURT	C 342	14	45.2	448	9	AG252910	AG252910	Lotus cor
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C 271	14	45.2	402	6	BY757153	BY757153	BY757153	C 344	14	45.2	449	5	BU954580	BU954580	AGENCOURT
C 272	14	45.2	403	4	BM357469	BM357469	131-H3_Tf	C 345	14	45.2	449	8	AQ814779	AQ814779	AGENCOURT
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C 274	14	45.2	404	4	BY503308	BY503308	BB170010B	C 347	14	45.2	451	7	D47478	D47478	RICS13004A
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C 278	14	45.2	408	5	BY228482	BY228482	BY228482	C 351	14	45.2	454	4	BG802487	BG802487	BG802487
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C 283	14	45.2	409	6	CD289297	CD289297	9_L5_abd	C 356	14	45.2	460	5	BY274061	BY274061	BY274061
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C 285	14	45.2	412	5	BY228713	BY228713	BY228713	C 358	14	45.2	461	5	BY291353	BY291353	FJ22906.y
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C 292	14	45.2	419	6	BY736784	BY736784	BY736784	C 365	14	45.2	469	7	CF135056	CF135056	UI-HF-CH0
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C 296	14	45.2	422	7	CF371978	CF371978	CSEC5047A	C 369	14	45.2	470	8	AQ359941	AQ359941	HU5034_B
C 297	14	45.2	424	1	AV792482	AV792482	AV792482	C 370	14	45.2	471	9	CG128551	CG128551	FUIEQ707D
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C 299	14	45.2	425	8	AQ050578	AQ050578	GSSTc0705	C 372	14	45.2	472	5	BY242100	BY242100	BY242100
C 300	14	45.2	426	2	AW596242	AW596242	sj01a04.y	C 373	14	45.2	473	8	AQ375331	AQ375331	RPCI-11-1
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C 302	14	45.2	428	5	BY266653	BY266653	BY266653	C 375	14	45.2	475	2	BE512212	BE512212	94606SH12
C 303	14	45.2	430	2	BF716809	BF716809	NCEST3a17	C 376	14	45.2	476	2	BE206737	BE206737	ba02d01.y
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C 310	14	45.2	432	4	BI457791	BI457791	603198445	C 383	14	45.2	480	4	BM694310	BM694310	UI-B-C11-
C 311	14	45.2	432	4	BI597368	BI597368	603251669	C 384	14	45.2	480	5	BP373523	BP373523	BP373523
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 142 GTTGAGTAGCGTGCTG 159

RESULT 2
CD309228/c
LOCUS
DEFINITION
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Strongylocentrotus purpuratus cDNA clone
MPMGp691H07137;MPI_SURUDI_137H7 5', mRNA sequence.
CD309228
CD309228.1 GI:34754277
EST.
Strongylocentrotus purpuratus
Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Echinoidea; Echinacea; Echinoida;
Strongylocentrotidae; Strongylocentrotus.
1 (bases 1 to 545)
Poustka, A.J., Groth, D., Hennig, S., Thamm, S., Cameron, A., Beck, A.,
Reinhardt, R., Herwig, R., Panopoulou, G. and Lehrach, H.
Generation, annotation, evolutionary analysis, and database
integration of 20,000 unique sea urchin EST clusters
Genome Res. 13 (12), 2736-2746 (2003)
Contact: Poustka AJ
Laboraty 145, dept Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Innestr.63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1235
Fax: +49 30 8413 1128
Email: poustka@molgen.mpg.de
The library was characterised by oligonucleotide fingerprinting
(ONF) to reduce sequencing redundancy. According to the ONF
procedure, clones that display the same hybridisation matrix with a
battery of 200 8mer oligonucleotides are grouped into clusters. One
clone per ONF cluster is selected for sequencing. The size of each
cluster is an indicator of the frequency of a transcript in the
analysed library. The cluster size as well as the coordinates of
the other clones assigned to the same ONF cluster as the clone from
which the above EST is generated is available at the sea urchin
project web site at: http://www.molgen.mpg.de/ag/seaurchin/ . cDNA
clones and filters are distributed via the Resource Center/Primary
Database of the German Human Genome Project (http://www.rzpd.de)
PCR Primers
FORWARD: 5' CCCAGGCTTACACTTATGCTTCGGGCTCG 3' (M13RSP) 5'-seq
BACKWARD: 5' GCTATTACCGAGTGGCGAAGGGGATGTG 3' (M13FSP) 3'-seq
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FEATURES
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Best Local Similarity 100.0%; Pred. No. 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GAAGTTGAGTAGACGGT 27
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Db 130 GAAGTTGAGTAGACGGT 114

RESULT 3
BH794414/c
LOCUS
DEFINITION
ME_MBa0002N14r Manihot esculenta Manihot esculenta genomic clone
BH794414
BH794414.1 GI:19892462
GSS.
Manihot esculenta (cassava)
ORGANISM
Manihot esculenta
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Malpighiales; Euphorbiaceae; Crotonoideae;
Manihoteae; Manihot.
1 (bases 1 to 737)
Tomkins, J.P., Fregene, M., Main, D., Goicoechea, J.L., Blackmon, B.,
Atkins, M., Tohme, J. and Wing, R.A.
New Genomic Resources for Cassava (Manihot esculenta): Development
of a Deep-Coverage BAC Library and Preliminary STC Analysis
Unpublished (2002)
Contact: Tomkins J
Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634, USA
Tel: 864 656 6419
Fax: 864 656 4293
Email: jtmkns@clemson.edu
Total High Quality bases = 383
Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
High quality sequence start: 130
High quality sequence stop: 737.
Location/Qualifiers
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For more details on library preparation and sequence
analysis see
http://www.genome.clemson.edu/projects/stc/cassava/ME_MBa
To order clones from this library see
http://www.genome.clemson.edu/orders "
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Best Local Similarity 100.0%; Pred. No. 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
BH794414/c
LOCUS
DEFINITION
ME_MBa0002N14r Manihot esculenta Manihot esculenta genomic clone
BH794414
BH794414.1 GI:19892462
GSS.
Manihot esculenta (cassava)
ORGANISM
Manihot esculenta
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Malpighiales; Euphorbiaceae; Crotonoideae;
Manihoteae; Manihot.
1 (bases 1 to 737)
Tomkins, J.P., Fregene, M., Main, D., Goicoechea, J.L., Blackmon, B.,
Atkins, M., Tohme, J. and Wing, R.A.
New Genomic Resources for Cassava (Manihot esculenta): Development
of a Deep-Coverage BAC Library and Preliminary STC Analysis
Unpublished (2002)
Contact: Tomkins J
Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634, USA
Tel: 864 656 6419
Fax: 864 656 4293
Email: jtmkns@clemson.edu
Total High Quality bases = 383
Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
High quality sequence start: 130
High quality sequence stop: 737.
Location/Qualifiers
1..737
/organism="Manihot esculenta"
/mol_type="genomic DNA"
/strains="MECW72"
/db_xref="taxon:3983"
/clone="ME_MBa0002N14r"
/tissue_type="Leaf"
/lab_host="E. coli"
/clone_lib="Manihot esculenta"
/note="Vector: pCUGIBAC-1; Site 1: HindIII; Site 2: NotI;
For more details on library preparation and sequence
analysis see
http://www.genome.clemson.edu/projects/stc/cassava/ME_MBa
To order clones from this library see
http://www.genome.clemson.edu/orders "
```

```

RESULT 4
CF824029 LOCUS EST701411 Coccidioides posadasii saprobic phase cDNA library, 2 to 4 kb Coccidioides posadasii cDNA clone CIDAP04 5' end, mRNA
DEFINITION
CF824029 895 bp mRNA linear EST 01-APR-2004
4 kb Coccidioides posadasii cDNA clone CIDAP04 5' end, mRNA
sequence.
ACCESSION CF824029 GI:45930086
VERSION CF824029.1
KEYWORDS EST.
SOURCE Coccidioides posadasii
ORGANISM Coccidioides posadasii
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.
REFERENCE 1 (bases 1 to 895)
AUTHORS Gardner, M.J. and Cole, G.T.
TITLE Analysis of gene expression in Coccidioides posadasii mycelia and
spherules via expressed sequence tags
JOURNAL Unpublished (2003)
COMMENT Other_ESTs: EST701410
Contact: Gardner MJ
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org
Seq primer: M13 Reverse.
Location/Qualifiers
1..895
/organism="Coccidioides posadasii"
/mol_type="mRNA"
/strain="C735"
/db_xref="taxon:199306"
/clone="CIDAP04"
/dev_stage="saprobic phase (mycelia)"
/lab_host="E. coli DH10B, T1 phage resistant"
/clone_lib="Coccidioides posadasii saprobic phase cDNA
library, 2 to 4 kb"
/notes="Vector: pExpress 1; Site 1: Not I; Site 2: Eco RV;
Coccidioides posadasii saprobic phase cDNA library, size
fractionated cDNA 2 to 4 kb"
ORIGIN
Query Match 54.8%; Score 17; DB 7; Length 895;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GCCACCGGAAGTTGAGT 20
|||||
Db 829 GCCACCGGAAGTTGAGT 845
Query Match 54.8%; Score 17; DB 7; Length 895;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GCCACCGGAAGTTGAGT 20
|||||
Db 829 GCCACCGGAAGTTGAGT 845
RESULT 5
AK029674/c LOCUS AK029674.1 3008 bp mRNA linear HTC 03-APR-2004
DEFINITION
AK029674 Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:4930452119 product:unclassifiable, full insert
sequence.
ACCESSION AK029674
VERSION AK029674.1 GI:26081467
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

```

```

TITLE Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
JOURNAL Normalization and subtraction of cap-trapper-selected cDNAs to
MEDLINE Prepare full-length cDNA libraries for rapid discovery of new genes
PUBMED Genome Res. 10 (10), 1617-1630 (2000)
REFERENCE 20499374
11042159
3
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
Yamamoto, R., Matsumoto, S., Hazama, M., Nishine, T., Harada, A.,
Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Iehikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 3008)
AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saichou, R., Saichou, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Tanaka, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/.
Location/Qualifiers
1..3008
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:4930452119"
/db_xref="taxon:10090"
/clone="4930452119"
/sex="male"
/tissue_type="testis"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
1..3008
misc_feature
/note="unclassifiable"

```

ORIGIN

Query Match 54.8%; Score 17; DB 3; Length 3008;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 AAGTTGAGTAGACGGTG 28
 |||||
 Db 317 AAGTTGAGTAGACGGTG 301

RESULT 6

BF545230/c 334 bp mRNA linear EST 11-DEC-2000
 LOCUS UI-R-CO-10-f-06-0-UI-r1 UI-R-CO Rattus norvegicus cDNA clone
 DEFINITION UI-R-CO-10-f-06-0-UI 5', mRNA sequence.

ACCESSION BF545230
 VERSION BF545230.1 GI:11636337
 KEYWORDS EST.

SOURCE

ORGANISM Rattus norvegicus (Norway rat)
 Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE

AUTHORS 1 (bases 1 to 334)
 TITLE Bonaldo,M.F., Lennon,G. and Soares,M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 PUBMED 8889548

COMMENT

Contact: Soares, MB
 Coordinated Laboratory for Computational Genomics
 University of Iowa
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565

Email: bento-soares@uiowa.edu
 cDNA Library Preparation: M.B. Soares Lab Clone distribution:
 clones will be available through Research Genetics (www.resgen.com)
 This clone is also available through the I.M.A.G.E. Consortium at
 LLNL (info@image.llnl.gov). IMAGE ID= 1782453 The following
 repetitive elements were found in this cDNA sequence: 27-117,
 >PB1D10#SINE/Alu 61-138, >B4A#SINE/B4 61-204, >B4#SINE/B4
 Seq primer: M13 Forward.

FEATURES

source

1..334
 Location/Qualifiers
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-CO-10-f-06-0-UI"
 /dev_stage="adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="UI-R-CO"

/notes="Vector: pTT3D-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not 1; Site 2: Eco RI; The UI-R-CO
 library is a subtracted library derived from the UI-R-A1
 and UI-R-E1 libraries. The UI-R-A1 library consisted of a
 mixture of individually tagged normalized libraries
 constructed from rat placenta, adult lung, brain, liver,
 kidney, heart, spleen, ovary, and muscle. The UI-R-E1
 library consisted of a mixture of individually tagged
 normalized libraries constructed from 8, 12 and 18-day
 embryo. The tag is a string of 3-5 nucleotides present
 between the Not I site and the oligo-dr track which
 allows identification of the library of origin of a clone
 within the mixture. The subtracted library (UI-R-CO) was
 constructed as follows: PCR amplified cDNA inserts from a
 pool of UI-R-A1 and UI-R-E1 clones from which 3' ESTs had
 been derived was used as a driver in a hybridization with
 the pooled UI-R-A1 and UI-R-E1 library in the form of
 single-stranded circles. The remaining single-stranded

ORIGIN

Query Match 51.6%; Score 16; DB 2; Length 334;
 Best Local Similarity 100.0%; Pred. No. 69;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AGTTGAGTAGACGGTG 28
 |||||
 Db 191 AGTTGAGTAGACGGTG 176

RESULT 7

AI029009 410 bp mRNA linear EST 04-JUL-1999
 LOCUS UI-R-CO-10-f-06-0-UI-s1 UI-R-CO Rattus norvegicus cDNA clone
 DEFINITION UI-R-CO-10-f-06-0-UI 3', mRNA sequence.

ACCESSION AI029009
 VERSION AI029009.1 GI:4295595
 KEYWORDS EST.

SOURCE

ORGANISM Rattus norvegicus (Norway rat)
 Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE

AUTHORS 1 (bases 1 to 410)
 TITLE Bonaldo,M.F., Lennon,G. and Soares,M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 PUBMED 8889548

COMMENT

On Jun 22, 1998 this sequence version replaced gi:3246835.
 Contact: Soares, MB
 Coordinated Laboratory for Computational Genomics
 University of Iowa
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565

Email: bento-soares@uiowa.edu

cDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone
 distribution: clones will be available through Research Genetics
 This clone is also available through the I.M.A.G.E. Consortium at
 LLNL (info@image.llnl.gov). IMAGE ID=1782453 The following
 repetitive elements were found in this cDNA sequence: 204-347,
 >B4#SINE/B4 270-347, >B4A#SINE/B4 291-381, >PB1D10#SINE/Alu
 Seq primer: M13 Forward

POLYA=No.

Location/Qualifiers

1..410
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-CO-10-f-06-0-UI"
 /dev_stage="adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="UI-R-CO"

/note="Vector: pTT3D-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not 1; Site 2: Eco RI; The UI-R-CO
 library is a subtracted library derived from the UI-R-A1
 and UI-R-E1 libraries. The UI-R-A1 library consisted of a
 mixture of individually tagged normalized libraries
 constructed from rat placenta, adult lung, brain, liver,
 kidney, heart, spleen, ovary, and muscle. The UI-R-E1
 library consisted of a mixture of individually tagged
 normalized libraries constructed from 8, 12 and 18-day

FEATURES

source

embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-CO) was constructed as follows: PCR amplified cDNA inserts from a pool of UI-R-A1 and UI-R-E1 clones from which 3' ESTs had been derived was used as a driver in a hybridization with the pooled UI-R-A1 and UI-R-E1 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-CO library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996)"

ORIGIN

Query Match 51.6%; Score 16; DB 1; Length 410;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 ACTTGAGTAGACGGTG 28
|||||
Db 217 ACTTGAGTAGACGGTG 232

RESULT 8

CD174634/c
LOCUS CD174634 434 bp mRNA linear EST 19-MAY-2003
DEFINITION AGENCOURT_13961755 NIH_MGC_172 Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CD174634
VERSION CD174634.1 GI:30858406
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 434)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jamie Thompson, University of WI
cDNA Library Preparation: Gina Zastrow-Hayes
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDKM42 row: f column: 23
High quality sequence start: 3
High quality sequence stop: 434.

FEATURES

source
1..434
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, WA01, passage 38"
/lab_host="DH10B Tona"
/clone_lib="NIH MGC 172"
/note="Vector: pDONR201; Site 1: attP2; Site 2: attP1;
LIBR_PRIMING - oligo dT; METHOD - full-length enriched;
Embryonic Stem Cells H1; LIBR PROVIDER - Bradfield"

ORIGIN

Query Match 51.6%; Score 16; DB 6; Length 434;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCCACCGGAAGTT 16
|||||

Db

31 TCCGCCACCGGAAGTT 16

RESULT 9

CD177046/c
LOCUS CD177046 438 bp mRNA linear EST 19-MAY-2003
DEFINITION AGENCOURT_13975662 NIH_MGC_173 Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CD177046
VERSION CD177046.1 GI:30863289
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 438)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jamie Thompson, University of WI
cDNA Library Preparation: Gina Zastrow-Hayes
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDKM35 row: o column: 01
High quality sequence start: 14
High quality sequence stop: 438.

FEATURES

source
1..438
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic trophoblasts, made from WA01 stem cells"
/lab_host="DH10B Tona"
/clone_lib="NIH MGC 173"
/note="Vector: pDONR201; Site 1: attP2; Site 2: attP1;
LIBR_PRIMING - oligo dT; METHOD - full-length enriched;
LIBR PROVIDER - Bradfield"

ORIGIN

Query Match 51.6%; Score 16; DB 6; Length 438;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCCACCGGAAGTT 16
|||||

Db 37 TCCGCCACCGGAAGTT 22

RESULT 10

AQ951732/c
LOCUS AQ951732 470 bp DNA linear GSS 27-JAN-2000
DEFINITION Sheared DNA-48L4-TR Sheared DNA Trypanosoma brucei genomic clone
ACCESSION AQ951732
VERSION AQ951732.1 GI:6774997
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 470)
El-Sayed,N., Zhao,S., Zhao,H., Gill,S., Suh,E., Malek,J., Fujii,C., Gerrard,C., Leech,V., de Jong,P., Ullu,E., Melville,S., Donelson,J., Fraser,C. and Adams,M.
Determination of clone end sequences from Trypanosoma brucei GUTat
10.1 sheared DNA library
Unpublished (1999)
Contact: Najib M. El-Sayed

Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: nelsayed@tigr.org
Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
DNA library constructed at TIGR. Clones will be available for
distribution through ATCC. Sheared DNA end sequences search page:
<http://www.tigr.org/tcdb/mbd/tbdb/>.
Seq primer: M13-Reverse
Class: shotgun.

FEATURES

Location/Qualifiers

```
1. .470
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927/4 GUTat 10.1"
/db_xref="taxon:5691"
/clone_lib="Sheared DNA-48L4"
/clone_lib="Sheared DNA"
/Note="Vector: pUC18; Site 1: SmaI; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically
sheared to give a tight size distribution (approx 2 kb).
The v + i method used for the library construction is
described in detail in Smith, H.O. and Venter, J.C.
(Making small insert libraries for whole genome shotgun
sequencing projects. In Genome Sequencing: A Practical
Approach, eds. M. Vaudin and B. Borell, Oxford University
Press, 1999)."
```

ORIGIN

```
Query Match 51.6%; Score 16; DB 8; Length 470;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 11 GAAGTTGAGTAGACGG 26

Db 246 GAAGTTGAGTAGACGG 231

```
RESULT 11
BQ559427/c 480 bp mRNA linear EST 20-JUN-2002
LOCUS H4058B07 5' NIA Mouse 7.4K cDNA Clone Set Mus musculus cDNA clone
DEFINITION BQ559427 5' mRNA sequence.
```

```
ACCESSION BQ559427
VERSION BQ559427.1 GI:21460312
KEYWORDS EST.
```

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 480)

AUTHORS VanBuren, V., Piao, Y., Dudekula, D.B., Qian, Y., Carter, M.G.,
Martin, P.R., Stagg, C.A., Bassey, U., Alba K., Hamatani, T.,
Kargul, G.J., Luo, A.G., Kelso, J., Hide, W. and KO, M.S.H.

TITLE Assembly, verification, and initial annotation of NIA 7.4K mouse
cDNA clone set

JOURNAL Genome Res. 12 (12), 1999-2003 (2002)

MEDLINE 22354164

PUBMED 12466305

COMMENT Other_ESTs: H4058B07-3

Contact: Yong Qian

Laboratory of Genetics

National Institute on Aging/National Institutes of Health

333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA

Email: cdna@lgsun.grc.nia.nih.gov

This clone set has been freely distributed to the community. Please
visit http://lgsun.grc.nia.nih.gov/cDNA/NIA_7.4k.html for details.

Plate: H4058 row: B column: 07

Seq primer: -21M13 Reverse

High quality sequence stop: 480
POLYA=No.

FEATURES

Location/Qualifiers

```
1. 480
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CS7BL/6"
/db_xref="niaEST:H4058B07-5"
/db_xref="taxon:10090"
/clone="H4058B07"
/sex="mixed"
/dev_stage="mixed"
/lab_host="DH10B"
/clone_lib="NIA Mouse 7.4K cDNA Clone Set"
/Note="Vector: pSPORT1; Site 1: Sall; Site 2: NotI; This
clone is among a rearranged set of 7,407 clones from more
than 20 cDNA libraries."
```

ORIGIN

```
Query Match 51.6%; Score 16; DB 5; Length 480;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 4 GCCACCGGAAGTTGAG 19

Db 440 GCCACCGGAAGTTGAG 425

RESULT 12

AZ952856

LOCUS 2M0217A22R

DEFINITION Mouse 10kb plasmid UUGC2M library Mus musculus genomic

ACCESSION AZ952856

VERSION AZ952856.1

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 520)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Bescorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Genome Center

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84112, USA

Tel: 801 585 5606

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Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0217 row: A column: 22

Seq primer: CACACGGAACAGTATGACC

Class: plasmid ends

High quality sequence stop: 520.

Location/Qualifiers

1. 520

organism="Mus musculus"

/mol_type="genomic DNA"

/strain="CS7BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0217A22"

/sex="Female"

/lab_host="E. coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC2M library"

/Note="Vector: PWD42nv; Purified genomic DNA from M.

musculus CS7BL/6J (female) was obtained from the Jackson

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 51.6%; Score 16; DB 8; Length 520;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 AAGTTGAGTAGACGGT 27
|||||
Db 432 AAGTTGAGTAGACGGT 447

RESULT 13
CA542435/c
LOCUS
DEFINITION
CA542435 539 bp mRNA linear EST 19-NOV-2002
musculus cDNA clone NIA:C0618H12 IMAGE:30021983 5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS
Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Lim, M.K., Luo, A.,
Tanaka, T., Kunath, T., Rossant, J. and Ko, M.S.H.
SYSTEMATIC ANALYSES OF NIA MOUSE TROPHOBLAST STEM CELL CDNA LIBRARY
(Long)
JOURNAL
COMMENT
Unpublished (2001)
Other ESTs: C0618H12-3
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgaun.grc.nia.nih.gov
Plate: C0618 row: H column: 12
Seq primer: M13 Reverse
High quality sequence stop: 539
POLYA=NO.

FEATURES
source

1. .539
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="B5/EGFP transgenic ICR mice"
/db_xref="niaEST:C0618H12-5N"
/db_xref="taxon:10090"
/clone="NIA:C0618H12 IMAGE:30021983"
/tissue_type="Trophoblast stem cell"
/dev_stage="3.5-dpc"
/lab_host="DH10B"
/clone_lib="NIA Mouse Trophoblast Stem Cell cDNA Library (Long)"
/note="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (<http://lgaun.grc.nia.nih.gov/cdna>). This is

a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were obtained from Dr. Janet Rossant and Tilo Kunath (Samuel Lunenfeld Research Institute, Canada). Double-stranded cDNAs were synthesized with an Oligo(dT) primer (Invitrogen):
5'-pGACATGATCTAGATCGGAGCGCCGCTTTT-3' from 4 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lona-linker Lu-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B *E. coli* host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.6 kb. The library was constructed by Yulan Piao (NIA)."

ORIGIN

Query Match 51.6%; Score 16; DB 6; Length 539;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCCACCGGAGCTTGAG 19
|||||
Db 440 GCCACCGGAGCTTGAG 425

RESULT 14
CF895091/c
LOCUS
DEFINITION
CF895091 587 bp mRNA linear EST 04-NOV-2003
Mus musculus cDNA clone NIA:A0143H02 IMAGE:30727765 5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS
Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.
CONSTRUCTION OF LONG-TRANSCRIPT ENRICHED cDNA LIBRARIES FROM
SUBMICROGRAM AMOUNTS OF TOTAL RNAs BY A UNIVERSAL PCR AMPLIFICATION
METHOD
Genome Res. 11 (9), 1553-1558 (2001)
21429098
11544199
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgaun.grc.nia.nih.gov
Plate: A0143 row: H column: 02
Seq primer: M13 Reverse
High quality sequence stop: 587
POLYA=NO.

FEATURES
source

1. .587
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129/Sv x 129/Sv-CP"
/db_xref="niaEST:A0143H02-5"
/db_xref="taxon:10090"
/clone="NIA:A0143H02 IMAGE:30727765"
/dev_stage="r1 ES cells"
/lab_host="DH10B"
/clone_lib="NIA Mouse Undifferentiated ES Cell cDNA Library (Long 1)"

/note="Vector: pCMV-SPORT6 (Invitrogen); Site 1: Sali; Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (<http://igsun.grc.nia.nih.gov/cDNA>). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001)). [PMID: 11544199]. Total RNAs were obtained from Dr. Kenneth R. Boheler (National Institute on Aging, USA). ES cells were cultured without feeder cells in the presence of LIF and BRL-conditioned media. Double-stranded cDNAs were synthesized with an Oligo(dT) primer (Invitrogen).
 5'-pGACTAGTCTGATCGGAGCGCGCCCTTTT-3' from 14.2 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Loxe-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with Sali and NotI enzymes and cloned into Sali/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.4 kb. The library was constructed by Yulan Piao."

ORIGIN

Query Match 51.6%; Score 16; DB 7; Length 587;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCACCGGAAGTTGAG 19

|||||

DB 214 GCACCGGAAGTTGAG 199

RESULT 15

BZ179360

LOCUS

DEFINITION CH230-44419, TJ CHORI-230 Segment 2 Rattus norvegicus genomic clone
 CH230-44419, genomic survey sequence.

ACCESSION

BZ179360

VERSION

BZ179360.1

KEYWORDS

GSS.

SOURCE

Rattus norvegicus

ORGANISM

Rattus norvegicus (Norway rat)

REFERENCE

1 (bases 1 to 590)

Zhang, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn, A., Gebregiorgis, E., Overton, L., Russell, D., Chen, D., Riggs, P., de Jong, P., and Fraser, C.M.

TITLE

Rat BAC End Sequences from Library CHORI-230 MboI segment

JOURNAL

Unpublished (1999)

COMMENT

Other GSSs: CH230-44419.TV

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230

(http://www.chori.org/bacpac/rat230.htm). For BAC library

availability, please contact Pieter de Jong (pdejong@mail.cho.org).

Clones may be purchased from BACPAC Resources

(http://www.chori.org/bacpac/or_xing/information.html). BAC end

page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html

Plate: 444 row: 1 column: 9

Seq.primer: SP6

Class: BAC ends.

Location/Qualifiers

source

1. 590
 /organism="Rattus norvegicus"
 /mol_type="genomic DNA"
 /strain="BN/SeNHsd/MCW"
 /db_xref="taxon:10116"
 /clone="CH230-44419"
 /sex="Female"
 /cell_type="Brain"
 /clone_lib="CHORI-230 Segment 2"
 /note="Vector: pTARBA1.3; Site 1: MboI; Site 2: MboI;
 CHORI-230 Rat (BN/SeNHsd/MCW) BAC library produced by
 Pieter de Jong"

ORIGIN

Query Match 51.6%; Score 16; DB 8; Length 590;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCGGAAGTTGAGTAGA 23

|||||

DB 489 CCGGAAGTTGAGTAGA 504

RESULT 16

AW338466/c

LOCUS

DEFINITION

AW338466 602 bp mRNA linear EST 31-JAN-2000
 xw78h03.x1 NCI CGAP Panl Homo sapiens cDNA clone IMAGE:2834165 3'
 similar to SM:ACDV HUMAN P49748 ACYL-COA DEHYDROGENASE.
 VERY-LONG-CHAIN SPECIFIC PRECURSOR ; contains Alu repetitive
 element; , mRNA sequence.

ACCESSION

AW338466

VERSION

AW338466.1

KEYWORDS

EST.

SOURCE

Homo sapiens

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 602)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov

Life Technologies catalog #: 11548-013

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Seq primer: -40UP from Gibco

High quality sequence stop: 359.

FEATURES

Location/Qualifiers

1. 602

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2834165"

/tissue_type="adenocarcinoma"

/lab_host="DH10B"

/clone_lib="NCI-CGAP_Panl"

/note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: Sali;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dr.
 Average insert size 1.72 kb. Life Technologies catalog #:
 11548-013"

ORIGIN

Query Match 51.6%; Score 16; DB 2; Length 602;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACCGGAAGTTGAGT 20

|||||

DB 564 CCACCGGAAGTTGAGT 549

```

RESULT 17
AQ447015/c
LOCUS
DEFINITION
  604 bp DNA linear GSS 08-APR-1999
  clone mgxb0002M12f BAC library Magnaporthe grisea genomic
  clone mgxb0002M12f, genomic survey sequence.
ACCESSION
  AQ447015
VERSION
  1
KEYWORDS
  GSS.
SOURCE
  Magnaporthe grisea (anamorph: Pyricularia grisea)
  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
  Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
  1 (bases 1 to 604)
AUTHORS
  Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
  Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
  A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
  Genome
  Unpublished (1998)
JOURNAL
  Contact: Dean RA
COMMENT
  Clemson University Genomics Institute
  100 Jordan Hall, Clemson University, Clemson, SC 29634
  Tel: 864 656 5737
  Fax: 864 656 4293
  Email: rdean@clemson.edu
  Seq primer: TAATACGACTCTACTATAGGG
  Class: BAC ends
  High quality sequence start: 61
  High quality sequence stop: 455.
  Location/Qualifiers
  1..604
  /organism="Magnaporthe grisea"
  /mol_type="genomic DNA"
  /strain="70-15"
  /db_xref="taxon:148305"
  /clone="mgxb0002M12f"
  /tissue_type="Protoplasts"
  /lab_host="B. coli DH10B"
  /note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;
  Rice blast is one of the most devastating fungal diseases
  of rice world wide. It is a filamentous ascomycete with
  a haploid genome (n=7) of approximately 40 Mbp. Rice
  blast is an important model fungal pathogen for studying
  numerous aspects of the fungal-host interaction. In
  order to facilitate genome wide analysis, a BAC library
  containing 9216 clones with an average insert size of 130
  kbp was constructed. This library represents greater
  than 25X genome coverage. High density colony filters
  are available upon request."
  ORIGIN
  Query Match 51.6%; Score 16; DB 8; Length 604;
  Best Local Similarity 100.0%; Pred. No. 68;
  Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 5 CCACCGGAAGTTGAGT 20
  |||||
  DB 558 CCACCGGAAGTTGAGT 543
  |||||

RESULT 18
CO430950/c
LOCUS
DEFINITION
  607 bp mRNA linear EST 06-JUL-2004
  UI-M-HX0-csc-e-14-0-UI.r1 NIH_BMAP_HX0 Mus musculus cDNA clone
  IMAGE:30685069 5', mRNA sequence.
ACCESSION
  CO430950
VERSION
  1
KEYWORDS
  EST.
SOURCE
  Mus musculus (house mouse)
  Unpublished (1997)
  Contact: Robert Strausberg, Ph.D.

```

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REFERENCE
  1 (bases 1 to 607)
  NIH-MGC http://mgc.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Robert Strausberg, Ph.D.
  Email: rsgapbs-remail.nih.gov
  Tissue Procurement: Dr. James Lin University of Iowa
  cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
  cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
  DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
  Clone Distribution: Distribution information can be found at
  http://genome.uiowa.edu/distribution/mouseefi.html
  This clone was contributed by the Brain Molecular Anatomy Project
  (BMAP)
  Seq primer: PYX-5.
  Location/Qualifiers
  1..607
  /organism="Mus musculus"
  /mol_type="mRNA"
  /strain="C57BL/6"
  /db_xref="taxon:10090"
  /clone="IMAGE:30685069"
  /tissue_type="whole eye"
  /dev_stage="newborn (1, 5, 15 days) and embryonic (15, 16,
  17, 18 dpc)"
  /lab_host="DH10B (T1 phage resistant)"
  /clone_lib="NIH BMAP HX0"
  /note="Organ: Eye; Vector: PYX-Asc; Site 1: EcoR I;
  Site 2: Not I; The library was constructed according
  Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
  1996. Denatured RNA was size fractionated on a 1% agarose
  gel. First strand cDNA synthesis was primed with oligo-dT
  primer containing a Not I site. Double strand cDNA was
  size selected according to mRNA size fraction, ligated
  with EcoR I adaptor, digested with NotI and then cloned
  directionally into PYX-Asc vector. The library tag
  sequence located between the Not I site and the polyA tail
  is AATAATTACG. This library was created for the University
  Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
  Developing Mouse Nervous System', supported by National
  Institute of Mental Health (NIMH)."
  ORIGIN
  Query Match 51.6%; Score 16; DB 7; Length 607;
  Best Local Similarity 100.0%; Pred. No. 68;
  Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 4 GCCACCGGAAGTTGAG 19
  |||||
  DB 101 GCCACCGGAAGTTGAG 86
  |||||

RESULT 19
AW173515/c
LOCUS
DEFINITION
  612 bp mRNA linear EST 16-NOV-1999
  xj08a06.x1 NCI CGAP Utc2 Homo sapiens cDNA clone IMAGE:2856594 3'
  similar to SW:ACDV_HUMAN P49748 ACYL-COA DEHYDROGENASE,
  VERY-LONG-CHAIN SPECIFIC PRECURSOR 1, mRNA sequence.
ACCESSION
  AW173515
VERSION
  1
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Carnivora; Hominidae; Homo.
  1 (bases 1 to 612)
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
  Unpublished (1997)
  Contact: Robert Strausberg, Ph.D.

```

Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: -40UP from Gibco
 High quality sequence stop: 416.
 Location/Qualifiers
 1. .612
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2656594"
 /tissue_type="moderately-differentiated endometrial adenocarcinoma, 3 pooled tumors"
 /lab_host="NCI CGAP Ut2"
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.85 kb. Life Technologies catalog #: 11539-012"

ORIGIN

Query Match 51.6%; Score 16; DB 2; Length 612;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACCGGAAGTTGAGT 20

Db 571 CCACCGGAAGTTGAGT 556

RESULT 20

AW173560/c

LOCUS

DEFINITION xj08g06.x1 NCI CGAP Ut2 Homo sapiens cDNA clone IMAGE:2656666 3', similar to SW-ACDV HUMAN P49748 ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR ;, mRNA sequence.

ACCESSION AW173560

VERSION AW173560.1 GI:6439508

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Greg Lennon, Ph.D.

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: -40UP from Gibco

High quality sequence stop: 415.

Location/Qualifiers

1. .614

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2656666"

/tissue_type="moderately-differentiated endometrial

adenocarcinoma, 3 pooled tumors"

/lab_host="NCI CGAP Ut2"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.85 kb. Life Technologies catalog #: 11539-012"

Seq primer: -40UP from Gibco

High quality sequence stop: 415.

Location/Qualifiers

1. .612

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2657267"

/tissue_type="moderately-differentiated endometrial

adenocarcinoma, 3 pooled tumors"

/lab_host="NCI CGAP Ut2"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.85 kb. Life Technologies catalog #: 11539-012"

Seq primer: -40UP from Gibco

High quality sequence stop: 425.

Location/Qualifiers

1. .626

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2657267"

/tissue_type="moderately-differentiated endometrial

adenocarcinoma, 3 pooled tumors"

/lab_host="NCI CGAP Ut2"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.85 kb. Life Technologies catalog #: 11539-012"

Seq primer: -40UP from Gibco

High quality sequence stop: 425.

Location/Qualifiers

1. .626

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2657267"

/tissue_type="moderately-differentiated endometrial

adenocarcinoma, 3 pooled tumors"

/lab_host="NCI CGAP Ut2"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.85 kb. Life Technologies catalog #: 11539-012"

Seq primer: -40UP from Gibco

High quality sequence stop: 425.

Location/Qualifiers

1. .626

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2657267"

/tissue_type="moderately-differentiated endometrial

adenocarcinoma, 3 pooled tumors"

/lab_host="NCI CGAP Ut2"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.85 kb. Life Technologies catalog #: 11539-012"

Seq primer: -40UP from Gibco

High quality sequence stop: 425.

Location/Qualifiers

1. .626

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2657267"

/tissue_type="moderately-differentiated endometrial

adenocarcinoma, 3 pooled tumors"

/lab_host="NCI CGAP Ut2"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.85 kb. Life Technologies catalog #: 11539-012"

Seq primer: -40UP from Gibco

High quality sequence stop: 425.

Location/Qualifiers

1. .626

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2657267"

/tissue_type="moderately-differentiated endometrial

adenocarcinoma, 3 pooled tumors"

/lab_host="NCI CGAP Ut2"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.85 kb. Life Technologies catalog #: 11539-012"

Seq primer: -40UP from Gibco

High quality sequence stop: 425.

Location/Qualifiers

1. .626

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2657267"

/tissue_type="moderately-differentiated endometrial

adenocarcinoma, 3 pooled tumors"

/lab_host="NCI CGAP Ut2"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.85 kb. Life Technologies catalog #: 11539-012"

Seq primer: -40UP from Gibco

High quality sequence stop: 425.

Location/Qualifiers

1. .626

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2657267"

/tissue_type="moderately-differentiated endometrial

adenocarcinoma, 3 pooled tumors"

/lab_host="NCI CGAP Ut2"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.85 kb. Life Technologies catalog #: 11539-012"

Seq primer: -40UP from Gibco

High quality sequence stop: 425.

Location/Qualifiers

1. .626

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2657267"

/tissue_type="moderately-differentiated endometrial

adenocarcinoma, 3 pooled tumors"

/lab_host="NCI CGAP Ut2"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.85 kb. Life Technologies catalog #: 11539-012"

Seq primer: -40UP from Gibco

High quality sequence stop: 425.

Location/Qualifiers

1. .626

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2657267"

/tissue_type="moderately-differentiated endometrial

adenocarcinoma, 3 pooled tumors"

/lab_host="NCI CGAP Ut2"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.85 kb. Life Technologies catalog #: 11539-012"

Seq primer: -40UP from Gibco

High quality sequence stop: 425.

Location/Qualifiers

1. .626

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2657267"

/tissue_type="moderately-differentiated endometrial

adenocarcinoma, 3 pooled tumors"

/lab_host="NCI CGAP Ut2"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.85 kb. Life Technologies catalog #: 11539-012"

Seq primer: -40UP from Gibco

High quality sequence stop: 425.

Location/Qualifiers

1. .626

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2657267"

/tissue_type="moderately-differentiated endometrial

adenocarcinoma, 3 pooled tumors"

/lab_host="NCI CGAP Ut2"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.85 kb. Life Technologies catalog #: 11539-012"

Seq primer: -40UP from Gibco

High quality sequence stop: 425.

Location/Qualifiers

1. .626

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2657267"

/tissue_type="moderately-differentiated endometrial

adenocarcinoma, 3 pooled tumors"

/lab_host="NCI CGAP Ut2"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.85 kb. Life Technologies catalog #: 11539-012"

Seq primer: -40UP from Gibco

High quality sequence stop: 425.

Location/Qualifiers

1. .626

/organism="Homo sapiens"

/mol_type="mRNA"

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/clone="IMAGE:2657267"

/tissue_type="moderately-differentiated endometrial

adenocarcinoma, 3 pooled tumors"

/lab_host="NCI CGAP Ut2"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.85 kb. Life Technologies catalog #: 11539-012"

Seq primer: -40UP from Gibco

High quality sequence stop: 425.

Location/Qualifiers

1. .626

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2657267"

/tissue_type="moderately-differentiated endometrial

adenocarcinoma, 3 pooled tumors"

/lab_host="NCI CGAP Ut2"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.85 kb. Life Technologies catalog #: 11539-012"

Seq primer: -40UP from Gibco

High quality sequence stop: 425.

Location/Qualifiers

1. .626

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2657267"

/tissue_type="moderately-differentiated endometrial

adenocarcinoma, 3 pooled tumors"

/lab_host="NCI CGAP Ut2"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.85 kb. Life Technologies catalog #: 11539-012"

Seq primer: -40UP from Gibco

High quality sequence stop: 425.

Location/Qualifiers

1. .626

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2657267"

/tissue_type="moderately-differentiated endometrial

adenocarcinoma, 3 pooled tumors"

/lab_host="NCI CGAP Ut2"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.85 kb. Life Technologies catalog #: 11539-012"

Seq primer: -40UP from Gibco

High quality sequence stop: 425.

Location/Qualifiers

1. .626

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2657267"

/tissue_type="moderately-differentiated endometrial

adenocarcinoma, 3 pooled tumors"

/lab_host="NCI CGAP Ut2"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.85 kb. Life Technologies catalog #: 11539-012"

Seq primer: -40UP from Gibco

High quality sequence stop: 425.

Location/Qualifiers

1. .626

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref

```

RESULT 22
AW172834/c
LOCUS
DEFINITION
XJ0403.x1 NCI_CGAP Ut2 Homo sapiens cDNA clone IMAGE:2656229 3'
similar to SW:ACDV_HUMAN P49748 ACYL-COA DEHYDROGENASE,
VERY-LONG-CHAIN SPECIFIC PRECURSOR ;, mRNA sequence.
ACCESSION
AW172834
VERSION
1 GI:6438782
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 627)
AUTHORS
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 401.
FEATURES
source
1..627
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2656229"
/tissue_type="moderately-differentiated endometrial
adenocarcinoma, 3 pooled tumors"
/lab_host="DH10B"
/clone_lib="NCI CGAP Ut2"
/notes="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Salt;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.85 kb. Life Technologies catalog #:
11539-012"
ORIGIN
Query Match 51.6%; Score 16; DB 2; Length 627;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 CCACCGGAAGTTGAGT 20
Db 562 CCACCGGAAGTTGAGT 547
CE654959 671 bp DNA linear GSS 29-SEP-2003
tigr-gss-dog-17000368030354 Dog Library Canis familiaris genomic,
genomic survey sequence.
ACCESSION
CE654959
VERSION
1 GI:36973823
KEYWORDS
GSS.
SOURCE
Canis familiaris (dog)
ORGANISM
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
1 (bases 1 to 671)
AUTHORS
Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
TITLE
The dog genome: survey sequencing and comparative analysis
JOURNAL
Science 301 (5641), 1898-1903 (2003)

```

```

MEDLINE
22875432
PUBMED
14512627
COMMENT
Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
FEATURES
source
1..671
Location/Qualifiers
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/notes="Site 1: BstXI; Libraries were prepared from
peripheral blood"
ORIGIN
Query Match 51.6%; Score 16; DB 9; Length 671;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 ACCCGAAGTTGAGTAG 22
Db 512 ACCCGAAGTTGAGTAG 497
BZ281548 691 bp DNA linear GSS 15-OCT-2002
CH230-384M7.TJ CHORI-230 Segment 2 Rattus norvegicus genomic clone
CH230-384M7, genomic survey sequence.
ACCESSION
BZ281548
VERSION
1 GI:24008985
KEYWORDS
GSS.
SOURCE
Rattus norvegicus (Norway rat)
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 691)
AUTHORS
Zhao,S., Shetty,J., Shatsman,S., Tsengaye,G., Geer,K.,
Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D.,
Riggs,F., de Jong,P. and Fraser,C.M.
TITLE
Rat BAC End Sequences from Library CHORI-230 MboI segment
JOURNAL
Unpublished (1999)
COMMENT
Other GSSs: CH230-384M7.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 384 row: M column: 7
Seq primer: SP6
Class: BAC ends.
FEATURES
source
1..691
Location/Qualifiers
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/SnHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-384M7"

```


Email: cgaabs-x@mail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)

Seq primer: pYX-5.

FEATURES

source

Location/Qualifiers
 1. .736
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:6833085"
 /tissue_type="whole brain"
 /dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="NIH BMAP_FY0"
 /notes="Organ: Brain; Vector: pYX-Asc; Site 1: EcoR I;
 Site 2: Not I; The library was constructed according
 to Bernaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured RNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was
 size selected according to mRNA size fraction, ligated
 with EcoR I adaptor, digested with NotI and then cloned
 directionally into pYX-Asc vector. The library tag
 sequence located between the Not I site and the polyA tail
 is ACCGACACAG. This library was created for the University
 of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
 Developing Mouse Nervous System', supported by National
 Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
 program coordinator."

ORIGIN

Query Match 51.6%; Score 16; DB 6; Length 736;
 Best Local Similarity 100.0%; Pred. No. 67;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 GCCACCGGAAGTTGAG 19
 |||||
 Db 438 GCCACCGGAAGTTGAG 423

RESULT 28

CV2233901

LOCUS

DEFINITION

CV2233901 743 bp mRNA linear EST 21-SEP-2004
 CS_hyp_06c11_M13Reverse Blue crab hypodermis, normalized
 Callinectes sapidus CDNA clone CS_hyp_06c11 5', similar to
 ref|XP_285910.2| similar to crossveinless 2 CGI5671-PA - Mus
 musculus. Score = 35.8 bits (81), Expect = 0.95, mRNA sequence.
 CV2233901

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Callinectes sapidus (blue crab)
 Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 Eubrachyura; Portunoidae; Portunidae; Callinectes.
 1 (bases 1 to 743)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Expressed sequence tags from normalized cDNA libraries prepared
 from gill and hypodermis tissues of the blue crab, *Callinectes*
sapidus
 Unpublished (2004)
 Contact: Thomas H. Shafer
 Department of Biological Sciences
 University of North Carolina Wilmington
 601 S. College Rd, Wilmington, NC 28403, USA

Tel: 910-962-7275
 Fax: 910-962-4066

Email: shafert@uncw.edu

Plate: 06 row: c column: 11

Seq primer: M13 Reverse

High quality sequence scop: 491.

FEATURES

source

Location/Qualifiers
 1. .743
 /organism="Callinectes sapidus"
 /mol_type="mRNA"
 /db_xref="taxon:6763"
 /clone="CS_hyp_06c11"
 /tissue_type="pooled hypodermal epithelium from the
 mid-dorsal region and arthroal membrane of premolt
 (stage D2) and 3-hour postmolt crabs"
 /dev_stage="Adult"
 /clone_lib="Blue crab hypodermis, normalized"
 /note="Vector: pCMV Sport 6.1; Total RNA samples were
 prepared individually from each tissue, checked for
 quality, and then pooled for construction and
 normalization of a cDNA library by Invitrogen. Plasmids
 were isolated and inserts sequenced from their 5'-ends by
 the Blue Crab Molecular Genetics Laboratory at the
 University of North Carolina Wilmington. Traces were
 trimmed, compared (BLASTx) to NCBI non-redundant protein
 database as of 19 July 2004, and processed for submission
 to dbEST by trace2dbEST software (Parkinson, Anthony and
 Blaxter, unpublished software)."

ORIGIN

Query Match 51.6%; Score 16; DB 7; Length 743;
 Best Local Similarity 100.0%; Pred. No. 67;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 CCGGAAGTTGAGTAGA 23
 |||||
 Db 632 CCGGAAGTTGAGTAGA 647

RESULT 29

CNS0088X/c

LOCUS

DEFINITION

CNS0088X 823 bp DNA linear GSS 03-JUN-1999
 Drosophila melanogaster genome survey sequence TET3 end of BAC #
 BACR16G18 of RPCI-98 library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 AL051573.1 GI:4933425
 GSS.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Drosophila melanogaster (fruit fly)
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 823)

REFERENCE

AUTHORS

TITLE

JOURNAL

Submitted (02-JUN-1999) Genoscope - Centre National de Sequençage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr)
 - Web : www.genoscope.cns.fr
 Determination of this BAC-end sequence was carried out as part of a
 collaboration with the Berkeley Drosophila Genome Project (BDGP).
 The BDGP is constructing a physical map of the Drosophila
 melanogaster genome using these BACs. For further information
 please see <http://www.fruitfly.org/TheBDGP/Drosophila>
 melanogaster BAC library was prepared by Kazutoyo Osoegawa and
 Aaron Mamoer in Peter de Jong's laboratory in the Department of
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
 NY. The library is named RPCI-98 and was constructed by partial
 EcoRI digestion of Drosophila DNA provided by the BDGP from the
 isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
 P1 and EST libraries. A more detailed description of the library
 and how to order individual BAC clones, the entire library, or
 filters for hybridization from the BACPAC Resource Center can be

found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source
Location/Qualifiers
1. 823
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone_lib="BACR16G18"
/clone_lib="RPCI-98"
/note="end : TET3"

ORIGIN

Query Match 51.6%; Score 16; DB 9; Length 823;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 CGCCACCGGAAGTTGA 18
Db 418 CGCCACCGGAAGTTGA 403

RESULT 30

BG440946
LOCUS
DEFINITION
GA_Ea0011B07f Gossypium arboreum 7-10 dpa fiber library Gossypium
arboresum cDNA clone GA_Ea0011B07f, mRNA sequence.
ACCESSION
BG440946
VERSION
BG440946.1 GI:13350598
KEYWORDS
EST.
SOURCE
Gossypium arboreum
ORGANISM
Gossypium arboreum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
1 (bases 1 to 837)

REFERENCE
Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J.,
Henry,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, development, and evolution
of the cotton fiber
Unpublished (2000)
CONTACT: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: TAATAGACTACTATAGG
High quality sequence stop: 273.

Location/Qualifiers
1. 837
/organism="Gossypium arboreum"
/mol_type="mRNA"
/strain="AKA"
/cultivar="8400"
/db_xref="taxon:29729"
/clone="GA_Ea0011B07f"
/tissue_type="Fibers isolated from bolls harvested 7-10
dpa"
/lab_host="E. coli"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"

FEATURES

source
Location/Qualifiers
1. 837
/organism="Gossypium arboreum"
/mol_type="mRNA"
/strain="AKA"
/cultivar="8400"
/db_xref="taxon:29729"
/clone="GA_Ea0011B07f"
/tissue_type="Fibers isolated from bolls harvested 7-10
dpa"
/lab_host="E. coli"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"

ORIGIN

Query Match 51.6%; Score 16; DB 4; Length 837;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 GGAAGTTGAGTAGACG 25
Db 643 GGAAGTTGAGTAGACG 658

RESULT 31

CNS00C0Q

LOCUS
DEFINITION
CNS00C0Q 897 bp DNA linear GSS 04-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BAC24G05 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
AL058582
VERSION
AL058582.1 GI:4946160
KEYWORDS
GSS.
SOURCE
Drosophila melanogaster (fruit fly)
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 897)

REFERENCE

AUTHORS
TITLE
JOURNAL
COMMENT
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr

Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammoser at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

Location/Qualifiers
1. 897
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BAC24G05"
/clone_lib="RPCI-98"
/note="end : TET3"

ORIGIN

Query Match 51.6%; Score 16; DB 9; Length 897;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 CGCCACCGGAAGTTGA 18
Db 372 CGCCACCGGAAGTTGA 387

RESULT 32

CD048769/c
LOCUS
DEFINITION
AGENCOURT_13965886 NIH_MGC_172 Homo sapiens cDNA 5', mRNA sequence.
CD048769
VERSION
CD048769.1 GI:30484080
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1021)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jamie Thompson, University of WI
cDNA Library Preparation: Gina Zastrow-Hayes
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

REFERENCE

AUTHORS
TITLE
JOURNAL
COMMENT

DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: NDKM47 row: b column: 05
 High quality sequence start: 13
 High quality sequence stop: 315.
 Location/Qualifiers

FEATURES

source

1. .1021
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="embryonic stem cells, WA01, passage 38"
 /lab_host="DH10B Tona"
 /clone_lib="NIH MGC 172"
 /notes="Vector: pDONR201; Site 1: attP2; Site 2: attP1;
 /LBR_PRIMING - oligo dr; METHOD - full-length enriched;
 Embryonic Stem Cells HI; LBR PROVIDER - Bradfield"

ORIGIN

Query Match 51.6%; Score 16; DB 6; Length 1021;
 Best Local Similarity 100.0%; Pred. No. 67;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCCACCGGAAGTT 16
 |||||
 Db 32 TCCGCCACCGGAAGTT 17

RESULT 33

CA467417/c

LOCUS

DEFINITION CA467417 1357 bp mRNA linear EST 09-MAR-2004
 IMAGE:30118765 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 1357)
 NIH-MGC <http://mgs.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Bradfield Laboratory
 CDNA Library Preparation: Mark Bittinger
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: NDKM016 row: a column: 14
 High quality sequence stop: 312.

FEATURES

source

1. .1357
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IMAGE:30118765"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 154"
 /note="Organ: Kidney; TCDD (DMSO vehicle) Treated 48
 Hours IP injections; Vector: pDONR201; Site 1: attP2;
 Site 2: attP1; CDNA made by oligo-dr with attB2 site and
 directionally cloned. Priming sequence:
 5'-TTCTCGAGGCGCCACCTTGTACAGAAAGCTGGGTTTTTTTTTTT
 TTATT-3'. Full-length enriched library was constructed
 using the GeneRacer kit by Invitrogen, library
 amplification 16 cycles. Library constructed by Mark
 Bittinger in the Bradfield laboratory (McArdle Laboratory

for Cancer Research, University of Wisconsin). Note: this
 is a NIH_MGC Library."

ORIGIN
 Query Match 51.6%; Score 16; DB 6; Length 1357;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCCACCGGAAGTT 16
 |||||
 Db 51 TCCGCCACCGGAAGTT 36

RESULT 34

AK040525/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

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JOURNAL

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REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
 Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
 Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
 Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
 Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
 Okazaki, Y., Saito, K., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,

AK040525 4639 bp mRNA linear HTC 03-APR-2004
 Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched
 library, clone: A430105D10 product: hypothetical protein, full insert
 sequence.

AK040525

AK040525.1 GI:26087907

HTC; CAP trapper.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

99279253

10349636

2

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

20499374

11042159

3

Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P.,

Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,

Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,

Yanamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,

Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, J.,

Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,

Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multipeptide sequencer

Genome Res. 10 (11), 1757-1771 (2000)

20530913

11076861

4

The RIKEN Genome Exploration Research Group Phase II Team and the

FANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection

Nature 409, 685-690 (2001)

5

The FANTOM Consortium and the RIKEN Genome Exploration Research

Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 4639)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,

Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,

Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,

Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,

Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,

Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,

Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,

Okazaki, Y., Saito, K., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,

Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE JOURNAL

Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: <http://genome.gsc.riken.jp/>

URL: <http://fantom.gsc.riken.jp/>

FEATURES

source

1..4639
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM DB:A430105D10"
/db_xref="taxon:10090"
/clone="A430105D10"
/tissue_type="thymus"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="0 day neonate"
misc_feature
1..4639
/note="hypothetical protein (evidence: rscds)"

ORIGIN

Query Match 51.6%; Score 16; DB 3; Length 4639;
Best Local Similarity 100.0%; Pred. NO. 63;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCCACCGGAAGTTGAG 19

Db 830 GCCACCGGAAGTTGAG 815

RESULT 35

AW222053
LOCUS
EST298864 tomato fruit red ripe, TAMU Lycopersicon esculentum cDNA clone cLENE6B4, mRNA sequence.
DEFINITION
AW222053
ACCESSION
AW222053.1 GI:6533737
VERSION
KEYWORDS
SOURCE
Lycopersicon esculentum (tomato)

ORGANISM

Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE
1 (bases 1 to 189)
Alcala, J., Vrebalov, J., White, R., Matern, A.L., Holt, I.E., Liang, F., Upton, J., Hansen, T., Craven, M.B., Bowman, C.L., Ahn, S., Roming, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and Giovannoni, J.

Generation of ESTs from tomato fruit tissue

Unpublished (1999)

TITLE

JOURNAL

COMMENT

Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>

5 prime sequence.

FEATURES

source

1..189
/organism="Lycopersicon esculentum"

/mol_type="mRNA"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLENE6B4"
/tissue_type="pericarp"
/dev_stage="red ripe (7-20 days post-breaker)"
/clone_lib="tomato fruit red ripe, TAMU"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; supplier: Giovannoni; Fruit were tagged at the breaker stage (first sign of lycopene accumulation on the blossom end of the fruit) and harvested 7 days post-breaker (fully red-ripe), 10 days post breaker, and 20 days post-breaker (over-ripe). 20 day fruit which showed external or internal signs of pathogenesis were discarded. Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."

ORIGIN

Query Match 48.4%; Score 15; DB 2; Length 189;
Best Local Similarity 100.0%; Pred. NO. 2.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CGCCACCGGAAGTTG 17

Db 19 CGCCACCGGAAGTTG 33

RESULT 36

AW576128/c

LOCUS

DEFINITION

ACCESSION

AW576128

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AW576128
UI-HF-BNO-aej-a-05-0-UI.s1 NIH MGC 50 Homo sapiens cDNA clone IMAGE:3064232 3', mRNA sequence.
AW576128
AW576128.1 GI:7247667
EST.
Homo sapiens (human)

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 201)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs@mail.nih.gov

The sequence contained an oligo-dT track that was present in the

oligonucleotide that was used to prime the synthesis of first

strand cDNA and therefore this may represent a bonafide poly A

tail. Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: M.B. Soares Lab

cDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

The following repetitive elements were found in this cDNA

sequence:

28-62, >AT-richLow_complexity

Seq primer: M13 Forward

POLYA=yes.

FEATURES

source

Location/Qualifiers

1..201

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3064232"

/tissue_type="lymph"

/cell_type="germinal center B cells"

/cell_line="MGC85"

/lab_host="DH10B (LT1)"

/clone_lib="NIH MGC 50"

/note="Vector: pT73-Pac; Site 1: NotI; Site 2: Eco RI;

Constructed from size fractionated cytoplasmic mRNA

RESULT 39
BY309989/c

LOCUS
DEFINITION

ACCESSION
VERSION

KEYWORDS
SOURCE

ORGANISM

REFERENCE

AUTHORS

BY309989 260 bp mRNA linear EST 11-DEC-2002
BY309989 RIKEN full-length enriched, stroma cell Mus musculus cDNA
clone J320012H13 5', mRNA sequence.

BY309989
BY309989.1 GI:26500326

EST.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 260)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,

Nikaido, I., Oato, N., Saito, R., Suzuki, H., Yamanaka, I.,

Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,

Schönbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,

Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,

Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,

Chochia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,

Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,

Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,

Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,

Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,

Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,

Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,

Numata, K., Okido, T., Pavan, W.J., Perte, G., Pesole, G.,

Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,

Ravasi, T., Reed, J.C., Reid, J., Reid, J., Ring, B.Z., Ringwald, M.,

Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,

Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,

Verardo, R., Wagner, L., Wahlstedt, C., Wang, Y., Watanabe, Y.,

Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,

Yang, L., Yuan, Z., Zvolan, M., Zhu, Y., Zimmer, A., Carninci, P.,

Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,

Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,

Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,

Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,

Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,

Rogers, J., Birney, E., and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

12466851

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/

Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,

Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,

Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,

Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,

Shiraki, T., Tgami, M., Waki, K., Watanishi, A., Muramatsu, M. and

Hayashizaki, Y. Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with

Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res.

10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA

encyclopedias: real-time sequence clustering for construction of a

nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

Tissues were provided by Takashi Ishikawa (Department of Surgery
2 Yokohama City University 3-9 Fukuura, Kanazawa-ku, Yokohama
236-0004 Japan) whose assistance we gratefully acknowledge.
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.

FEATURES
source

Location/Qualifiers

1..260

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="I320012H13"

/cell_type="stroma cell"

/clone_lib="RIKEN full-length enriched, stroma cell"

ORIGIN

Query Match

Best Local Similarity 48.4%; Score 15; DB 5; Length 260;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCGCCACCGGAAGTT 16

Db 31 CCGCCACCGGAAGTT 17

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BF412428 296 bp mRNA linear EST 28-NOV-2000
UI-R-BT1-bnd-b-06-0-UI-s1 UI-R-BT1 Rattus norvegicus cDNA clone
UI-R-BT1-bnd-b-06-0-UI-3', mRNA sequence.

BF412428

BF412428.1 GI:11400417

EST.

Rattus norvegicus (Norway rat)

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 296)

Bonaldo, M.F., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

97044477

8889548

Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

The sequence contained an oligo-dT track that was present in the

oligonucleotide that was used to prime the synthesis of first

strand cDNA and therefore this may represent a bonafide poly A

tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:

clones will be available through Research Genetics (www.resgen.com)

Seq primer: M13 Forward

POLVA=Yes.

Location/Qualifiers

1..296

/organism="Rattus norvegicus"

/mol_type="mRNA"

/strain="Sprague-Dawley"

/db_xref="taxon:10116"

/clone="UI-R-BT1-bnd-b-06-0-UI"

/dev_stage="adult"

/lab_host="DH10B (Life Technologies)"

/clone_lib="UI-R-BT1"

/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The library UI-R-FT1 is a substracted library derived from a mixture of the following tissues: hippocampus, thalamus, mid-brain, medulla, corpus striatum, cerebral cortex and testis. For a detailed description of the library from which this clone was derived, please visit our web site at rategest.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
TAG_SEQ=None found"

ORIGIN

Query Match 48.4%; Score 15; DB 2; Length 296;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCCACCGGAAGTTGA 18
|||||
Db 86 GCCACCGGAAGTTGA 72

RESULT 41

AU196235/c
LOCUS AU196235 Porphyra yezoensis TU-1 sporophytes Porphyra yezoensis
DEFINITION cDNA clone PFL086h02_r 5', mRNA sequence.
ACCESSION AU196235
VERSION AU196235.1 GI:31938671
KEYWORDS EST.
SOURCE Porphyra yezoensis
ORGANISM Porphyra yezoensis
Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae;
Porphyra.

1 (bases 1 to 304)
Asamizu,E., Nakajima,M., Kitade,Y., Saga,N., Nakamura,Y. and Tabata,S.
COMPARISON OF RNA EXPRESSION PROFILES BETWEEN THE TWO GENERATIONS OF PORPHYRA YEZOENSIS (RHODOPHYTA), BASED ON EXPRESSED SEQUENCE TAG FREQUENCY ANALYSIS
J. Phycol. 39 (5), 923-930 (2003)
Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:<http://www.kazusa.or.jp/en/plant/>.

FEATURES

Location/Qualifiers
1..304
/organism="Porphyra yezoensis"
/mol_type="mRNA"
/strain="TU-1"
/db_xref="taxon:2788"
/clone="PFL086h02_r"
/dev_stage="sporophytes"
/clone_lib="Porphyra yezoensis TU-1 sporophytes"
ORIGIN
Query Match 48.4%; Score 15; DB 1; Length 304;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FEATURES

Location/Qualifiers
1..304
/organism="Porphyra yezoensis"
/mol_type="mRNA"
/strain="TU-1"
/db_xref="taxon:2788"
/clone="PFL086h02_r"
/dev_stage="sporophytes"
/clone_lib="Porphyra yezoensis TU-1 sporophytes"
ORIGIN

ORIGIN

Query Match 48.4%; Score 15; DB 1; Length 304;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCCACCGGAAGT 15
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Db 39 TCCGCCACCGGAAGT 25

RESULT 42

CA190223/c
LOCUS CA190223 Porphyra yezoensis TU-1 sporophytes Porphyra yezoensis
DEFINITION cDNA clone SCCCLR1C10D04
5', mRNA sequence.
ACCESSION CA190223
VERSION CA190223.1 GI:35134164

KEYWORDS

SOURCE
ORGANISM

EST.

Saccharum officinarum
Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
complex.

REFERENCE

AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 326)
Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
<http://www.bcccenter.fcav.unesp.br>
Plate: C10 row: D column: 04
Seq primer: T7 Promoter Primer.
Location/Qualifiers
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/mol_type="mRNA"
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/clone_lib="LR1"
/note="Organ: Leaf roll from field grown adult plants
(large insert library); Vector: pSport1; Site 1: SalI;
Site 2: NotI; An unidirectional cDNA library generated
from [leaf roll from field grown adult plants (large
insert library)]. cDNA was prepared from polyA+ mRNA
using SuperScript Plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CL-2B 40cm-columns and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at <http://sucest.lad.ic.unicamp.br/public>"

FEATURES

source
1..326
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCCCLR1C10D04"
/lab_host="DH10B"
/clone_lib="LR1"
/note="Organ: Leaf roll from field grown adult plants
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1.5 Kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at <http://sucest.lad.ic.unicamp.br/public>"

ORIGIN

Query Match 48.4%; Score 15; DB 6; Length 326;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CGGAAGTTGAGTAGA 23
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Db 197 CGGAAGTTGAGTAGA 183
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RESULT 43

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DEFINITION SCBGLR1112D03.g LR1 Saccharum officinarum cDNA clone SCBGLR1112D03
5', mRNA sequence.
ACCESSION CA118676
VERSION CA118676.1 GI:34971984
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum

REFERENCE

AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 336)
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Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica

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Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089

Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 112 row: D column: 03
Seq primer: T7 Promoter Primer.

FEATURES

Location/Qualifiers

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/lab_host="DH10B"

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/notes="Organ: Leaf roll from field grown adult plants
(large insert library); Vector: pSport1; Site 1: SalI;
Site 2: NotI; An unidirectional cDNA library generated
from [Leaf roll from field grown adult plants (large
insert library)]. cDNA was prepared from polyA+ mRNA
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of each source of RNA and library construction can be
obtained at http://succestd.lad.ic.unicamp.br/public"

ORIGIN

Query Match 48.4%; Score 15; DB 6; Length 336;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CGGAGTTGAGTAGA 23

|||||

Db 197 CGGAGTTGAGTAGA 183

RESULT 44

BY106179/c

LOCUS

BY106179 RIKEN full-length enriched, 15 days embryo whole body Mus
musculus cDNA clone L330001H23 5', mRNA sequence.

DEFINITION

BY106179

BY106179.1 GI:26216796

EST.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 337)

Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,

Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,

Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,

Schombach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,

Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,

Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,

Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dregani,T.A.,

Fletcher,C.P., Forrest,A., Frazer,K.S., Gaasterland,T.,

Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,

Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,

Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,

Maitais,L., Marchionni,L., McKenzie,L., Miki,H., Negashima,I.,

Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,

Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,

Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,

Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,

Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,

Verardo,R., Wagner,L., Wahlstedt,C., Wang,Y., Watanabe,Y.,

Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,

Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
Rogers,J., Birney,E. and Hayashizaki,Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

12466851

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Email: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,

Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
Shiraki,T., Tsgami,M., Waki,K., Watanishi,A., Muramatsu,M. and

Hayashizaki,Y. Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with

Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

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RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res.

10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues.

Please visit our web site (http://genome.gsc.riken.go.jp) for

further details.

FEATURES

source

1..337

/organism="Mus musculus"

/mol_type="mRNA"

/strain="CS7BL/6J"

/db_xref="taxon:10090"

/clone="L330001H23"

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whole body"

ORIGIN

Query Match

Best Local Similarity 48.4%; Score 15; DB 5; Length 337;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGGCCACCGGAGTT 16

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Db 168 CGGCCACCGGAGTT 154

RESULT 45

BY215955

LOCUS

DEFINITION

BY215955

ACCESSION

BY215955.1

GI:26396697

BY215955 339 bp mRNA linear EST 10-DEC-2002
BY215955 RIKEN full-length enriched, activated spleen Mus musculus
cDNA clone F830039P10 5', mRNA sequence.

KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS EST.
 Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 339)
 Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
 Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,
 Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
 Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,
 Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
 Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,
 Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,
 Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
 Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
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 Kawajiri, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,
 Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
 Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
 Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,
 Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,
 Ravasi, T., Reed, J.C., Reid, J., Ring, B.Z., Ringwald, M.,
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 Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
 Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
 Wells, C., Wilming, L.G., Wyshaw-Boris, A., Yanagisawa, M., Yang, I.,
 Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
 Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
 Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
 Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
 Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
 Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
 Rogers, J., Birney, E. and Hayashizaki, Y.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 22354683
 12466851

TITLE
 Analysis of the mouse transcriptome based on functional annotation
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 Nature 420, 563-573 (2002)
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JOURNAL
MEDLINE
PUBLISHED
COMMENT
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 Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/
 Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
 Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
 Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
 Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
 Shiraki, T., Tagami, M., Waki, K., Watanabe, A., Muramatsu, M. and
 Hayashizaki, Y. Direct Submission
 Computational Analysis of Full-Length Mouse cDNAs Compared with
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 10 (11), 1757-1771 (2000)
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 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
 Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
 Trust/MRC building Addenbrookes Hospital Cambridge) whose
 assistance we gratefully acknowledge.
 Please visit our web site (http://genome.gsc.riken.go.jp) for

FEATURES
source further details.
 Location/Qualifiers
 1..339
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="NOD"
 /db_xref="taxon:10090"
 /clone="F830039P10"
 /tissue_type="activated spleen"
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ORIGIN
 Query Match 48.4%; Score 15; DB 5; Length 339;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 17 GAGTAGACGGTGCTG 31
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 DB 213 GAGTAGACGGTGCTG 227
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RESULT 46
 BY2233847
 LOCUS
 DEFINITION
 CDNA clone F830305P17 5', mRNA sequence.
 BY2233847
 EST.
 Mus musculus (house mouse)
 SOURCE
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 351)
 Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
 Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,
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 Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
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COMMENT
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
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 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
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Email: genome-res@gsr.riken.jp, URL: <http://genome.gsc.riken.jp/>
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 Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
 Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

FEATURES

Location/Qualifiers
 1. .351

/organism="Mus musculus"
 /mol_type="mRNA"
 /strain="NOD"
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ORIGIN

Query Match 48.4%; Score 15; DB 5; Length 351;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 GAGTAGACGGTGCTG 31

DB 213 GAGTAGACGGTGCTG 227

RESULT 47

LOCUS BY219248 352 bp mRNA linear EST 10-DEC-2002
 DEFINITION BY219248 RIKEN full-length enriched, activated spleen Mus musculus
 CDNA clone F830113N13 5', mRNA sequence.

ACCESSION BY219248

VERSION BY219248.1 GI:26400262

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 352)

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AUTHORS Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaudo, I., Oatso, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,

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 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
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 Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission
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 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
 Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

FEATURES

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COMMENT

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source

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Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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LOCUS

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ACCESSION

BY039415

VERSION

BY039415.1

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

AUTHORS

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 370)
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
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JOURNAL

MEDLINE

PUBMED

COMMENT

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GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Sequence 4025, Ap	1558	41.9	1558	4 US-09-949-016-4025	Sequence 4025, Ap
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Sequence 2352, Ap	1671	41.9	1671	4 US-09-252-991A-2352	Sequence 2352, Ap
Sequence 219, App	1671	41.9	1671	4 US-09-602-787A-219	Sequence 219, App
Sequence 4087, Ap	1680	41.9	1680	4 US-09-252-991A-4087	Sequence 4087, Ap

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102	13	41.9	1826	4	US-09-883-720-1	Sequence 1, Appl	13	41.9	818128	4	US-09-949-016-14553	Sequence 14553, A
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104	13	41.9	1833	3	US-08-705-438-3	Sequence 3, Appl	13	41.9	818128	4	US-09-949-016-14555	Sequence 14555, A
105	13	41.9	1833	4	US-09-489-039A-1045	Sequence 1045, Ap	13	41.9	818128	4	US-09-949-016-14556	Sequence 14556, A
106	13	41.9	1995	4	US-09-252-991A-5783	Sequence 5783, Ap	13	41.9	818128	4	US-09-949-016-14557	Sequence 14557, A
107	13	41.9	2811	4	US-09-252-991A-11998	Sequence 11998, A	13	41.9	818128	4	US-09-949-016-14558	Sequence 14558, A
108	13	41.9	2885	5	PCT-US94-05905-21	Sequence 21, Appl	13	41.9	818128	4	US-09-949-016-14559	Sequence 14559, A
109	13	41.9	2820	2	US-08-306-488-1	Sequence 1, Appl	13	41.9	818128	4	US-09-949-016-14560	Sequence 14560, A
110	13	41.9	2820	5	PCT-US94-05905-19	Sequence 19, Appl	13	41.9	818128	4	US-09-949-016-14561	Sequence 14561, A
111	13	41.9	2839	1	US-07-814-964-6	Sequence 6, Appl	13	41.9	818128	4	US-09-949-016-14562	Sequence 14562, A
112	13	41.9	2839	1	US-08-258-442-6	Sequence 1, Appl	13	41.9	818128	4	US-09-949-016-14563	Sequence 14563, A
113	13	41.9	2839	3	US-08-328-809-1	Sequence 1, Appl	13	41.9	818128	4	US-09-949-016-14564	Sequence 14564, A
114	13	41.9	2839	3	US-09-015-003-1	Sequence 1, Appl	13	41.9	818128	4	US-09-949-016-14565	Sequence 14565, A
115	13	41.9	2839	4	US-08-866-840-1	Sequence 1, Appl	13	41.9	818128	4	US-09-949-016-14566	Sequence 14566, A
116	13	41.9	2839	5	PCT-US92-11107-6	Sequence 6, Appl	13	41.9	818128	4	US-09-949-016-14567	Sequence 14567, A
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118	13	41.9	2887	4	US-09-949-016-2186	Sequence 2186, Ap	13	41.9	818128	4	US-09-949-016-14569	Sequence 14569, A
119	13	41.9	3459	4	US-09-902-540-433	Sequence 433, Ap	13	41.9	818128	4	US-09-949-016-14570	Sequence 14570, A
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122	13	41.9	8051	2	US-08-576-628A-2	Sequence 2, Appl	13	41.9	818128	4	US-09-949-016-14573	Sequence 14573, A
123	13	41.9	1026	4	US-09-949-016-16680	Sequence 16680, A	13	41.9	818128	4	US-09-949-016-14574	Sequence 14574, A
124	13	41.9	11358	4	US-09-902-540-1075	Sequence 1075, Ap	13	41.9	818128	4	US-09-949-016-14575	Sequence 14575, A
125	13	41.9	11808	4	US-09-949-016-15281	Sequence 15281, A	13	41.9	818128	4	US-09-949-016-14576	Sequence 14576, A
126	13	41.9	13259	4	US-09-949-016-16454	Sequence 16454, A	13	41.9	818128	4	US-09-949-016-14577	Sequence 14577, A
127	13	41.9	13466	4	US-09-902-540-1007	Sequence 1007, Ap	13	41.9	818128	4	US-09-949-016-14578	Sequence 14578, A
128	13	41.9	14823	4	US-09-902-540-1087	Sequence 1087, Ap	13	41.9	818128	4	US-09-949-016-14579	Sequence 14579, A
129	13	41.9	16541	4	US-09-949-016-11665	Sequence 11665, Ap	13	41.9	818128	4	US-09-949-016-14580	Sequence 14580, A
130	13	41.9	19253	4	US-09-949-016-15131	Sequence 15131, Ap	13	41.9	818128	4	US-09-949-016-14581	Sequence 14581, A
131	13	41.9	19728	4	US-09-949-016-12506	Sequence 12506, A	13	41.9	818128	4	US-09-949-016-14582	Sequence 14582, A
132	13	41.9	19728	4	US-09-949-016-15767	Sequence 15767, A	13	41.9	818128	4	US-09-949-016-14583	Sequence 14583, A
133	13	41.9	20495	4	US-09-949-016-17198	Sequence 17198, A	13	41.9	818128	4	US-09-949-016-14584	Sequence 14584, A
134	13	41.9	23445	4	US-09-949-016-12955	Sequence 12955, A	13	41.9	818128	4	US-09-949-016-14585	Sequence 14585, A
135	13	41.9	24459	4	US-09-902-540-5004	Sequence 5004, Ap	13	41.9	818128	4	US-09-949-016-14586	Sequence 14586, A
136	13	41.9	25686	4	US-09-902-540-1246	Sequence 1246, Ap	13	41.9	818128	4	US-09-949-016-14587	Sequence 14587, A
137	13	41.9	26933	4	US-09-949-016-12045	Sequence 12045, A	13	41.9	818128	4	US-09-949-016-14588	Sequence 14588, A
138	13	41.9	29321	4	US-09-949-016-15872	Sequence 15872, A	13	41.9	818128	4	US-09-949-016-14589	Sequence 14589, A
139	13	41.9	29321	4	US-09-949-016-14257	Sequence 14257, A	13	41.9	818128	4	US-09-949-016-14590	Sequence 14590, A
140	13	41.9	29321	4	US-09-949-016-14258	Sequence 14258, A	13	41.9	818128	4	US-09-949-016-14591	Sequence 14591, A
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142	13	41.9	32573	4	US-09-949-016-13359	Sequence 13359, A	13	41.9	818128	4	US-09-949-016-14593	Sequence 14593, A
143	13	41.9	39754	4	US-09-949-016-14689	Sequence 14689, A	13	41.9	818128	4	US-09-949-016-14594	Sequence 14594, A
144	13	41.9	41171	4	US-08-311-731A-122	Sequence 122, Ap	13	41.9	818128	4	US-09-949-016-14595	Sequence 14595, A
145	13	41.9	45862	4	US-09-949-016-13928	Sequence 13928, A	13	41.9	818128	4	US-09-949-016-14596	Sequence 14596, A
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151	13	41.9	68720	4	US-09-949-016-14296	Sequence 14296, A	13	41.9	818128	4	US-09-949-016-14602	Sequence 14602, A
152	13	41.9	113042	4	US-09-949-016-12343	Sequence 12343, A	13	41.9	818128	4	US-09-949-016-14603	Sequence 14603, A
153	13	41.9	113042	4	US-09-949-016-15246	Sequence 15246, A	13	41.9	818128	4	US-09-949-016-14604	Sequence 14604, A
154	13	41.9	118999	4	US-09-791-105B-32	Sequence 32, Appl	13	41.9	818128	4	US-09-949-016-14605	Sequence 14605, A
155	13	41.9	118999	4	US-09-791-105B-32	Sequence 32, Appl	13	41.9	818128	4	US-09-949-016-14606	Sequence 14606, A
156	13	41.9	127771	4	US-09-949-016-14982	Sequence 14982, A	13	41.9	818128	4	US-09-949-016-14607	Sequence 14607, A
157	13	41.9	134292	4	US-09-949-016-12158	Sequence 12158, A	13	41.9	818128	4	US-09-949-016-14608	Sequence 14608, A
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159	13	41.9	174259	4	US-09-949-016-11968	Sequence 11968, A	13	41.9	818128	4	US-09-949-016-14610	Sequence 14610, A
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162	13	41.9	209210	4	US-09-949-016-15094	Sequence 15094, A	13	41.9	818128	4	US-09-949-016-14613	Sequence 14613, A
163	13	41.9	636591	4	US-09-949-016-11808	Sequence 11808, A	13	41.9	818128	4	US-09-949-016-14614	Sequence 14614, A
164	13	41.9	636591	4	US-09-949-016-13388	Sequence 13388, A	13	41.9	818128	4	US-09-949-016-14615	Sequence 14615, A
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166	13	41.9	767877	4	US-09-949-016-17361	Sequence 17361, A	13	41.9	818128	4	US-09-949-016-14617	Sequence 14617, A
167	13	41.9	784019	4	US-09-949-016-14033	Sequence 14033, A	13	41.9	818128	4	US-09-949-016-14618	Sequence 14618, A
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169	13	41.9	818128	4	US-09-949-016-14547	Sequence 14547, A	13	41.9	818128	4	US-09-949-016-14620	Sequence 14620, A
170	13	41.9	818128	4	US-09-949-016-14548	Sequence 14548, A	13	41.9	818128	4	US-09-949-016-14621	Sequence 14621, A
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173	13	41.9	818128	4	US-09-949-016-14551	Sequence 14551, A	13	41.9	818128	4	US-09-949-016-14624	Sequence 14624, A

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248	12	38.7	432	4	US-09-902-540-1638	Sequence 1638, Ap	c 321	12	38.7	903	4	US-09-328-352-1510	Sequence 1510, Ap
249	12	38.7	433	4	US-09-270-767-6917	Sequence 6917, Ap	c 322	12	38.7	903	4	US-09-902-540-4584	Sequence 4584, Ap
250	12	38.7	436	4	US-09-270-767-22199	Sequence 22199, A	c 323	12	38.7	936	5	PCT-US95-01185-66	Sequence 66, Appl
251	12	38.7	452	4	US-09-322-357-47	Sequence 47, Appl	c 324	12	38.7	936	4	US-09-248-796A-912	Sequence 912, App
252	12	38.7	459	3	US-09-199-637A-268	Sequence 268, App	c 325	12	38.7	951	4	US-09-134-000C-1037	Sequence 1037, App
253	12	38.7	465	4	US-09-621-976-3332	Sequence 3332, Ap	c 326	12	38.7	969	4	US-09-328-352-1763	Sequence 1763, Ap
254	12	38.7	468	4	US-09-621-976-13677	Sequence 13677, A	c 327	12	38.7	983	4	US-09-640-211A-15	Sequence 15, Appl
255	12	38.7	494	4	US-09-621-976-18300	Sequence 18300, A	c 328	12	38.7	998	2	US-08-105-989-6	Sequence 6, Appli
256	12	38.7	495	4	US-09-710-279-5	Sequence 5, Appli	c 329	12	38.7	998	3	US-09-138-922-6	Sequence 6, Appli
257	12	38.7	495	4	US-09-710-279-473	Sequence 473, App	c 330	12	38.7	1001	3	US-09-641-638-198	Sequence 198, App
258	12	38.7	495	4	US-09-248-796A-9077	Sequence 9077, Ap	c 331	12	38.7	1001	3	US-09-641-638-198	Sequence 198, App
259	12	38.7	504	3	US-09-370-838-250	Sequence 250, App	c 332	12	38.7	1017	3	US-08-469-318-67	Sequence 67, Appl
260	12	38.7	504	3	US-09-854-133-250	Sequence 250, App	c 333	12	38.7	1017	3	US-08-468-609A-67	Sequence 67, Appl
261	12	38.7	510	3	US-09-134-001C-2594	Sequence 2594, Ap	c 334	12	38.7	1017	3	US-08-446-872A-67	Sequence 67, Appl
262	12	38.7	528	4	US-09-621-976-3331	Sequence 3331, Ap	c 335	12	38.7	1017	3	US-08-446-872A-67	Sequence 67, Appl
263	12	38.7	567	4	US-09-252-991A-3149	Sequence 3149, Ap	c 336	12	38.7	1017	3	US-09-902-540-9102	Sequence 9102, Ap
264	12	38.7	570	4	US-09-248-796A-5804	Sequence 5804, Ap	c 337	12	38.7	1017	5	PCT-US95-01185-67	Sequence 67, Appl
265	12	38.7	573	4	US-09-328-352-1033	Sequence 1033, Ap	c 338	12	38.7	1047	3	US-08-469-318-65	Sequence 65, Appl
266	12	38.7	601	4	US-09-949-016-22002	Sequence 22002, A	c 339	12	38.7	1047	3	US-08-469-318-74	Sequence 74, Appl
267	12	38.7	601	4	US-09-949-016-22003	Sequence 22003, A	c 340	12	38.7	1047	3	US-08-469-318-76	Sequence 76, Appl
268	12	38.7	601	4	US-09-949-016-22004	Sequence 22004, A	c 341	12	38.7	1047	3	US-08-468-609A-65	Sequence 65, Appl
269	12	38.7	601	4	US-09-949-016-25005	Sequence 25005, A	c 342	12	38.7	1047	3	US-08-468-609A-74	Sequence 74, Appl
270	12	38.7	601	4	US-09-949-016-25006	Sequence 25006, A	c 343	12	38.7	1047	3	US-08-468-609A-76	Sequence 76, Appl
271	12	38.7	601	4	US-09-949-016-4650	Sequence 4650, A	c 344	12	38.7	1047	3	US-08-446-872A-65	Sequence 65, Appl
272	12	38.7	601	4	US-09-949-016-52288	Sequence 52288, A	c 345	12	38.7	1047	3	US-08-446-872A-74	Sequence 74, Appl
273	12	38.7	601	4	US-09-949-016-53918	Sequence 53918, A	c 346	12	38.7	1047	3	US-08-446-872A-76	Sequence 76, Appl
274	12	38.7	601	4	US-09-949-016-57347	Sequence 57347, A	c 347	12	38.7	1047	3	US-08-762-227A-65	Sequence 65, Appl
275	12	38.7	601	4	US-09-949-016-60149	Sequence 60149, A	c 348	12	38.7	1047	3	US-08-762-227A-74	Sequence 74, Appl
276	12	38.7	601	4	US-09-949-016-60150	Sequence 60150, A	c 349	12	38.7	1047	3	US-08-762-227A-76	Sequence 76, Appl
277	12	38.7	601	4	US-09-949-016-60646	Sequence 60646, A	c 350	12	38.7	1047	5	PCT-US95-01185-65	Sequence 65, Appl
278	12	38.7	601	4	US-09-949-016-83423	Sequence 83423, A	c 351	12	38.7	1047	5	PCT-US95-01185-74	Sequence 74, Appl
279	12	38.7	601	4	US-09-949-016-83459	Sequence 83459, A	c 352	12	38.7	1047	5	PCT-US95-01185-76	Sequence 76, Appl
280	12	38.7	601	4	US-09-949-016-84323	Sequence 84323, A	c 353	12	38.7	1074	3	US-09-134-001C-542	Sequence 542, App
281	12	38.7	601	4	US-09-949-016-84324	Sequence 84324, A	c 354	12	38.7	1078	4	US-09-522-689A-1	Sequence 1, Appli
282	12	38.7	601	4	US-09-949-016-84325	Sequence 84325, A	c 355	12	38.7	1089	5	PCT-US95-03866-31	Sequence 31, Appl
283	12	38.7	601	4	US-09-949-016-86532	Sequence 86532, A	c 356	12	38.7	1092	4	US-09-489-039A-6864	Sequence 6864, Ap
284	12	38.7	601	4	US-09-949-016-86533	Sequence 86533, A	c 357	12	38.7	1100	3	US-08-920-422-22	Sequence 22, Appl
285	12	38.7	601	4	US-09-949-016-86534	Sequence 86534, A	c 358	12	38.7	1101	3	US-09-152-060-23	Sequence 23, Appl
286	12	38.7	601	4	US-09-949-016-128409	Sequence 128409, A	c 359	12	38.7	1106	5	PCT-US92-02977-5	Sequence 5, Appli
287	12	38.7	601	4	US-09-949-016-140349	Sequence 140349, A	c 360	12	38.7	1106	5	PCT-US95-03032-4	Sequence 4, Appli
288	12	38.7	601	4	US-09-949-016-140350	Sequence 140350, A	c 361	12	38.7	1107	4	US-09-252-991A-14565	Sequence 14565, A
289	12	38.7	601	4	US-09-949-016-142625	Sequence 142625, A	c 362	12	38.7	1110	4	US-09-489-039A-416	Sequence 416, App
290	12	38.7	601	4	US-09-949-016-162628	Sequence 162628, A	c 363	12	38.7	1140	4	US-09-252-991A-2912	Sequence 2912, App
291	12	38.7	601	4	US-09-949-016-162629	Sequence 162629, A	c 364	12	38.7	1170	3	US-09-491-577-49	Sequence 49, Appl
292	12	38.7	601	4	US-09-949-016-169472	Sequence 169472, A	c 365	12	38.7	1173	3	US-08-706-216-5	Sequence 5, Appli
293	12	38.7	601	4	US-09-949-016-176054	Sequence 176054, A	c 366	12	38.7	1173	4	US-09-650-284B-5	Sequence 5, Appli
294	12	38.7	601	4	US-09-949-016-176055	Sequence 176055, A	c 367	12	38.7	1230	4	US-09-502-540-7025	Sequence 7025, Ap
295	12	38.7	601	4	US-09-949-016-186031	Sequence 186031, A	c 368	12	38.7	1245	4	US-09-252-991A-4537	Sequence 4537, Ap
296	12	38.7	601	4	US-09-949-016-186031	Sequence 186031, A	c 369	12	38.7	1291	1	US-07-952-755-2	Sequence 2, Appli
297	12	38.7	601	4	US-09-949-016-199453	Sequence 199453, A	c 370	12	38.7	1291	1	US-08-443-679-2	Sequence 2, Appli
298	12	38.7	603	4	US-09-252-991A-4238	Sequence 4238, Ap	c 371	12	38.7	1304	4	US-09-270-767-678	Sequence 678, App
299	12	38.7	610	4	US-09-270-767-15117	Sequence 15117, A	c 372	12	38.7	1304	4	US-09-270-767-15960	Sequence 15960, A
300	12	38.7	640	4	US-09-854-133-431	Sequence 431, App	c 373	12	38.7	1311	4	US-09-248-796A-5537	Sequence 5537, Ap
301	12	38.7	647	5	PCT-US94-04174-27	Sequence 27, Appl	c 374	12	38.7	1320	1	US-07-681-704A-1	Sequence 1, Appli
302	12	38.7	657	4	US-09-489-039A-651	Sequence 651, App	c 375	12	38.7	1320	4	US-09-602-787A-159	Sequence 159, App
303	12	38.7	658	3	US-08-476-120-7	Sequence 7, Appli	c 376	12	38.7	1326	4	US-09-328-352-2243	Sequence 2243, Ap
304	12	38.7	672	4	US-09-252-991A-3957	Sequence 3957, Ap	c 377	12	38.7	1341	3	US-09-199-637A-266	Sequence 266, App
305	12	38.7	702	4	US-09-489-039A-6546	Sequence 6546, Ap	c 378	12	38.7	1347	3	US-09-342-681C-13	Sequence 13, Appl
306	12	38.7	744	4	US-09-270-767-13516	Sequence 13516, A	c 379	12	38.7	1353	4	US-09-252-991A-4921	Sequence 4921, Ap
307	12	38.7	771	4	US-09-543-681A-2936	Sequence 2936, Ap	c 380	12	38.7	1368	4	US-09-270-767-5066	Sequence 5066, Ap
308	12	38.7	832	4	US-09-270-767-12770	Sequence 12770, A	c 381	12	38.7	1374	4	US-09-270-767-20348	Sequence 20348, A
309	12	38.7	840	4	US-09-248-796A-6353	Sequence 6353, Ap	c 382	12	38.7	1374	4	US-09-252-991A-4024	Sequence 4024, Ap
310	12	38.7	840	4	US-09-949-016-5446	Sequence 5446, Ap	c 383	12	38.7	1382	2	US-08-596-387B-123	Sequence 123, App
311	12	38.7	858	4	US-09-248-796A-8715	Sequence 8715, Ap	c 384	12	38.7	1382	2	US-09-067-615-123	Sequence 123, App
312	12	38.7	862	1	US-08-379-280-4	Sequence 4, Appli	c 385	12	38.7	1382	5	PCT-US95-09816A-123	Sequence 123, App
313	12	38.7	889	2	US-08-832-883-52	Sequence 52, Appl	c 386	12	38.7	1385	2	US-08-596-387B-121	Sequence 121, App
314	12	38.7	889	2	US-08-832-877-52	Sequence 52, Appl	c 387	12	38.7	1385	3	US-09-067-615-121	Sequence 121, App
315	12	38.7	891	4	US-09-543-681A-204	Sequence 204, App	c 388	12	38.7	1385	5	PCT-US95-09816A-121	Sequence 121, App
316	12	38.7	894	4	US-09-902-540-6908	Sequence 6908, Ap	c 389	12	38.7	1393	4	US-09-902-540-9055	Sequence 9055, Ap
317	12	38.7	903	3	US-08-469-318-66	Sequence 66, Appl	c 390	12	38.7	1395	4	US-10-029-180-43	Sequence 43, Appl
318	12	38.7	903	3	US-08-468-609A-66	Sequence 66, Appl	c 391	12	38.7	1400	1	PCT-US93-845-1	Sequence 1, Appli
319	12	38.7	903	3	US-08-446-872A-66	Sequence 66, Appl	c 392	12	38.7	1400	5	PCT-US93-11298-1	Sequence 1, Appli


```
RESULT 2
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: PRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37RV
US-09-103-840A-1

Query Match      51.6%; Score 16; DB 3; Length 4411529;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 GCACCGGAAGTTGAG 19
DB      1450409 GCACCGGAAGTTGAG 1450394

RESULT 3
US-09-313-294A-1931/c
; Sequence 1931, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 1931
; LENGTH: 214
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6476212 700551761H1
US-09-313-294A-1931

Query Match      48.4%; Score 15; DB 4; Length 214;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCCGCCACCGGAAGT 15
DB      113 TCCGCCACCGGAAGT 99

RESULT 4
US-09-464-535-13/c
; Sequence 13, Application US/09464535
; Patent No. 6545200
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Sakai, Hajime
; APPLICANT: Rafalski, J. Antoni
; TITLE OF INVENTION: STEROL BIOSYNTHETIC ENZYMES
; FILE REFERENCE: BB1306 US NA
; CURRENT APPLICATION NUMBER: US/09/464,535
; CURRENT FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
; LENGTH: 436
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-09-464-535-13

Query Match      48.4%; Score 15; DB 4; Length 436;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 CCACCGGAAGTTGAG 19
DB      157 CCACCGGAAGTTGAG 143

RESULT 5
US-09-464-535-39/c
; Sequence 39, Application US/09464535
; Patent No. 6545200
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Sakai, Hajime
; APPLICANT: McGonigle, Brian
; APPLICANT: Rafalski, J. Antoni
; TITLE OF INVENTION: STEROL BIOSYNTHETIC ENZYMES
; FILE REFERENCE: BB1306 US NA
; CURRENT APPLICATION NUMBER: US/09/464,535
; CURRENT FILING DATE: 1999-12-15
; EARLIER APPLICATION NUMBER: 60/112,555
; EARLIER FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 39
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-09-464-535-39

Query Match      48.4%; Score 15; DB 4; Length 600;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 CCACCGGAAGTTGAG 19
DB      164 CCACCGGAAGTTGAG 150

RESULT 6
US-09-464-535-33/c
; Sequence 33, Application US/09464535
; Patent No. 6545200
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Sakai, Hajime
; APPLICANT: McGonigle, Brian
; APPLICANT: Rafalski, J. Antoni
; TITLE OF INVENTION: STEROL BIOSYNTHETIC ENZYMES
; FILE REFERENCE: BB1306 US NA
; CURRENT APPLICATION NUMBER: US/09/464,535
; CURRENT FILING DATE: 1999-12-15
```

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; EARLIER APPLICATION NUMBER: 60/112,555
; CURRENT FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 33
; LENGTH: 616
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (387)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (415)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (489)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (491)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (544)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (551)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (558)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (562)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (567)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (569)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (592)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (600)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (611)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (616)
; LOCATION: (616)
US-09-464-535-33

```

```

Query Match 48.4%; Score 15; DB 4; Length 616;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 5 CCACCGGAAGTTGAG 19
Db 376 CCACCGGAAGTTGAG 362

```

```

RESULT 7
US-09-464-535-31/c
; Sequence 31, Application US/09464535
; Patent No. 6545200
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Sakai, Hajime
; APPLICANT: McGonigle, Brian
; APPLICANT: Rafaleki, J. Antoni
; TITLE OF INVENTION: STEROL BIOSYNTHETIC ENZYMES
; FILE REFERENCE: BB1306 US NA

```

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; CURRENT APPLICATION NUMBER: US/09/464,535
; CURRENT FILING DATE: 1999-12-15
; EARLIER APPLICATION NUMBER: 60/112,555
; EARLIER FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 31
; LENGTH: 673
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (3)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (41)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (95)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (227)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (385)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (388)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (390)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (487)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (491)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (554)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (557)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (560)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (626)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (634)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (650)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (664)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (668)
US-09-464-535-31

```

```

Query Match 48.4%; Score 15; DB 4; Length 673;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 5 CCACCGGAAGTTGAG 19
Db 362 CCACCGGAAGTTGAG 348

```

RESULT 8

PCT-US95-08354A-1
 ; Sequence 1, Application PC/TUS9508354A
 ; GENERAL INFORMATION:
 ; APPLICANT: Temple University - Of The
 ; APPLICANT: Commonwealth System of Higher Education
 ; TITLE OF INVENTION: JAK3 PROTEIN TYROSINE
 ; TITLE OF INVENTION: KINASE AND DNA ENCODING THE SAME
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Seidel, Gonda, Lavorigna
 ; ADDRESSEE: & Monaco, P.C.
 ; STREET: Suite 1800, Two Penn Center
 ; CITY: Philadelphia
 ; STATE: Pennsylvania
 ; COUNTRY: U.S.A.
 ; ZIP: 19102
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
 ; COMPUTER: IBM PS/2
 ; OPERATING SYSTEM: MS-DOS
 ; SOFTWARE: WordPerfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/08354A
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/272,368
 ; FILING DATE: 8 July 1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Monaco, Daniel A.
 ; REGISTRATION NUMBER: 30,480
 ; REFERENCE/DOCKET NUMBER: 6056-203 PC
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (215) 568-8383
 ; TELEFAX: (215) 568-5549
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4016 nucleotides
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single stranded
 ; TOPOLOGY: linear
 ; PCT-US95-08354A-1

Query Match 48.4%; Score 15; DB 5; Length 4016;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 GAGTAGACGGTGCTG 31
 Db 2033 GAGTAGACGGTGCTG 2047

RESULT 9
 US-09-949-016-12182/c
 ; Sequence 12182, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 12182
 ; LENGTH: 92581

; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-016-12182
 ; Query Match 48.4%; Score 15; DB 4; Length 92581;
 ; Best Local Similarity 100.0%; Pred. No. 16;
 ; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ; QY 10 GGAAGTTGAGTAGAC 24
 ; Db 55600 GGAAGTTGAGTAGAC 55586
 ; RESULT 10
 ; US-09-949-016-16542/c
 ; Sequence 16542, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 16542
 ; LENGTH: 92581
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-016-16542

Query Match 48.4%; Score 15; DB 4; Length 92581;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GGAAGTTGAGTAGAC 24
 Db 55600 GGAAGTTGAGTAGAC 55586

RESULT 11
 US-09-621-976-17715/c
 ; Sequence 17715, Application US/09621976
 ; Patent No. 6639063
 ; GENERAL INFORMATION:
 ; APPLICANT: Dumas Milne Edwards, J.B.
 ; APPLICANT: Jobert, S.
 ; APPLICANT: Giordano, J.Y.
 ; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
 ; FILE REFERENCE: GENSET.054PR2
 ; CURRENT APPLICATION NUMBER: US/09/621,976
 ; CURRENT FILING DATE: 2000-07-21
 ; NUMBER OF SEQ ID NOS: 19335
 ; SOFTWARE: Patent.pm
 ; SEQ ID NO 17715
 ; LENGTH: 223
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; LOCATION: 208
 ; OTHER INFORMATION: n=a, g, c o r t
 ; US-09-621-976-17715
 ; Query Match 45.2%; Score 14; DB 4; Length 223;
 ; Best Local Similarity 100.0%; Pred. No. 74;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCCACCGGAAG 14
Db 15 TCCGCCACCGGAAG 2

RESULT 12

US-09-471-276-430/c
; Sequence 430, Application US/09471276
; Patent No. 6822072
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6822072
; FILE REFERENCE: GENSET.025CP1
; CURRENT APPLICATION NUMBER: US/09/471,276
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 09/057,719
; EARLIER FILING DATE: 1998-04-09
; EARLIER APPLICATION NUMBER: 09/069,047
; EARLIER FILING DATE: 1998-04-28
; EARLIER APPLICATION NUMBER: PCT/IB99/00712
; EARLIER FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1622
; SOFTWARE: Patent.pm
; SEQ ID NO 430
; LENGTH: 236
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 52..234
; NAME/KEY: sig_peptide
; LOCATION: 52..159
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 4.8000019073486
; OTHER INFORMATION: seq VLLAIGMFFTAWF/FV
US-09-471-276-430

Query Match 45.2%; Score 14; DB 4; Length 236;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCCACCGGAAG 14
Db 25 TCCGCCACCGGAAG 12

RESULT 13

US-09-247-155-137/c
; Sequence 137, Application US/09247155A
; Patent No. 6312922
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Complementary DNAs
; FILE REFERENCE: GENSET.021A
; CURRENT APPLICATION NUMBER: US/09/247,155A
; CURRENT FILING DATE: 1999-02-09
; EARLIER APPLICATION NUMBER: 60/074,121
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/081,563
; EARLIER FILING DATE: 1998-04-13
; EARLIER APPLICATION NUMBER: 60/096,116
; EARLIER FILING DATE: 1998-08-10
; EARLIER APPLICATION NUMBER: 60/099,273
; EARLIER FILING DATE: 1998-10-04
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patent.pm

; SEQ ID NO 137
; LENGTH: 419
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 50..286
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 50..157
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 4.8000019073486
; OTHER INFORMATION: seq VLLAIGMFFTAWF/FV
; FEATURE:
; NAME/KEY: polyA signal
; LOCATION: 385..390
; FEATURE:
; NAME/KEY: polyA site
; LOCATION: 405..416
US-09-247-155-137

Query Match 45.2%; Score 14; DB 3; Length 419;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCCACCGGAAG 14
Db 23 TCCGCCACCGGAAG 10

RESULT 14

US-09-247-155-73/c
; Sequence 73, Application US/09247155A
; Patent No. 6312922
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Complementary DNAs
; FILE REFERENCE: GENSET.021A
; CURRENT APPLICATION NUMBER: US/09/247,155A
; CURRENT FILING DATE: 1999-02-09
; EARLIER APPLICATION NUMBER: 60/074,121
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/081,563
; EARLIER FILING DATE: 1998-04-13
; EARLIER APPLICATION NUMBER: 60/096,116
; EARLIER FILING DATE: 1998-08-10
; EARLIER APPLICATION NUMBER: 60/099,273
; EARLIER FILING DATE: 1998-10-04
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patent.pm
; SEQ ID NO 73
; LENGTH: 425
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 55..291
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 55..255
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 4.4
; OTHER INFORMATION: seq LISLVASLFMGFG/VL
; FEATURE:
; NAME/KEY: polyA signal
; LOCATION: 390..395
; FEATURE:
; NAME/KEY: polyA site
; LOCATION: 410..425
US-09-247-155-73

Query Match 45.2%; Score 14; DB 3; Length 425;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCCACCGGAAG 14
| | | | | | | | | | | | | | | |
Db 27 TCCGCCACCGGAAG 14

RESULT 15
US-09-621-976-17717/c
; Sequence 17717, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 17717
; LENGTH: 440
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-17717

Query Match 45.2%; Score 14; DB 4; Length 440;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCCACCGGAAG 14
| | | | | | | | | | | | | | | |
Db 29 TCCGCCACCGGAAG 16

RESULT 16
US-09-270-767-14483
; Sequence 14483, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14483
; LENGTH: 443
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-14483

Query Match 45.2%; Score 14; DB 4; Length 443;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCCACCGGAAGTTG 17
| | | | | | | | | | | | | | | |
Db 334 GCCACCGGAAGTTG 347

RESULT 17
US-09-621-976-17361
; Sequence 17361, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.

; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 17361
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-17361

Query Match 45.2%; Score 14; DB 4; Length 468;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCCACCGGAAG 14
| | | | | | | | | | | | | | | |
Db 259 TCCGCCACCGGAAG 272

RESULT 18
US-09-621-976-17716/c
; Sequence 17716, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 17716
; LENGTH: 536
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 300,454,457
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-17716

Query Match 45.2%; Score 14; DB 4; Length 536;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCCACCGGAAG 14
| | | | | | | | | | | | | | | |
Db 15 TCCGCCACCGGAAG 2

RESULT 19
US-09-513-999C-12104/c
; Sequence 12104, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 12104
; LENGTH: 564

; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 173059
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-173059

Query Match 45.2%; Score 14; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCCACCGGAAG 14
|||||
Db 98 TCCGCCACCGGAAG 111

RESULT 24
US-09-902-540-4310/c
; Sequence 4310, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 4310
; LENGTH: 663
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-4310

Query Match 45.2%; Score 14; DB 4; Length 663;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 TGAGTAGACGGTGC 29
|||||
Db 288 TGAGTAGACGGTGC 275

RESULT 25
US-09-127-219B-2/c
; Sequence 2, Application US/09127219B
; Patent No. 637272
; GENERAL INFORMATION:
; APPLICANT: KIRKPATRICK, D. LYNN
; APPLICANT: POWIS, GARTH
; TITLE OF INVENTION: INHIBITORS OF REDOX SIGNALING AND METHODS OF USING SAME
; FILE REFERENCE: 98-571-us
; CURRENT APPLICATION NUMBER: US/09/127,219B
; CURRENT FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: 60/054,566
; PRIOR FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2187
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-127-219B-2

Query Match 45.2%; Score 14; DB 3; Length 2187;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCCACCGGAAG 14
|||||
Db 251 TCCGCCACCGGAAG 238

RESULT 26
US-09-252-991A-10206/c
; Sequence 10206, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 10206
; LENGTH: 2310
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-10206

Query Match 45.2%; Score 14; DB 4; Length 2310;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCGCCACCGGAAGT 15
|||||
Db 1292 CCGCCACCGGAAGT 1279

RESULT 27
US-09-902-540-8535/c
; Sequence 8535, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 8535
; LENGTH: 2850
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-8535

Query Match 45.2%; Score 14; DB 4; Length 2850;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CGCCACCGGAAGTT 16
|||||
Db 1752 CGCCACCGGAAGTT 1739

RESULT 28

US-09-949-016-12296
; Sequence 12296, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12296
; LENGTH: 2913
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12296

Query Match 45.2%; Score 14; DB 4; Length 2913;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CGCCACCGGAAGTT 16
|||
Db 758 CGCCACCGGAAGTT 771

RESULT 29
US-09-949-016-12327
; Sequence 12327, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12327
; LENGTH: 8073
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12327

Query Match 45.2%; Score 14; DB 4; Length 8073;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCCACCGGAAG 14
|||
Db 1909 TCCGCCACCGGAAG 1922

RESULT 30
US-09-949-016-16645
; Sequence 16645, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16645
; LENGTH: 8074
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16645

Query Match 45.2%; Score 14; DB 4; Length 8074;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCCACCGGAAG 14
|||
Db 1909 TCCGCCACCGGAAG 1922

RESULT 31
US-09-902-540-899
; Sequence 899, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 899
; LENGTH: 8518
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-899

Query Match 45.2%; Score 14; DB 4; Length 8518;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CGCCACCGGAAGTT 16
|||
Db 6766 CGCCACCGGAAGTT 6779

RESULT 32
US-09-902-540-1219
; Sequence 1219, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883

; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1219
; LENGTH: 22761
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(22761)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1219

Query Match 45.2%; Score 14; DB 4; Length 22761;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCGCCACCGGAAGT 15
Db 18791 CCGCCACCGGAAGT 18804

RESULT 33

US-09-902-540-1214/C
; Sequence 1214, Application US/09902540
; Patent No. 6833447

GENERAL INFORMATION:

; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1214
; LENGTH: 22807
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1214

Query Match 45.2%; Score 14; DB 4; Length 22807;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 TGAGTAGACGGTGC 29
Db 21474 TGAGTAGACGGTGC 21461

RESULT 34

US-09-902-540-1214/C
; Sequence 1214, Application US/09902540
; Patent No. 6833447
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1214
; LENGTH: 22807
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1214

Query Match 45.2%; Score 14; DB 4; Length 22807;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 TGAGTAGACGGTGC 29
Db 21474 TGAGTAGACGGTGC 21461

; FILING DATE: 20-JAN-1988
; APPLICATION NUMBER: 485,614
; FILING DATE: 15-APR-1983
; APPLICATION NUMBER: 713,624
; FILING DATE: 10-JUN-1991
; APPLICATION NUMBER: 260,574
; FILING DATE: 21-OCT-1988
; APPLICATION NUMBER: 848,733
; FILING DATE: 01-APR-1986
; APPLICATION NUMBER: 535,354
; FILING DATE: 26-SEP-1983
; SEQ ID NO:1:
; LENGTH: 24595
5428147-1

Query Match 45.2%; Score 14; DB 6; Length 24595;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCGCCACCGGAAGT 15
Db 22666 CCGCCACCGGAAGT 22679

RESULT 35

US-09-902-540-1214/C
; Sequence 1214, Application US/09902540
; Patent No. 6833447
; APPLICANT: Barker, Richard F.; Kemp, John D.
; TITLE OF INVENTION: OCTOPINE T-DNA PROMOTERS
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/91,538
; FILING DATE: 13-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 869,216
; FILING DATE: 13-APR-1992
; APPLICATION NUMBER: 869,216
; FILING DATE: 13-APR-1992
; APPLICATION NUMBER: 440,432
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 553,786
; FILING DATE: 19-NOV-1983
; APPLICATION NUMBER: 741,034
; FILING DATE: 06-AUG-1991
; APPLICATION NUMBER: 144,775
; FILING DATE: 20-JAN-1988
; APPLICATION NUMBER: 485,614
; FILING DATE: 15-APR-1983
; APPLICATION NUMBER: 713,624
; FILING DATE: 10-JUN-1991
; APPLICATION NUMBER: 260,574
; FILING DATE: 21-OCT-1988
; APPLICATION NUMBER: 848,733
; FILING DATE: 01-APR-1986
; APPLICATION NUMBER: 535,354
; FILING DATE: 26-SEP-1983
; SEQ ID NO:1:
; LENGTH: 24595
5428147-1

QY 2 CCGCCACCGGAAGT 15
Db 22666 CCGCCACCGGAAGT 22679

US-09-902-540-1214/C
; Sequence 1214, Application US/09902540
; Patent No. 6833447
; APPLICANT: Barker, Richard F.; Kemp, John D.
; TITLE OF INVENTION: OCTOPINE T-DNA PROMOTERS
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/91,538
; FILING DATE: 13-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 869,216
; FILING DATE: 13-APR-1992
; APPLICATION NUMBER: 869,216
; FILING DATE: 13-APR-1992
; APPLICATION NUMBER: 440,432
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 553,786
; FILING DATE: 19-NOV-1983
; APPLICATION NUMBER: 741,034
; FILING DATE: 06-AUG-1991
; APPLICATION NUMBER: 144,775
; FILING DATE: 20-JAN-1988
; APPLICATION NUMBER: 485,614
; FILING DATE: 15-APR-1983
; APPLICATION NUMBER: 713,624
; FILING DATE: 10-JUN-1991
; APPLICATION NUMBER: 260,574
; FILING DATE: 21-OCT-1988
; APPLICATION NUMBER: 848,733
; FILING DATE: 01-APR-1986
; APPLICATION NUMBER: 535,354
; FILING DATE: 26-SEP-1983
; SEQ ID NO:1:
; LENGTH: 24595
5428147-1

QY 2 CCGCCACCGGAAGT 15
Db 22666 CCGCCACCGGAAGT 22679

US-09-902-540-1214/C
; Sequence 1214, Application US/09902540
; Patent No. 6833447
; APPLICANT: Barker, Richard F.; Kemp, John D.
; TITLE OF INVENTION: OCTOPINE T-DNA PROMOTERS
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/91,538
; FILING DATE: 13-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 869,216
; FILING DATE: 13-APR-1992
; APPLICATION NUMBER: 869,216
; FILING DATE: 13-APR-1992
; APPLICATION NUMBER: 440,432
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 553,786
; FILING DATE: 19-NOV-1983
; APPLICATION NUMBER: 741,034
; FILING DATE: 06-AUG-1991
; APPLICATION NUMBER: 144,775
; FILING DATE: 20-JAN-1988
; APPLICATION NUMBER: 485,614
; FILING DATE: 15-APR-1983
; APPLICATION NUMBER: 713,624
; FILING DATE: 10-JUN-1991
; APPLICATION NUMBER: 260,574
; FILING DATE: 21-OCT-1988
; APPLICATION NUMBER: 848,733
; FILING DATE: 01-APR-1986
; APPLICATION NUMBER: 535,354
; FILING DATE: 26-SEP-1983
; SEQ ID NO:1:
; LENGTH: 24595
5428147-1

QY 2 CCGCCACCGGAAGT 15
Db 22666 CCGCCACCGGAAGT 22679

US-09-902-540-1214/C
; Sequence 1214, Application US/09902540
; Patent No. 6833447
; APPLICANT: Barker, Richard F.; Kemp, John D.
; TITLE OF INVENTION: OCTOPINE T-DNA PROMOTERS
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/91,538
; FILING DATE: 13-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 869,216
; FILING DATE: 13-APR-1992
; APPLICATION NUMBER: 869,216
; FILING DATE: 13-APR-1992
; APPLICATION NUMBER: 440,432
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 553,786
; FILING DATE: 19-NOV-1983
; APPLICATION NUMBER: 741,034
; FILING DATE: 06-AUG-1991
; APPLICATION NUMBER: 144,775
; FILING DATE: 20-JAN-1988
; APPLICATION NUMBER: 485,614
; FILING DATE: 15-APR-1983
; APPLICATION NUMBER: 713,624
; FILING DATE: 10-JUN-1991
; APPLICATION NUMBER: 260,574
; FILING DATE: 21-OCT-1988
; APPLICATION NUMBER: 848,733
; FILING DATE: 01-APR-1986
; APPLICATION NUMBER: 535,354
; FILING DATE: 26-SEP-1983
; SEQ ID NO:1:
; LENGTH: 24595
5428147-1

QY 2 CCGCCACCGGAAGT 15
Db 22666 CCGCCACCGGAAGT 22679

US-09-902-540-1214/C
; Sequence 1214, Application US/09902540
; Patent No. 6833447
; APPLICANT: Barker, Richard F.; Kemp, John D.
; TITLE OF INVENTION: OCTOPINE T-DNA PROMOTERS
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/91,538
; FILING DATE: 13-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 869,216
; FILING DATE: 13-APR-1992
; APPLICATION NUMBER: 869,216
; FILING DATE: 13-APR-1992
; APPLICATION NUMBER: 440,432
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 553,786
; FILING DATE: 19-NOV-1983
; APPLICATION NUMBER: 741,034
; FILING DATE: 06-AUG-1991
; APPLICATION NUMBER: 144,775
; FILING DATE: 20-JAN-1988
; APPLICATION NUMBER: 485,614
; FILING DATE: 15-APR-1983
; APPLICATION NUMBER: 713,624
; FILING DATE: 10-JUN-1991
; APPLICATION NUMBER: 260,574
; FILING DATE: 21-OCT-1988
; APPLICATION NUMBER: 848,733
; FILING DATE: 01-APR-1986
; APPLICATION NUMBER: 535,354
; FILING DATE: 26-SEP-1983
; SEQ ID NO:1:
; LENGTH: 24595
5428147-1

QY 2 CCGCCACCGGAAGT 15
Db 22666 CCGCCACCGGAAGT 22679

US-09-902-540-1214/C
; Sequence 1214, Application US/09902540
; Patent No. 6833447
; APPLICANT: Barker, Richard F.; Kemp, John D.
; TITLE OF INVENTION: OCTOPINE T-DNA PROMOTERS
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/91,538
; FILING DATE: 13-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 869,216
; FILING DATE: 13-APR-1992
; APPLICATION NUMBER: 869,216
; FILING DATE: 13-APR-1992
; APPLICATION NUMBER: 440,432
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 553,786
; FILING DATE: 19-NOV-1983
; APPLICATION NUMBER: 741,034
; FILING DATE: 06-AUG-1991
; APPLICATION NUMBER: 144,775
; FILING DATE: 20-JAN-1988
; APPLICATION NUMBER: 485,614
; FILING DATE: 15-APR-1983
; APPLICATION NUMBER: 713,624
; FILING DATE: 10-JUN-1991
; APPLICATION NUMBER: 260,574
; FILING DATE: 21-OCT-1988
; APPLICATION NUMBER: 848,733
; FILING DATE: 01-APR-1986
; APPLICATION NUMBER: 535,354
; FILING DATE: 26-SEP-1983
; SEQ ID NO:1:
; LENGTH: 24595
5428147-1

US-09-949-016-13407
; Sequence 13407, Application US/09949016
; Patent No. 6812339

```
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13407
; LENGTH: 32616
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13407
```

```
Query Match 45.2%; Score 14; DB 4; Length 32616;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 9 CGGAAGTTGAGTAG 22
      |||||
Db 8287 CGGAAGTTGAGTAG 8300
```

```
RESULT 37
US-09-949-016-16785/c
; Sequence 16785, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16785
; LENGTH: 35784
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16785
```

```
Query Match 45.2%; Score 14; DB 4; Length 35784;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 TCCGCCACCGGAAG 14
      |||||
Db 1184 TCCGCCACCGGAAG 1171
```

```
RESULT 38
US-09-949-016-16786/c
; Sequence 16786, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
```

```
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16786
; LENGTH: 35784
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16786
```

```
Query Match 45.2%; Score 14; DB 4; Length 35784;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 TCCGCCACCGGAAG 14
      |||||
Db 1184 TCCGCCACCGGAAG 1171
```

```
RESULT 39
US-09-949-016-15846
; Sequence 15846, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15846
; LENGTH: 40951
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc feature
; LOCATION: (1)...(40951)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15846
```

```
Query Match 45.2%; Score 14; DB 4; Length 40951;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 10 GGAAGTTGAGTAGA 23
      |||||
Db 15796 GGAAGTTGAGTAGA 15809
```

```
RESULT 40
US-09-949-016-15794
; Sequence 15794, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
```

```
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15794
; LENGTH: 123513
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(123513)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15794

Query Match      45.2%; Score 14; DB 4; Length 123513;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 CCACCGGAGTTGCA 18
Db      118414 CCACCGGAGTTGCA 118427

RESULT 41
US-09-949-016-15444/c
; Sequence 15444, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15444
; LENGTH: 145928
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(145928)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15444

Query Match      45.2%; Score 14; DB 4; Length 145928;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 GGAAGTTGAGTAGA 23
Db      1160 GGAAGTTGAGTAGA 1147

RESULT 42
US-09-949-016-14182/c
; Sequence 14182, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14182
; LENGTH: 422592
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(422592)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14182

Query Match      45.2%; Score 14; DB 4; Length 422592;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 AAGTTGAGTAGACG 25
Db      402008 AAGTTGAGTAGACG 401995

RESULT 43
US-08-483-528B-87
; Sequence 87, Application US/08483528B
; Patent No. 5939532
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUWANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,528B
; FILING DATE: 07-JUN-95
; CLASSIFICATION: 536
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 87 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA"
US-08-483-528B-87
```

Query Match 41.9%; Score 13; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GAAGTTGAGTAGA 23
|||||
Db 57 GAAGTTGAGTAGA 69

RESULT 44

US-08-673-799C-87
; Sequence 87, Application US/08673799C
; Patent No. 6042828
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUWANA, YOSHITISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/673,799C
; FILING DATE: 27-JUN-96

CLASSIFICATION: 536
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4100
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 87 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA"
US-08-673-799C-87

Query Match 41.9%; Score 13; DB 3; Length 87;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GAAGTTGAGTAGA 23
|||||
Db 57 GAAGTTGAGTAGA 69

RESULT 45

US-09-393-385B-87
; Sequence 87, Application US/09393385B
; Patent No. 6423511
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUWANA, YOSHITISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/393,385B
; FILING DATE: 27-JUN-96

CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4100
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 87 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA"
US-09-393-385B-87

Query Match 41.9%; Score 13; DB 3; Length 87;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GAAGTTGAGTAGA 23
|||||
Db 57 GAAGTTGAGTAGA 69

RESULT 46

US-09-252-991A-14219/c
; Sequence 14219, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 14219
; LENGTH: 216
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-14219

Query Match 41.9%; Score 13; DB 4; Length 216;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GTAGACGGTGCTG 31
|||||
Db 203 GTAGACGGTGCTG 191

RESULT 47

US-09-270-767-8307/c
; Sequence 8307, Application US/09270767
; Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION-NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8307
LENGTH: 363
TYPE: DNA
ORGANISM: Drosophila melanogaster
US-09-270-767-8307

Query Match 41.9%; Score 13; DB 4; Length 363;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCGCCACCGGAAG 14
|||||
DB 18 CCGCCACCGGAAG 6

RESULT 48
US-09-270-767-23589/c
Sequence 23589, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION-NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 23589
LENGTH: 363
TYPE: DNA
ORGANISM: Drosophila melanogaster
US-09-270-767-23589

Query Match 41.9%; Score 13; DB 4; Length 363;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCGCCACCGGAAG 14
|||||
DB 18 CCGCCACCGGAAG 6

RESULT 49
US-08-483-528B-90/c
Sequence 90, Application US/08483528B
Patent No. 5939532
GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KUNAWA, YOSHIHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHVE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,528B
FILING DATE: 07-JUN-95
CLASSIFICATION: 536
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 90:
SEQUENCE CHARACTERISTICS:
LENGTH: 390 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
ORIGINAL SOURCE:
ORGANISM: Homo sapiens and mouse
FEATURE:
NAME/KEY: sig_peptide
LOCATION: -22..-1
IDENTIFICATION METHOD: by similarity with known sequence or to an established c
FEATURE:
NAME/KEY: domain
LOCATION: 24..33
IDENTIFICATION METHOD: by similarity with known sequence or to an established c
OTHER INFORMATION: /product= "CDR1"
FEATURE:
NAME/KEY: domain
LOCATION: 49..55
IDENTIFICATION METHOD: by similarity with known sequence or to an established c
OTHER INFORMATION: /product= "CDR2"
FEATURE:
NAME/KEY: domain
LOCATION: 88..96
IDENTIFICATION METHOD: by similarity with known sequence or to an established c
OTHER INFORMATION: /product= "CDR3"
US-08-483-528B-90

Query Match 41.9%; Score 13; DB 2; Length 390;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GAAGTTGAGTAGA 23
|||||
DB 218 GAAGTTGAGTAGA 206

RESULT 50
US-08-673-799C-90/c
Sequence 90, Application US/08673799C
Patent No. 6042828
GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KUNAWA, YOSHIHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHVE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/673,799C
; FILING DATE: 27-JUN-96
; CLASSIFICATION: 536
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 90:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 390 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA"
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens and mouse
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: -22..-1
; IDENTIFICATION METHOD: by similarity with known sequence or to an established co
; FEATURE:
; NAME/KEY: domain
; LOCATION: 24..33
; IDENTIFICATION METHOD: by similarity with known sequence or to an established co
; OTHER INFORMATION: /product= "CDR1"
; FEATURE:
; NAME/KEY: domain
; LOCATION: 49..55
; IDENTIFICATION METHOD: by similarity with known sequence or to an established co
; OTHER INFORMATION: /product= "CDR2"
; FEATURE:
; NAME/KEY: domain
; LOCATION: 88..96
; IDENTIFICATION METHOD: by similarity with known sequence or to an established co
; OTHER INFORMATION: /product= "CDR3"
; US-08-673-799C-90

```

```

Query Match          41.9%; Score 13; DB 3; Length 390;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      11 GAAGTTGAGTAGA 23
        |||||
Db      218 GAAGTTGAGTAGA 206

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Job time : 92.7595 secs

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OM nucleic - nucleic search, using sw model

Run on: March 25, 2005, 09:07:11 ; Search time 190.709 Seconds
(without alignments)
968.698 Million cell updates/sec

Title: US-10-688-489-59
Perfect score: 31
Sequence: 1 tcgcacacggaagttagtagcgtgctg 31

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Minimum DB seq length: 0
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Post-processing: Listing first 500 summaries

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10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
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C 283	13	41.9	1045	9	US-09-822-849A-368	Sequence 368, App	C 356	13	41.9	2005	17	US-10-425-114-32279	Sequence 32279, A
C 284	13	41.9	1058	9	US-09-925-301-108	Sequence 108, App	C 357	13	41.9	2016	18	US-10-437-963-33080	Sequence 33080, A
C 285	13	41.9	1058	19	US-10-873-593-1	Sequence 1, Appl	C 358	13	41.9	2037	9	US-09-738-626-2495	Sequence 2495, Ap
C 286	13	41.9	1077	17	US-10-424-599-130988	Sequence 130988,	C 359	13	41.9	2043	11	US-09-938-842A-1337	Sequence 1337, Ap
C 287	13	41.9	1085	17	US-10-276-774-1339	Sequence 1339, Ap	C 360	13	41.9	2043	19	US-10-495-918-153	Sequence 153, App
C 288	13	41.9	1085	18	US-10-425-115-41755	Sequence 41755, A	C 361	13	41.9	2043	17	US-10-369-493-35516	Sequence 35516, A
C 289	13	41.9	1097	18	US-10-437-963-76733	Sequence 76733, A	C 362	13	41.9	2061	17	US-10-369-493-35516	Sequence 35516, A
C 290	13	41.9	1116	9	US-09-974-300-3015	Sequence 3015, Ap	C 363	13	41.9	2073	17	US-10-369-493-35516	Sequence 35516, A
C 291	13	41.9	1121	17	US-10-425-114-2848	Sequence 2848, Ap	C 364	13	41.9	2100	13	US-10-027-632-97188	Sequence 97188, A
C 292	13	41.9	1121	17	US-10-425-114-20946	Sequence 20946, A	C 365	13	41.9	2100	13	US-10-027-632-97189	Sequence 97189, A
C 293	13	41.9	1131	15	US-10-156-761-2320	Sequence 2320, Ap	C 366	13	41.9	2100	13	US-10-027-632-97190	Sequence 97190, A
C 294	13	41.9	1135	18	US-10-739-930-5023	Sequence 5023, Ap	C 367	13	41.9	2100	17	US-10-027-632-97188	Sequence 97188, A
C 295	13	41.9	1146	15	US-10-126-279-3	Sequence 3, Appl	C 368	13	41.9	2100	17	US-10-027-632-97189	Sequence 97189, A
C 296	13	41.9	1146	16	US-10-286-606-3	Sequence 3, Appl	C 369	13	41.9	2100	17	US-10-027-632-97190	Sequence 97190, A
C 297	13	41.9	1146	18	US-10-891-383-3	Sequence 3, Appl	C 370	13	41.9	2106	13	US-10-027-632-99059	Sequence 99059, A
C 298	13	41.9	1196	17	US-10-425-114-19357	Sequence 19357, A	C 371	13	41.9	2106	13	US-10-027-632-99060	Sequence 99060, A
C 299	13	41.9	1209	9	US-10-437-963-7581	Sequence 7581, Ap	C 372	13	41.9	2106	17	US-10-027-632-99059	Sequence 99059, A
C 300	13	41.9	1212	9	US-09-938-842A-1566	Sequence 1566, Ap	C 373	13	41.9	2106	17	US-10-027-632-99060	Sequence 99060, A
C 301	13	41.9	1212	11	US-09-938-842A-1566	Sequence 1566, Ap	C 374	13	41.9	2116	18	US-10-695-089-2	Sequence 2, Appl
C 302	13	41.9	1225	18	US-10-425-115-127953	Sequence 127953,	C 375	13	41.9	2116	18	US-10-695-089-4	Sequence 4, Appl
C 303	13	41.9	1235	18	US-10-437-963-59964	Sequence 59964, A	C 376	13	41.9	2160	18	US-10-695-546-6	Sequence 6, Appl

; PRIOR APPLICATION NUMBER: 60/429,006
 ; PRIOR FILING DATE: 2002-11-25
 ; PRIOR APPLICATION NUMBER: 60/449,810
 ; PRIOR FILING DATE: 2003-02-24
 ; NUMBER OF SEQ ID NOS: 196
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 59
 ; LENGTH: 31
 ; TYPE: DNA
 ; ORGANISM: West Nile Virus
 US-10-688-489-59

Query Match 100.0%; Score 31; DB 18; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.4e-08;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCCACCGGAAGTTGAGTAGACGGTGCTG 31
 Db 1 TCCGCCACCGGAAGTTGAGTAGACGGTGCTG 31

RESULT 2
 US-10-361-002-5
 ; Sequence 5, Application US/10361002
 ; Publication No. US20040170954A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Clearant, Inc.
 ; APPLICANT: McKenney, Keith
 ; APPLICANT: Gillmeister, Lidja
 ; APPLICANT: Marlowe, Kristina
 ; APPLICANT: Armistead, David
 ; TITLE OF INVENTION: Pathogen Inactivation Assay
 ; FILE REFERENCE: CI-0043
 ; CURRENT APPLICATION NUMBER: US/10/361,002
 ; CURRENT FILING DATE: 2003-02-10
 ; NUMBER OF SEQ ID NOS: 99
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 5
 ; LENGTH: 10945
 ; TYPE: DNA
 ; ORGANISM: West Nile virus
 US-10-361-002-5

Query Match 96.8%; Score 30; DB 18; Length 10945;
 Best Local Similarity 100.0%; Pred. No. 3.7e-08;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 31
 Db 10481 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 10510

RESULT 3
 US-10-361-004-5
 ; Sequence 5, Application US/10361004
 ; Publication No. US20040170981A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Clearant, Inc.
 ; APPLICANT: McKenney, Keith
 ; APPLICANT: Gillmeister, Lidja
 ; APPLICANT: Marlowe, Kristina
 ; APPLICANT: Armistead, David
 ; TITLE OF INVENTION: Real-Time Polymerase Chain Reaction Using Large Target Amplicons
 ; FILE REFERENCE: CI-0042
 ; CURRENT APPLICATION NUMBER: US/10/361,004
 ; CURRENT FILING DATE: 2003-02-10
 ; NUMBER OF SEQ ID NOS: 99
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 5
 ; LENGTH: 10945
 ; TYPE: DNA
 ; ORGANISM: West Nile virus
 US-10-361-004-5

Query Match 96.8%; Score 30; DB 18; Length 10945;
 Best Local Similarity 100.0%; Pred. No. 3.7e-08;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 31
 Db 10481 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 10510

RESULT 4
 US-10-699-550-1
 ; Sequence 1, Application US/10699550
 ; Publication No. US20040197769A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WONG, SUSAN J.
 ; APPLICANT: SHI, PEI-YONG
 ; TITLE OF INVENTION: DIAGNOSTIC TEST FOR WEST NILE VIRUS
 ; FILE REFERENCE: 454311-2232.1
 ; CURRENT APPLICATION NUMBER: US/10/699,550
 ; CURRENT FILING DATE: 2003-10-31
 ; PRIOR APPLICATION NUMBER: 60/476,513
 ; PRIOR FILING DATE: 2003-06-06
 ; PRIOR APPLICATION NUMBER: 60/422,755
 ; PRIOR FILING DATE: 2002-10-31
 ; PRIOR APPLICATION NUMBER: PCT/US02/09036
 ; PRIOR FILING DATE: 2002-03-11
 ; PRIOR APPLICATION NUMBER: 60/402,860
 ; PRIOR FILING DATE: 2002-08-08
 ; PRIOR APPLICATION NUMBER: 60/281,947
 ; PRIOR FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: 60/275,025
 ; PRIOR FILING DATE: 2001-03-12
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: PatentIn Ver. 3.2
 ; SEQ ID NO 1
 ; LENGTH: 10975
 ; TYPE: DNA
 ; ORGANISM: West Nile virus
 US-10-699-550-1

Query Match 96.8%; Score 30; DB 18; Length 10975;
 Best Local Similarity 100.0%; Pred. No. 3.7e-08;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 31
 Db 10505 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 10534

RESULT 5
 US-10-699-550-2
 ; Sequence 2, Application US/10699550
 ; Publication No. US20040197769A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WONG, SUSAN J.
 ; APPLICANT: SHI, PEI-YONG
 ; TITLE OF INVENTION: DIAGNOSTIC TEST FOR WEST NILE VIRUS
 ; FILE REFERENCE: 454311-2232.1
 ; CURRENT APPLICATION NUMBER: US/10/699,550
 ; CURRENT FILING DATE: 2003-10-31
 ; PRIOR APPLICATION NUMBER: 60/476,513
 ; PRIOR FILING DATE: 2003-06-06
 ; PRIOR APPLICATION NUMBER: 60/422,755
 ; PRIOR FILING DATE: 2002-10-31
 ; PRIOR APPLICATION NUMBER: PCT/US02/09036
 ; PRIOR FILING DATE: 2002-03-11
 ; PRIOR APPLICATION NUMBER: 60/402,860
 ; PRIOR FILING DATE: 2002-08-08
 ; PRIOR APPLICATION NUMBER: 60/281,947
 ; PRIOR FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: 60/275,025
 ; PRIOR FILING DATE: 2001-03-12

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; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 11029
; TYPE: DNA
; ORGANISM: West Nile virus
US-10-699-550-2

Query Match          96.8%; Score 30; DB 18; Length 11029;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 31
|||||
Db 10523 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 10552

RESULT 6
US-10-679-520A-66
; Sequence 66, Application US/10679520A
; Publication No. US20050031641A1
; GENERAL INFORMATION:
; APPLICANT: LOOSMORE, SHEENA MAY
; APPLICANT: AUDONNET, JEAN-CHRISTOPHE FRANCIS
; APPLICANT: MINKE, JULES MAARTEN
; TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST WEST NILE VIRUS
; FILE REFERENCE: 574313-3161.4
; CURRENT APPLICATION NUMBER: US/10/679,520A
; PRIOR FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: 10/374,953
; PRIOR FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: 10/116,298
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/281,923
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: PCT/FR02/01200
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: FR 01/04737
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 66
; LENGTH: 11029
; TYPE: DNA
; ORGANISM: West Nile virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (97)..(10395)
US-10-679-520A-66

Query Match          96.8%; Score 30; DB 19; Length 11029;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 31
|||||
Db 10523 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 10552

RESULT 7
US-10-706-892-1
; Sequence 1, Application US/10706892
; Publication No. US20050058987A1
; GENERAL INFORMATION:
; APPLICANT: SHI, PEI-YONG
; TITLE OF INVENTION: SCREENING FOR WEST NILE VIRUS ANTIVIRAL THERAPY
; FILE REFERENCE: 454311-2231.1
; CURRENT APPLICATION NUMBER: US/10/706,892
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/427,117
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 11029
; TYPE: DNA
; ORGANISM: West Nile virus
US-10-706-892-1

Query Match          96.8%; Score 30; DB 19; Length 11029;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 31
|||||
Db 10523 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 10552

RESULT 8
US-10-706-892-2
; Sequence 2, Application US/10706892
; Publication No. US20050058987A1
; GENERAL INFORMATION:
; APPLICANT: SHI, PEI-YONG
; TITLE OF INVENTION: SCREENING FOR WEST NILE VIRUS ANTIVIRAL THERAPY
; FILE REFERENCE: 454311-2231.1
; CURRENT APPLICATION NUMBER: US/10/706,892
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/427,117
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 11029
; TYPE: DNA
; ORGANISM: West Nile virus
US-10-706-892-2

Query Match          96.8%; Score 30; DB 19; Length 11029;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 31
|||||
Db 10523 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 10552

RESULT 9
US-10-688-489-68
; Sequence 68, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GPI40-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 68
; LENGTH: 22
; TYPE: DNA
; ORGANISM: West Nile virus
US-10-688-489-68
```

```
Query Match      71.0%; Score 22; DB 18; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GGAAGTTGAGTAGACGGTGCTG 31
    |||||
Db 1 GGAAGTTGAGTAGACGGTGCTG 22

RESULT 10
US-10-688-489-63
; Sequence 63, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GPI40-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 21
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-63

Query Match      67.7%; Score 21; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCCACCGGAAGTTGACTA 21
    |||||
Db 1 TCCGCCACCGGAAGTTGACTA 21

RESULT 11
US-10-688-489-67
; Sequence 67, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GPI40-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 21
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-67

Query Match      71.0%; Score 22; DB 18; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GGAAGTTGAGTAGACGGTGCTG 31
    |||||
Db 1 GGAAGTTGAGTAGACGGTGCTG 22

RESULT 10
US-10-688-489-63
; Sequence 63, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GPI40-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 21
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-63

Query Match      67.7%; Score 21; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCCACCGGAAGTTGACTA 21
    |||||
Db 1 TCCGCCACCGGAAGTTGACTA 21

RESULT 11
US-10-688-489-67
; Sequence 67, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GPI40-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 21
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-67

Query Match      67.7%; Score 21; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGAAGTTGAGTAGACGGTGCTG 31
    |||||
Db 1 GGAAGTTGAGTAGACGGTGCTG 21

RESULT 13
US-10-688-489-62
; Sequence 62, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GPI40-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 62
; LENGTH: 21
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-62

Query Match      67.7%; Score 21; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGAAGTTGAGTAGACGGTGCTG 31
    |||||
Db 1 GGAAGTTGAGTAGACGGTGCTG 21

RESULT 13
US-10-688-489-62
; Sequence 62, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GPI40-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 62
; LENGTH: 21
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-62
```

```
; SEQ ID NO 62
; LENGTH: 20
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-62

Query Match      64.5%; Score 20; DB 18; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCCACCGGAAGTTGAGT 20
    |||||
DB 1 TCCGCCACCGGAAGTTGAGT 20

RESULT 14
US-10-688-489-69
; Sequence 69, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GPI40-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2002-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 69
; LENGTH: 20
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-69

Query Match      64.5%; Score 20; DB 18; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GAAGTTGAGTAGACGGTGCT 30
    |||||
DB 1 GAAGTTGAGTAGACGGTGCT 20

RESULT 15
US-10-688-489-71
; Sequence 71, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GPI40-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2002-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 71
; LENGTH: 20
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-71

Query Match      61.3%; Score 19; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCCACCGGAAGTTGAG 19
    |||||
DB 1 TCCGCCACCGGAAGTTGAG 19

RESULT 17
US-10-688-489-66
; Sequence 66, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GPI40-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2002-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 66
; LENGTH: 19
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-66

Query Match      61.3%; Score 19; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCCACCGGAAGTTGAG 19
    |||||
DB 1 TCCGCCACCGGAAGTTGAG 19
```

```

; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 66
; LENGTH: 19
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-66

```

```

Query Match          61.3%; Score 19; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 3 CGCCACCGGAAGTTGAGTA 21
Db 1 CGCCACCGGAAGTTGAGTA 19

```

```

RESULT 18
US-10-688-489-64
; Sequence 64, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Wu, Wen
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 64
; LENGTH: 18
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-64

```

```

Query Match          58.1%; Score 18; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 3 CGCCACCGGAAGTTGAGT 20
Db 1 CGCCACCGGAAGTTGAGT 18

```

```

RESULT 19
US-10-688-489-61
; Sequence 61, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Wu, Wen
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489

```

```

; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 61
; LENGTH: 19
; TYPE: DNA
; ORGANISM: West Nile Virus
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1)...(1)
; OTHER INFORMATION: I
US-10-688-489-61

```

```

Query Match          58.1%; Score 18; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 CGCCACCGGAAGTTGAG 19
Db 2 CGCCACCGGAAGTTGAG 19

```

```

RESULT 20
US-10-688-489-147/c
; Sequence 147, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 147
; LENGTH: 26
; TYPE: RNA
; ORGANISM: West Nile Virus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)_(26)
; OTHER INFORMATION: 2'-OME nucleotide analogs
US-10-688-489-147

```

```

Query Match          58.1%; Score 18; DB 18; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.79;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 14 GTTGAGTAGACGGTGCTG 31
Db 26 GTTGAGTAGACGGTGCTG 9

```

```

RESULT 21
US-10-688-489-65
; Sequence 65, Application US/10688489

```

; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; TITLE OF INVENTION: West Nile Virus
; FILE REFERENCE: GPI40-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 65
; LENGTH: 18
; TYPE: DNA
; ORGANISM: West Nile Virus
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1)....(1)
; OTHER INFORMATION: I
US-10-688-489-65

Query Match 54.8%; Score 17; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCCACCGGAAGTTGAGT 20
|||||
DB 2 GCCACCGGAAGTTGAGT 18

RESULT 22
US-10-653-047-918/c
; Sequence 918, Application US/10653047
; Publication No. US20040229367A1
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjarke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 5849-200-US
; CURRENT APPLICATION NUMBER: US/10/653,047
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/533,559
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/273,623
; PRIOR FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 918
; LENGTH: 628
; TYPE: DNA
; ORGANISM: Fusarium venenatum
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)....(628)
; OTHER INFORMATION: n = A,T,C or G
US-10-653-047-918

Query Match 51.6%; Score 16; DB 18; Length 628;
Best Local Similarity 100.0%; Pred. No. 9.9;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 GTTGAGTAGACGGTGC 29
|||||
DB 205 GTTGAGTAGACGGTGC 190

RESULT 23
US-10-027-632-274317/c
; Sequence 274317, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 274317
; LENGTH: 632
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-274317

Query Match 51.6%; Score 16; DB 13; Length 632;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GGAAGTTGAGTAGACG 25
|||||
DB 547 GGAAGTTGAGTAGACG 532

RESULT 24
US-10-027-632-274317/c
; Sequence 274317, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002

; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 274317
; LENGTH: 632
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-274317

Query Match 51.6%; Score 16; DB 17; Length 632;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GGAAGTTGAGTAGACG 25
|||
DB 547 GGAAGTTGAGTAGACG 532

RESULT 25
US-10-481-265-136/c
; Sequence 136, Application US/10481265
; Publication No. US20040254349A1
; GENERAL INFORMATION:
; APPLICANT: James, Brian William
; APPLICANT: Bacon, Joanna
; APPLICANT: Marsh, Philip
; TITLE OF INVENTION: Mycobacterial Antigens Expressed Under Low Oxygen Tension
; FILE REFERENCE: 1581.1020000
; CURRENT APPLICATION NUMBER: US/10/481,265
; PRIOR FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: GB 0115365.9
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: GB 0121780.1
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: PCT/GB02/02845
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 136
; LENGTH: 1323
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-481-265-136

Query Match 51.6%; Score 16; DB 18; Length 1323;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCCACCGGAAGTTGAG 19
|||
DB 1037 GCCACCGGAAGTTGAG 1022

RESULT 26
US-09-712-363-49/c
; Sequence 49, Application US/09712363
; Patent No. US20020164588A1
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David
; APPLICANT: Rotstein, Sergio H.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
; FILE REFERENCE: 07419-032001
; CURRENT APPLICATION NUMBER: US/09/712,363
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/US00/02246
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206,

; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 1326
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-49

Query Match 51.6%; Score 16; DB 9; Length 1326;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCCACCGGAAGTTGAG 19
|||
DB 1037 GCCACCGGAAGTTGAG 1022

RESULT 27
US-10-688-489-104
; Sequence 104, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 104
; LENGTH: 21
; TYPE: DNA
; ORGANISM: West Nile Virus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(21)
; OTHER INFORMATION: 2'-OME nucleotide analogs
US-10-688-489-104

Query Match 48.4%; Score 15; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 GAGTAGACGGTCTG 31
|||
DB 1 GAGTAGACGGTCTG 15

RESULT 28
US-10-688-489-185
; Sequence 185, Application US/10688489

```
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 185
; LENGTH: 22
; TYPE: RNA
; ORGANISM: West Nile Virus
; NAME/KEY: misc_feature
; LOCATION: (1)..(22)
; OTHER INFORMATION: 2'-OME nucleotide analogs
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(22)
; OTHER INFORMATION: Molecular beacon arm sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (18)..(22)
; OTHER INFORMATION: Molecular beacon arm sequence
US-10-688-489-185

Query Match      48.4%; Score 15; DB 18; Length 22;
Best Local Similarity 80.0%; Pred. No. 49;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      17 GAGTAGACGGTGCTG 31
      |||:|||||:|:|:|
Db      3 GAGUAGACGGUGUG 17

RESULT 29
US-10-098-263B-27587
; Sequence 27587, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 27587
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
; US-10-098-263B-27587

Query Match      48.4%; Score 15; DB 15; Length 25;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 CACCGAAGTTGAGT 20
      |||||||:|||||
```

```
Db      2 CACCGAAGTTGAGT 16

RESULT 30
US-10-688-489-186
; Sequence 186, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 186
; LENGTH: 28
; TYPE: RNA
; ORGANISM: West Nile Virus
; NAME/KEY: misc_feature
; LOCATION: (1)..(28)
; OTHER INFORMATION: 2'-OME nucleotide analogs
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(5)
; OTHER INFORMATION: Molecular beacon arm sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (24)..(28)
; OTHER INFORMATION: Molecular beacon arm sequence
US-10-688-489-186

Query Match      48.4%; Score 15; DB 18; Length 28;
Best Local Similarity 80.0%; Pred. No. 48;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      17 GAGTAGACGGTGCTG 31
      |||:|||||:|:|:|
Db      3 GAGUAGACGGUGUG 17

RESULT 31
US-10-688-489-102
; Sequence 102, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
```

; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 102
; LENGTH: 69
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-102

Query Match 48.4%; Score 15; DB 18; Length 69;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 GAGTAGACGGTGCTG 31
| | | | | | | | | | | | | | | | | | | | |
DB 1 GAGTAGACGGTGCTG 15

RESULT 32
US-10-688-489-101
; Sequence 101, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linmen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; TITLE OF INVENTION: West Nile Virus
; FILE REFERENCE: GPI40-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 101
; LENGTH: 87
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-101

Query Match 48.4%; Score 15; DB 18; Length 87;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 GAGTAGACGGTGCTG 31
| | | | | | | | | | | | | | | | | | | | |
DB 1 GAGTAGACGGTGCTG 15

RESULT 33
US-10-425-115-139988/c
; Sequence 139988, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 139988
; LENGTH: 351

; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_59153C.1
US-10-425-115-139988

Query Match 48.4%; Score 15; DB 18; Length 351;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACCGGAGGTTGAG 19
| | | | | | | | | | | | | | | | | | | | |
DB 268 CCACCGGAGGTTGAG 254

RESULT 34
US-10-767-701-25132/c
; Sequence 25132, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 25132
; LENGTH: 685
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 30947447
US-10-767-701-25132

Query Match 48.4%; Score 15; DB 18; Length 685;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACCGGAGGTTGAG 19
| | | | | | | | | | | | | | | | | | | | |
DB 250 CCACCGGAGGTTGAG 236

RESULT 35
US-10-027-632-156396
; Sequence 156396, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 32520
; SOFTWARE: FastSeq for Windows Version 4.0

```
; SEQ ID NO 156396
; LENGTH: 795
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-156396

Query Match          48.4%; Score 15; DB 13; Length 795;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GGAAGTTGAGTAGAC 24
   |||||
Db 659 GGAAGTTGAGTAGAC 673

RESULT 36
US-10-027-632-156396
; Sequence 156396, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 156396
; LENGTH: 795
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-156396

Query Match          48.4%; Score 15; DB 17; Length 795;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GGAAGTTGAGTAGAC 24
   |||||
Db 659 GGAAGTTGAGTAGAC 673

RESULT 37
US-10-027-632-120761/c
; Sequence 120761, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 120761
; LENGTH: 910
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-120761

Query Match          48.4%; Score 15; DB 13; Length 910;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TTGAGTAGACGGTGC 29
   |||||
Db 333 TTGAGTAGACGGTGC 319

RESULT 38
US-10-027-632-120762/c
; Sequence 120762, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 120762
; LENGTH: 910
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-120762

Query Match          48.4%; Score 15; DB 13; Length 910;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TTGAGTAGACGGTGC 29
   |||||
Db 333 TTGAGTAGACGGTGC 319

RESULT 39
US-10-027-632-120761/c
; Sequence 120761, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
```

APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 120761
LENGTH: 910
TYPE: DNA
ORGANISM: Human
US-10-027-632-120761

Query Match 48.4%; Score 15; DB 17; Length 910;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TTGAGTAGACGGTGC 29
|||||
Db 333 TTGAGTAGACGGTGC 319

RESULT 40
US-10-027-632-120762/c
Sequence 120762, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 120762
LENGTH: 910
TYPE: DNA
ORGANISM: Human
US-10-027-632-120762

Query Match 48.4%; Score 15; DB 17; Length 910;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TTGAGTAGACGGTGC 29
|||||
Db 333 TTGAGTAGACGGTGC 319

RESULT 41
US-10-363-345A-29275
Sequence 29275, Application US/10363345A
Publication No. US20040234960A1
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Method for determining the degree of methylation of defined
cytosines in genomic DNA in the sequence context of 5'-CpG-3
FILE REFERENCE: E01/1227
CURRENT APPLICATION NUMBER: US/10/363,345A
CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
SEQ ID NO 29275
LENGTH: 1795
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Chemically treated genomic DNA (Homo sapiens)
OTHER INFORMATION: CpG-island No: 29275
US-10-363-345A-29275

Query Match 48.4%; Score 15; DB 18; Length 1795;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AGTTGAGTAGACGGT 27
|||||
Db 1002 AGTTGAGTAGACGGT 1016

RESULT 42
US-10-363-345A-29276/c
Sequence 29276, Application US/10363345A
Publication No. US20040234960A1
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Method for determining the degree of methylation of defined
cytosines in genomic DNA in the sequence context of 5'-CpG-3
FILE REFERENCE: E01/1227
CURRENT APPLICATION NUMBER: US/10/363,345A
CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
SEQ ID NO 29276
LENGTH: 1795
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Chemically treated genomic DNA (Homo sapiens)
OTHER INFORMATION: CpG-island No: 29276
US-10-363-345A-29276

Query Match 48.4%; Score 15; DB 18; Length 1795;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AGTTGAGTAGACGGT 27
|||||
Db 794 AGTTGAGTAGACGGT 780

RESULT 43
US-09-738-626-437/c
Sequence 437, Application US/09738626

Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 437
LENGTH: 1863
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
US-09-738-626-437

Query Match 48.4%; Score 15; DB 9; Length 1863;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACCGGAAGTTGAG 19
|||||
DB 734 CCACCGGAAGTTGAG 720

RESULT 44
US-10-425-115-16225/c
Sequence 16225, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 16225
LENGTH: 1891
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(1891)
OTHER INFORMATION: unsure at all n locations
FEATURE:
OTHER INFORMATION: Clone ID: MPT4577_114797C.1
US-10-425-115-16225

Query Match 48.4%; Score 15; DB 18; Length 1891;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGCCACCGGAAGT 15
|||||
DB 884 TCGCCACCGGAAGT 870

RESULT 45
US-10-494-672-341/c
Sequence 341, Application US/10494672
Publication No. US2005003494A1
GENERAL INFORMATION:
APPLICANT: Zelder, Oskar
APPLICANT: Pompejus, Markus
APPLICANT: Schroder, Hartwig
APPLICANT: Kroger, Burkhard
APPLICANT: Klopptogge, Corinna
APPLICANT: Haberhauser, Gregor
TITLE OF INVENTION: Genes coding for novel proteins
FILE REFERENCE: BGI-169US
CURRENT APPLICATION NUMBER: US/10/494,672
CURRENT FILING DATE: 2004-05-04
PRIOR APPLICATION NUMBER: PCT/EP02/12134
PRIOR FILING DATE: 2002-10-31
PRIOR APPLICATION NUMBER: DE 10154177
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 434
SEQ ID NO 341
LENGTH: 1969
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
FEATURE:
NAME/KEY: CDS
LOCATION: (101)..(1939)
OTHER INFORMATION: RXA02825
US-10-494-672-341

Query Match 48.4%; Score 15; DB 18; Length 1969;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACCGGAAGTTGAG 19
|||||
DB 810 CCACCGGAAGTTGAG 796

RESULT 46
US-10-425-114-35701/c
Sequence 35701, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 35701
LENGTH: 2066
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: UC-ZMROB73080G04_FLI
US-10-425-114-35701

Query Match 48.4%; Score 15; DB 17; Length 2066;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACCGGAAGTTGAG 19
|||||
DB 1689 CCACCGGAAGTTGAG 1675

RESULT 47
US-10-280-576-23
; Sequence 23, Application US/10280576
; Publication No. US20040044405A1
; GENERAL INFORMATION:
; APPLICANT: Wolff, Matthew R.
; TITLE OF INVENTION: VASCULAR STENT OR GRAFT COATED OR IMPREGNATED WITH PROTEIN
; FILE REFERENCE: 09820.189
; CURRENT APPLICATION NUMBER: US/10/280,576
; CURRENT FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: 60/343,732
; PRIOR FILING DATE: 2001-10-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 3246
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-280-576-23

Query Match 48.4%; Score 15; DB 17; Length 3246;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 GAGTAGACGGTGCTG 31
|||||
DB 1370 GAGTAGACGGTGCTG 1384

RESULT 48
US-09-738-626-1/c
; Sequence 1, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1
; LENGTH: 3309400
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1

Query Match 48.4%; Score 15; DB 9; Length 3309400;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACCGGAAGTTGAG 19
|||||
DB 411416 CCACCGGAAGTTGAG 411402

RESULT 49
US-09-803-719-272/c
; Sequence 272, Application US/09803719
; Publication No. US20030044783A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Lewis T.
; APPLICANT: Escobedo, Jaime
; APPLICANT: Innis, Michael A.
; APPLICANT: Garcia, Pablo Dominiguez
; APPLICANT: Sudduth-Klinger, Julie
; APPLICANT: Reinhard, Christoph
; APPLICANT: Giese, Klaus
; APPLICANT: Randazzo, Filippo
; APPLICANT: Kennedy, Giulia C.
; APPLICANT: Pot, David
; APPLICANT: Kassam, Altaf
; APPLICANT: Lamson, George
; APPLICANT: Drmanac, Radoje
; APPLICANT: Crkvenjakov, Radomir
; APPLICANT: Dickson, Mark
; APPLICANT: Drmanac, Snezana
; APPLICANT: Labat, Ivan
; APPLICANT: Leshkowitz, Dena
; APPLICANT: Kita, David
; APPLICANT: Garcia, Veronica
; APPLICANT: Jones, Lee William
; APPLICANT: Stache-Crain, Birgit
; TITLE OF INVENTION: Human Genes and Gene Products
; FILE REFERENCE: 1624.002
; CURRENT APPLICATION NUMBER: US/09/803,719
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,609
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 2396
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 272
; LENGTH: 151
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-803-719-272

Query Match 45.2%; Score 14; DB 10; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCCACCGGAAG 14
|||||
DB 28 TCCGCCACCGGAAG 15

RESULT 50
US-10-719-993-27926
; Sequence 27926, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27926
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-27926

Query Match 45.2%; Score 14; DB 18; Length 201;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GGAAGTTGAGTAGA 23
| | | | | | | | | |
Db 128 GGAAGTTGAGTAGA 141

Search completed: March 25, 2005, 11:07:28
Job time : 226.709 secs